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Key indicators

Single-crystal X-ray study
T = 298 K
Mean $\sigma(\text{C}-\text{C}) = 0.004 \text{ \AA}$
R factor = 0.076
wR factor = 0.095
Data-to-parameter ratio = 10.8

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

7-Nitro-1,2,3a,4-tetrahydrobenzo[*b*]-[1,3]oxazolo[3,2-*d*]oxazine: a new heterocycle

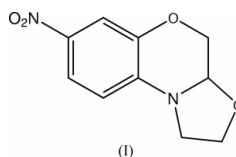
The title compound, $\text{C}_{10}\text{H}_{10}\text{N}_2\text{O}_4$, crystallizes with two independent molecules (*A* and *B*) in the asymmetric unit. The five-membered ring of the oxazole moiety adopts a half-chair conformation in molecule *A* and an envelope conformation in molecule *B*. The oxazine ring adopts a sofa conformation in both molecules.

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Comment

The oxazole moiety is frequently found in biologically active molecules and natural products. During the development of facile synthetic methods for compounds having this moiety, we synthesized 7-nitro-1,2,3a,4-tetrahydrobenzo[*b*]-[1,3]oxazolo[3,2-*d*]oxazine, (I), for the first time.



The molecular structure of (I) is shown in Fig. 1. The title compound crystallizes with two independent molecules (*A* and *B*) in the asymmetric unit. All the bond lengths and angles have normal values (Allen *et al.*, 1987). The five-membered ring adopts a half-chair conformation in molecule *A* and an envelope conformation in molecule *B*. The oxazine ring adopts a sofa conformation in both molecules..

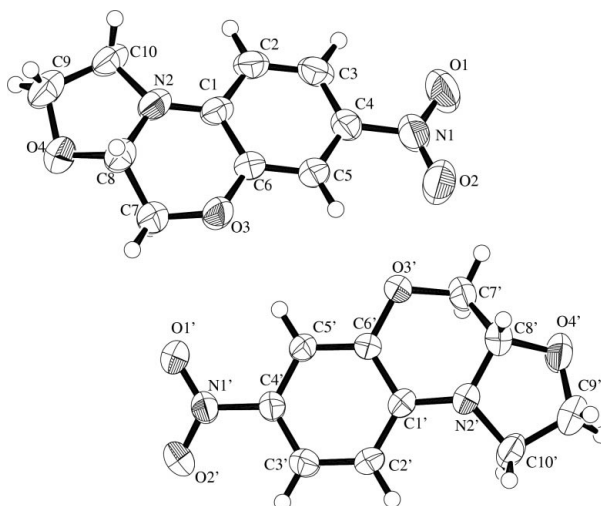


Figure 1

A perspective view of the asymmetric unit of the title compound, with displacement ellipsoids drawn at the 50% probability level.

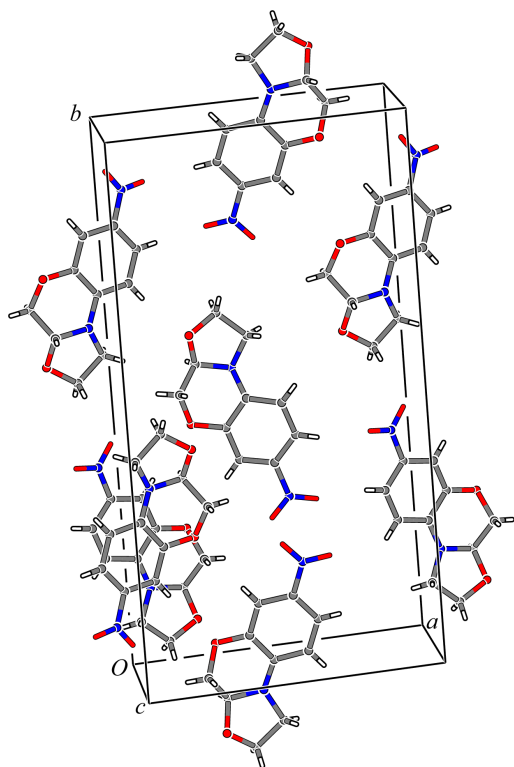


Figure 2
Packing diagram, viewed down the *c* axis.

Experimental

The title compound was prepared by nitration (using fuming nitric acid) of tricyclic oxazolooxazine, *i.e.* 1,2,3a,4-tetrahydrobenzo-*[b][1,3]oxazolo[3,2-d]oxazine*, which was synthesized according to the method of Lohray *et al.* (2000). Crystals suitable for X-ray diffraction analysis were grown from a mixture of *n*-butanol and chloroform (ratio 9:1).

Crystal data

$C_{10}H_{10}N_2O_4$	$D_x = 1.518 \text{ Mg m}^{-3}$
$M_r = 222.20$	Cu $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 25 reflections
$a = 12.164 (2) \text{ \AA}$	$\theta = 25.8\text{--}29.5^\circ$
$b = 22.079 (4) \text{ \AA}$	$\mu = 1.02 \text{ mm}^{-1}$
$c = 7.373 (2) \text{ \AA}$	$T = 298.2 \text{ K}$
$\beta = 100.86 (2)^\circ$	Block, yellow
$V = 1944.6 (6) \text{ \AA}^3$	$0.45 \times 0.30 \times 0.20 \text{ mm}$
$Z = 8$	

Data collection

Rigaku AFC-7S diffractometer	$R_{\text{int}} = 0.082$
ω - 2θ scans	$\theta_{\text{max}} = 70.0^\circ$
Absorption correction: ψ scans (North <i>et al.</i> , 1968)	$h = -14 \rightarrow 14$
$T_{\text{min}} = 0.586$, $T_{\text{max}} = 0.816$	$k = 0 \rightarrow 26$
4615 measured reflections	$l = -8 \rightarrow 3$
3769 independent reflections	3 standard reflections every 150 reflections
3111 reflections with $I > 0.5\sigma(I)$	intensity decay: <i>ca.</i> 1.0%

Refinement

Refinement on F	H-atom parameters constrained
$R = 0.076$	$w = 1/[\sigma^2(F_o) + 0.00016 F_o ^2]$
$wR = 0.095$	$(\Delta/\sigma)_{\text{max}} = 0.002$
$S = 1.98$	$\Delta\rho_{\text{max}} = 0.33 \text{ e \AA}^{-3}$
3111 reflections	$\Delta\rho_{\text{min}} = -0.42 \text{ e \AA}^{-3}$
289 parameters	

Table 1

Selected geometric parameters (\AA , $^\circ$).

O1A—N1A	1.221 (4)	O4B—C8B	1.406 (3)
O2A—N1A	1.228 (4)	O4B—C9B	1.413 (4)
O3A—C6A	1.383 (3)	N1A—C4A	1.446 (4)
O3A—C7A	1.426 (3)	N2A—C8A	1.446 (4)
O4A—C8A	1.399 (3)	N2A—C1A	1.354 (3)
O4A—C9A	1.433 (4)	N2A—C10A	1.455 (3)
O1B—N1B	1.231 (3)	N1B—C4B	1.438 (3)
O2B—N1B	1.231 (3)	N2B—C1B	1.371 (3)
O3B—C6B	1.371 (3)	N2B—C8B	1.453 (3)
O3B—C7B	1.432 (3)	N2B—C10B	1.458 (3)
C6A—O3A—C7A	112.74 (19)	O3A—C6A—C1A	119.9 (2)
C8A—O4A—C9A	104.8 (2)	O3A—C6A—C5A	118.2 (2)
C6B—O3B—C7B	113.23 (18)	O3A—C7A—C8A	110.0 (2)
C8B—O4B—C9B	105.7 (2)	C2B—O4B—N2A	105.5 (2)
O1A—N1A—C4A	118.9 (2)	O4A—C8A—C7A	110.9 (3)
O1A—N1A—O2A	122.8 (3)	N2A—C8A—C7A	110.5 (2)
O2A—N1A—C4A	118.3 (3)	O4A—C9A—C10A	104.8 (2)
C8A—N2A—C10A	109.3 (2)	N2A—C10A—C9A	101.5 (3)
C1A—N2A—C10A	126.7 (2)	N2B—C1B—C2B	122.5 (2)
C1A—N2A—C8A	121.0 (2)	N2B—C1B—C6B	118.3 (2)
O2B—N1B—C4B	118.65 (19)	N1B—C4B—C3B	119.5 (2)
O1B—N1B—O2B	122.1 (2)	N1B—C4B—C5B	118.28 (19)
O1B—N1B—C4B	119.2 (2)	O3B—C6B—C1B	120.96 (18)
C1B—N2B—C10B	124.4 (2)	O3B—C6B—C5B	118.56 (19)
C8B—N2B—C10B	110.2 (2)	O3B—C7B—C8B	109.7 (2)
C1B—N2B—C8B	120.67 (19)	O4B—C8B—N2B	105.2 (2)
N2A—C1A—C2A	123.2 (2)	O4B—C8B—C7B	112.0 (2)
N2A—C1A—C6A	119.1 (2)	N2B—C8B—C7B	110.5 (2)
N1A—C4A—C5A	118.4 (2)	O4B—C9B—C10B	107.2 (2)
N1A—C4A—C3A	119.6 (2)	N2B—C10B—C9B	100.7 (3)

Table 2

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

$D\text{---}H\cdots A$	$D\text{---}H$	$H\cdots A$	$D\cdots A$	$D\text{---}H\cdots A$
C3A—H2A \cdots O2B ⁱ	0.95	2.42	3.200 (3)	140
C5B—H3B \cdots O3A	0.95	2.59	3.517 (3)	165
C7A—H5A \cdots O1B	0.95	2.54	3.222 (4)	129
C8A—H6A \cdots O2B ⁱⁱ	0.95	2.57	3.325 (4)	136

Symmetry codes: (i) $1 + x, y, z$; (ii) $-x, -y, 1 - z$.

H atoms were included in calculated positions and refined using a riding model, with $C\text{---}H = 0.95 \text{ \AA}$.

Data collection: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1994); cell refinement: *MSC/AFC Diffractometer Control Software*; data reduction: *TEXSAN* (Molecular Structure Corporation, 1995); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1993); program(s) used to refine structure: *TEXSAN*; molecular graphics: *TEXSAN*; software used to prepare material for publication: *TEXSAN*.

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