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## Daniel E. Lynch<sup>a\*</sup> and Ian McClenaghan<sup>b</sup>

<sup>a</sup>School of Science and the Environment, Coventry University, Coventry CV1 5FB, England, and <sup>b</sup>Key Organics Ltd, Highfield Industrial Estate, Camelford, Cornwall PL32 9QZ, England

Correspondence e-mail: apx106@coventry.ac.uk

#### **Key indicators**

Single-crystal X-ray study T = 150 KMean  $\sigma(C-C) = 0.006 \text{ Å}$ R factor = 0.080 wR factor = 0.206 Data-to-parameter ratio = 13.0

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

# Ethyl 4-phenyl-2-(N-pyrrolyl)-1,3-thiazole-5-carboxylate

The structure of the title compound,  $C_{16}H_{14}N_2O_2S$ , comprises a twisted molecule with dihedral angles of 11.3 (2) and 45.8 (1)° between the thiazole and, respectively, the pyrrole and phenyl rings.

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#### Comment

The title compound, (I), has been studied as part of a larger investigation into the solid-state packing of 2-aminothiazoles and their carboxylic acid cocrystals. The structure of (I) (Fig. 1)

comprises a twisted molecule with dihedral angles of 11.3 (2) and 45.8 (1)° between the thiazole and, respectively, the pyrrole and phenyl rings.

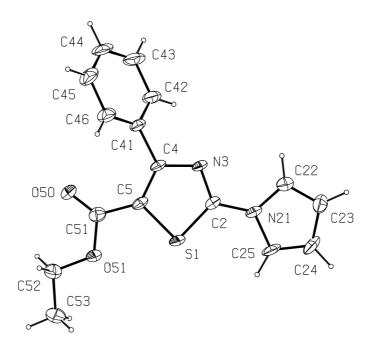


Figure 1 The molecular configuration and the atom-numbering scheme for (I), showing 50% probability ellipsoids.

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## organic papers

## **Experimental**

The title compound was obtained from Key Organics Ltd and crystals were grown from an ethanol solution.

#### Crystal data

$C_{16}H_{14}N_2O_2S$	$D_x = 1.399 \text{ Mg m}^{-3}$
$M_r = 298.35$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 6999
a = 10.2375 (4)  Å	reflections
b = 3.9460 (2)  Å	$\theta = 2.9 - 27.5^{\circ}$
c = 35.075 (2) Å	$\mu = 0.23 \text{ mm}^{-1}$
$\beta = 91.979 (2)^{\circ}$	T = 150 (2)  K
$V = 1416.1 (1) \text{ Å}^3$	Needle, colourless
Z = 4	$0.30 \times 0.08 \times 0.03 \text{ mm}$

#### Data collection

Bruker-Nonius KappaCCD area-	2486 independent reflections
detector diffractometer	1643 reflections with $I > 2\sigma(I)$
$\varphi$ and $\omega$ scans	$R_{\rm int} = 0.171$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.0^{\circ}$
(SORTAV; Blessing, 1995)	$h = -12 \rightarrow 12$
$T_{\min} = 0.933, T_{\max} = 0.993$	$k = -4 \rightarrow 4$
6999 measured reflections	$l = -37 \rightarrow 41$

### Refinement

Refinement on $F^2$	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.080$	$w = 1/[\sigma^{2}(F_{o}^{2}) + (0.1059P)^{2}]$
$wR(F^2) = 0.206$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.04	$(\Delta/\sigma)_{\rm max} < 0.001$
2486 reflections	$\Delta \rho_{\text{max}} = 1.26 \text{ e Å}^{-3}$
191 parameters	$\Delta \rho_{\min} = -0.95 \text{ e Å}^{-3}$

All H atoms were included in the refinement, at calculated positions, as riding models, with C—H distances set to 0.95 (Ar-H), 0.99 (CH<sub>2</sub>) and 0.98 Å (CH<sub>3</sub>). An  $R_{\rm int}$  value of 0.171 was the result of weak high-angle data. An unassigned maximum (positive) residual density of 1.26 e Å<sup>-3</sup> and a minimum (negative) residual density of -0.95 e Å<sup>-3</sup> are both observed, approximately 0.9 Å from the S atom but 1.37 Å apart.

Data collection: *DENZO* (Otwinowski & Minor, 1997) and *COLLECT* (Hooft, 1998); cell refinement: *DENZO* and *COLLECT*; data reduction: *DENZO* and *COLLECT*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLATON*97 (Spek, 1997); software used to prepare material for publication: *SHELXL*97.

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