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#### **Key indicators**

Single-crystal X-ray study T = 294 K Mean  $\sigma$ (C–C) = 0.005 Å R factor = 0.042 wR factor = 0.091 Data-to-parameter ratio = 13.4

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

# Diphenylmethyl 3-azido-1,1-dioxocephalosporanate

The title compound,  $C_{21}H_{20}N_4O_5S$ , crystallizes with two molecules in the asymmetric unit. The crystal structure is stabilized by a network of  $C-H\cdots O$  hydrogen bonds.

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## Comment

Tazobactam is a widely used beta-lactamase inhibitor (Bai *et al.*, 2001, Micetich *et al.*, 1987). The title compound, (I), is a byproduct of the synthesis of tazobactam and the structure of its benzene solvate has been reported (Liu, 2006). The unsolvated material, (I), was obtained from 6-aminopenicillanic acid, and its structure is reported here (Figs. 1 and 2).



Compound (I) crystallizes with two independent, but structurally quite similar, molecules in the asymmetric unit. All bond lengths and angles in (I) are within normal ranges (Allen *et al.*, 1987) and similar to those reported for the solvated material (Liu, 2006). The four-membered azetedinone rings are planar (r.m.s. deviations 0.0246 and 0.0249 Å). The thiazine rings adopt chair conformations. The C1/O1/O2/C14/C15 and C22/O6/O7/C35/C36 carboxylate units are also planar (r.m.s. deviations 0.0232 and 0.0383 Å, respectively) and lie approximately orthogonal to the respective thiazine rings. The crystal structure is stabilized by a network of intermolecular C–H···O hydrogen bonds (Fig. 3 and Table 1).

### **Experimental**

The title compound was prepared by the procedure of Bai *et al.* (2001). Colourless single crystals of (I) were grown by slow evaporation of a methanol solution.

Crystal data  $C_{21}H_{20}N_4O_5S$   $M_r = 440.47$ Orthorhombic,  $P_{21}^2 2_1 2_1$  a = 10.9030 (13) Å b = 11.3796 (14) Å c = 34.293 (4) Å V = 4254.8 (9) Å<sup>3</sup>

Z = 8  $D_x$  = 1.375 Mg m<sup>-3</sup> Mo K $\alpha$  radiation  $\mu$  = 0.19 mm<sup>-1</sup> T = 294 (2) K Block, colourless 0.24 × 0.22 × 0.18 mm

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### Figure 1

One of the two molecules (molecule 1) in the asymmetric unit of (I), with the atom-numbering scheme and 30% probability displacement ellipsoids.



#### Figure 2

The other molecule (molecule 2) in the asymmetric unit of (I), with the atom-numbering scheme and 30% probability displacement ellipsoids.



#### Figure 3

Packing diagram for (I), with hydrogen bonds drawn as dashed lines.

#### Data collection

Bruker SMART-1000 CCD areadetector diffractometer  $\varphi$  and  $\omega$  scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)

(3ADAB3, Shednek, 1990) $T_{\rm min} = 0.943, T_{\rm max} = 0.966$ 

## Refinement

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.042$   $wR(F^2) = 0.092$  S = 1.037497 reflections 561 parameters H-atom parameters constrained 20301 measured reflections 7497 independent reflections 5529 reflections with  $I > 2\sigma(I)$  $R_{\text{int}} = 0.037$  $\theta_{\text{max}} = 25.0^{\circ}$ 

# Table 1Hydrogen-bond geometry (Å, °).

$D-\mathrm{H}\cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
$C19-H19B\cdots O3^{i}$	0.97	2.44	3.364 (3)	160
C31-H31···O9 <sup>ii</sup>	0.93	2.57	3.446 (6)	157
C36−H36···O10 <sup>iii</sup>	0.98	2.25	3.196 (4)	162
$C40 - H40B \cdots O8^{iv}$	0.97	2.29	3.235 (4)	166
$C18-H18\cdots O7^{ii}$	0.98	2.50	3.262 (3)	135

Symmetry codes: (i)  $x + \frac{1}{2}, -y + \frac{5}{2}, -z + 2$ ; (ii) x, y + 1, z; (iii)  $-x + 1, y + \frac{1}{2}, -z + \frac{3}{2}$ ; (iv)  $-x + 1, y - \frac{1}{2}, -z + \frac{3}{2}$ .

All H atoms were positioned geometrically and refined using a riding model, with C-H = 0.93 Å and  $U_{iso}(H) = 1.2U_{eq}(C)$  for aromatic, C-H = 0.98 Å and  $U_{iso}(H) = 1.2U_{eq}(C)$  for CH, C-H = 0.97 Å and  $U_{iso}(H) = 1.2U_{eq}(C)$  for CH<sub>2</sub>, and C-H = 0.96 Å and  $U_{iso}(H) = 1.5U_{eq}(C)$  for CH<sub>3</sub> H atoms.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SAINT* (Bruker, 1997); 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, 1997); software used to prepare material for publication: *SHELXTL*.

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