

6,7,8,9-Tetrahydro-2*H*-1,2,4-triazolo[4,3-*a*]-
azepin-3(5*H*)-oneGui-Sheng Yu, Hai-Zhen Xu* and
Xin ZhangCollege of Chemistry and Life Science, Tianjin
Normal University, Weijin Road No. 241,
Tianjin, People's Republic of China

Correspondence e-mail: tj_xhz@126.com

In the title compound, C₇H₁₁N₃O, the seven-membered hetero-ring adopts a chair conformation. The five-membered ring is essentially coplanar with the fused back of the chair. The compound is stabilized by a strong intermolecular N—H···O hydrogen bond, forming a chain.

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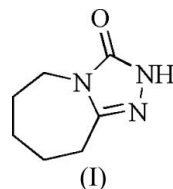
Key indicators

Single-crystal X-ray study
T = 294 K
 Mean σ (C—C) = 0.004 Å
R factor = 0.058
wR factor = 0.154
 Data-to-parameter ratio = 14.1

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

Comment

Recently, bicyclic 1,2,4-triazol-3(2*H*)-ones have been designed and synthesized as potential 5-HT₂ antagonists (Yoshifumi *et al.*, 1992). It was noticed that many hetero-ring compounds possess high herbicidal activities; however, the use of their derivatives as herbicides has rarely been reported. This provides us with a chance to obtain the herbicidal lead compound with bicyclic 1,2,4-triazol-3(2*H*)-ones. In this paper, we describe the crystal structure of the title compound, (I).



In (I), the seven-membered heterocyclic ring adopts a chair conformation. The five-membered ring is essentially coplanar with the fused back of the chair, *viz.* atoms C1, N1, C6 and C5 (Fig. 1). The dihedral angles formed by the plane C1/C2/C4/C5 with C1/C5/C6/C7/N1/N2/N3 and C2/C3/C4 are 51.9 (1) and 56.1 (2)°, respectively. The packing form of the molecule is a sandwich, and the compound is stabilized by an intermolecular

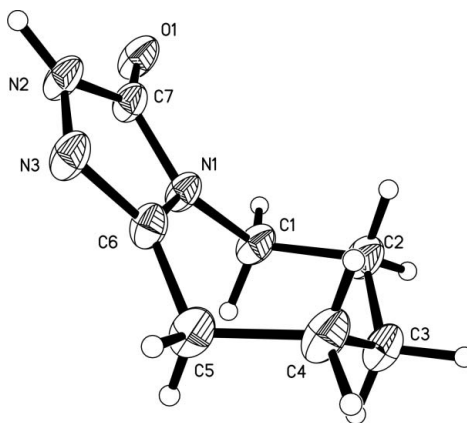


Figure 1
View of the title compound, with displacement ellipsoids drawn at the 30% probability level.

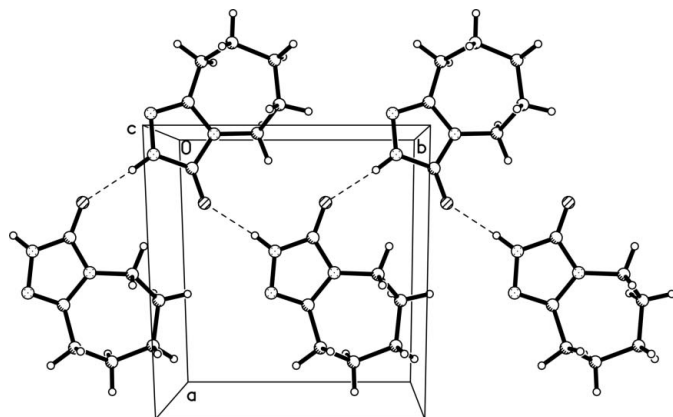


Figure 2
The packing of (I), viewed along the *c* axis. Dashed lines indicate hydrogen bonds.

N—H···O hydrogen bond, forming a chain along the *b* axis (Fig. 2 and Table 2).

Experimental

The title compound, (I), was synthesized by the procedure of Petersen & Tietze (1957). The product was recrystallized from ethanol, affording colorless crystals suitable for X-ray analysis.

Crystal data

$C_7H_{11}N_3O$	$D_x = 1.417 \text{ Mg m}^{-3}$
$M_r = 153.19$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 1141 reflections
$a = 9.069 (9) \text{ \AA}$	$\theta = 3.3\text{--}25.3^\circ$
$b = 7.884 (8) \text{ \AA}$	$\mu = 0.10 \text{ mm}^{-1}$
$c = 10.780 (11) \text{ \AA}$	$T = 294 (2) \text{ K}$
$\beta = 111.279 (17)^\circ$	Prism, colorless
$V = 718.2 (12) \text{ \AA}^3$	$0.28 \times 0.24 \times 0.20 \text{ mm}$
$Z = 4$	

Data collection

Bruker SMART CCD area-detector diffractometer	1426 independent reflections
φ and ω scans	898 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	$R_{\text{int}} = 0.049$
$T_{\text{min}} = 0.973$, $T_{\text{max}} = 0.980$	$\theta_{\text{max}} = 26.1^\circ$
3655 measured reflections	$h = -11 \rightarrow 8$
	$k = -9 \rightarrow 9$
	$l = -13 \rightarrow 12$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.08P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.058$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.155$	$(\Delta/\sigma)_{\text{max}} = 0.004$
$S = 1.07$	$\Delta\rho_{\text{max}} = 0.26 \text{ e \AA}^{-3}$
1426 reflections	$\Delta\rho_{\text{min}} = -0.25 \text{ e \AA}^{-3}$
101 parameters	Extinction correction: SHELXL97
H-atom parameters constrained	Extinction coefficient: 0.032 (8)

Table 1

Selected torsion angles ($^\circ$).

C7—N1—C1—C2	122.9 (2)	C3—C4—C5—C6	−74.0 (3)
N1—C1—C2—C3	75.2 (3)	C4—C5—C6—N3	−122.6 (3)

Table 2

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

$D\text{—}H\cdots A$	$D\text{—}H$	$H\cdots A$	$D\cdots A$	$D\text{—}H\cdots A$
N2—H2···O1 ⁱ	0.86	1.95	2.776 (3)	160

Symmetry code: (i) $-x - \frac{1}{2}, y + \frac{1}{2}, -z + \frac{3}{2}$.

The H atom bonded to N2 was located in a difference map but then placed in a calculated position. All other H atoms were positioned geometrically. The H atoms were refined using a riding model, with N—H = 0.86 \AA and C—H = 0.97 \AA , and with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C}, \text{N})$.

Data collection: SMART (Bruker, 1999); cell refinement: SAINT (Bruker, 1999); 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, 1999); software used to prepare material for publication: SHELXTL.

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