Acta Crystallographica Section E

Structure Reports

Online

ISSN 1600-5368

2-(2-Thienyl)-4,5-dihydro-1*H*-imidazole. Corrigendum

Reza Kia, a‡ Hoong-Kun Funa*§ and Hadi Kargarb

^aX-ray Crystallography Unit, School of Physics, Universiti Sains Malaysia, 11800 USM, Penang, Malaysia, and ^bDepartment of Chemistry, School of Science, Payame Noor University (PNU), Ardakan, Yazd, Iran Correspondence e-mail: hkfun@usm.my

Received 5 May 2009; accepted 18 May 2009

Key indicators: single-crystal X-ray study; T = 100 K; mean $\sigma(C-C) = 0.001 \text{ Å}$; R factor = 0.027; wR factor = 0.080; data-to-parameter ratio = 32.3.

Consideration of a previous unrecognized twinning of the original investigated crystal of the title compound [Kia *et al.* (2009). *Acta Cryst.* E**65**, o301] led to improved reliability factors and to a slightly higher precision for all geometric parameters. The crystal under investigation was twinned by pseudo-merohedry with $[100, 0\overline{10}, 00\overline{1}]$ as the twin matrix and a refined twin domain fraction of 0.9610 (5):0.0390 (5). The results of the new crystal structure refinement are given here.

Experimental

Crystal data

 $C_7H_8N_2S$ $M_r = 152.21$ Monoclinic, $P2_1/c$ a = 6.1321 (2) Å b = 11.5663 (3) Å c = 10.0098 (3) Å $\beta = 90.154$ (1)° V = 709.95 (4) Å³ Z = 4Mo $K\alpha$ radiation $\mu = 0.37 \text{ mm}^{-1}$ T = 100 K $0.54 \times 0.28 \times 0.22 \text{ mm}$

Data collection

Bruker SMART APEXII CCD area-detector diffractometer Absorption correction: multi-scan (SADABS; Bruker, 2005) $T_{\min} = 0.825$, $T_{\max} = 0.922$

28316 measured reflections 3100 independent reflections 3040 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.021$

Refinement

 $R[F^2 > 2\sigma(F^2)] = 0.027$ $wR(F^2) = 0.080$ S = 1.153100 reflections 96 parameters H atoms treated by a mixture of independent and constrained refinement $\Delta \rho_{\rm max} = 0.52 \ {\rm e} \ {\rm \mathring{A}}^{-3}$ $\Delta \rho_{\rm min} = -0.24 \ {\rm e} \ {\rm \mathring{A}}^{-3}$

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

D $ H$ $\cdot \cdot \cdot A$	D-H	$H \cdot \cdot \cdot A$	$D \cdot \cdot \cdot A$	$D-\mathrm{H}\cdots A$
$ \begin{array}{c} N1 - H1 \cdots N2^{i} \\ C3 - H3A \cdots N2^{i} \end{array} $	0.857 (16)	2.130 (16)	2.9803 (10)	171.5 (16)
	0.95	2.59	3.4815 (11)	156

Symmetry code: (i) $x, -y + \frac{1}{2}, z + \frac{1}{2}$.

Data collection: *APEX2* (Bruker, 2005); cell refinement: *SAINT* (Bruker, 2005); data reduction: *SAINT*; program(s) used to solve structure: *SHELXTL* (Sheldrick, 2008); program(s) used to refine structure: *SHELXTL* (Sheldrick, 2008); molecular graphics: *SHELXTL* (Sheldrick, 2008); software used to prepare material for publication: *SHELXTL* (Sheldrick, 2008) and *PLATON* (Spek, 2009).

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: WM2233).

References

Bruker (2005). APEX2, SAINT and SADABS. Bruker AXS Inc. Madison, Wisconsin, USA.

Kia, R., Fun, H.-K. & Kargar, H. (2009). Acta Cryst. E65, o301.
Sheldrick, G. M. (2008). Acta Cryst. A64, 112–122.
Spek, A. L. (2009). Acta Cryst. D65, 148–155.

[‡] Thomson Reuters ResearcherID: A-5471-2009.

[§] Thomson Reuters ResearcherID: A-3561-2009.