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## Structure Reports

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## 2,7-Dimethyl-1,3-thiazolo[4,5-d]-pyridazin-4(5H)-one

Abdulrahman O. Al-Youbi,<sup>a</sup> Abdullah M. Asiri,<sup>a</sup> Hassan M. Faidallah<sup>a</sup> and Seik Weng Ng<sup>b,a\*</sup><sup>a</sup>Chemistry Department, Faculty of Science, King Abdulaziz University, PO Box 80203, Jeddah, Saudi Arabia, and <sup>b</sup>Department of Chemistry, University of Malaya, 50603 Kuala Lumpur, Malaysia  
Correspondence e-mail: seikweng@um.edu.my

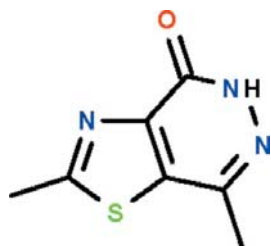
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Key indicators: single-crystal X-ray study;  $T = 100$  K; mean  $\sigma(\text{C}-\text{C}) = 0.002$  Å;  $R$  factor = 0.029;  $wR$  factor = 0.080; data-to-parameter ratio = 13.4.

The nine-membered fused-ring system of the title pyridazine derivative,  $\text{C}_7\text{H}_7\text{N}_3\text{OS}$ , is almost planar (r.m.s. deviation 0.012 Å). In the crystal, the amino H atom forms a hydrogen bond to the ketonic O atom of a neighboring molecule to generate a centrosymmetric dimer.

## Related literature

For a related structure, see: Abdel-Aziz *et al.* (2010). For the biological activity of the class of pyridazines, see: Faid-Allah *et al.* (2011); Makki & Faid-Allah (1996).



## Experimental

## Crystal data

 $\text{C}_7\text{H}_7\text{N}_3\text{OS}$   
 $M_r = 181.22$ Triclinic,  $P\bar{1}$   
 $a = 6.9262$  (4) Å $b = 7.0540$  (4) Å  
 $c = 8.8079$  (6) Å  
 $\alpha = 71.002$  (6)°  
 $\beta = 75.845$  (5)°  
 $\gamma = 85.570$  (5)°  
 $V = 394.54$  (4) Å<sup>3</sup> $Z = 2$ Cu  $K\alpha$  radiation  
 $\mu = 3.26$  mm<sup>-1</sup>  
 $T = 100$  K  
0.30 × 0.25 × 0.20 mm

## Data collection

Agilent Technologies SuperNova  
Dual diffractometer with Atlas  
detector  
Absorption correction: multi-scan  
(*CrysAlis PRO*; Agilent, 2010)  
 $T_{\min} = 0.442$ ,  $T_{\max} = 0.562$ 2363 measured reflections  
1539 independent reflections  
1523 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.012$ 

## Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.029$   
 $wR(F^2) = 0.080$   
 $S = 1.05$   
1539 reflections  
115 parametersH atoms treated by a mixture of  
independent and constrained  
refinement  
 $\Delta\rho_{\max} = 0.41$  e Å<sup>-3</sup>  
 $\Delta\rho_{\min} = -0.30$  e Å<sup>-3</sup>

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{N2}-\text{H2}\cdots\text{O1}^i$	0.88 (2)	1.97 (2)	2.845 (2)	173 (2)

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

Data collection: *CrysAlis PRO* (Agilent, 2010); cell refinement: *CrysAlis PRO*; data reduction: *CrysAlis PRO*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *X-SEED* (Barbour, 2001); software used to prepare material for publication: *publCIF* (Westrip, 2010).

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: XU5288).

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