

Acta Crystallographica Section E

## Structure Reports

Online

ISSN 1600-5368

## 3,4-Dimethyl-1*H*-1,2,4-triazepino[2,3-*a*]-benzimidazol-2(3*H*)-one

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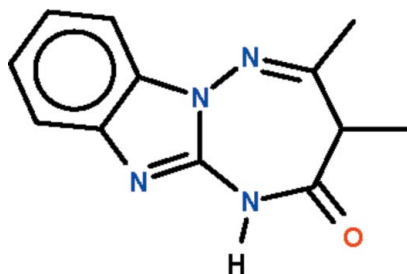
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Received 9 April 2010; accepted 12 April 2010

 Key indicators: single-crystal X-ray study;  $T = 293$  K; mean  $\sigma(\text{C}-\text{C}) = 0.003$  Å;  $R$  factor = 0.049;  $wR$  factor = 0.157; data-to-parameter ratio = 19.3.

In the molecule of the title compound,  $\text{C}_{12}\text{H}_{12}\text{N}_4\text{O}$ , a C atom and an N atom of the benzimidazole fused-ring portion are part of a seven-membered ring; this ring adopts a boat-shaped conformation (with the fused-ring atoms representing the stern and the  $sp^3$ -hybridized C atom the prow). The amino group is a hydrogen-bond donor to the imidazole group of an inversion-related molecule, the pair of  $\text{N}-\text{H}\cdots\text{N}$  hydrogen bonds giving rise to a hydrogen-bonded dimer.

## Related literature

 For the synthesis, see: Romano *et al.* (1988).


## Experimental

## Crystal data

$\text{C}_{12}\text{H}_{12}\text{N}_4\text{O}$   
 $M_r = 228.26$   
 Monoclinic,  $P2_1/c$   
 $a = 7.2899$  (3) Å  
 $b = 14.4888$  (5) Å  
 $c = 10.9932$  (4) Å  
 $\beta = 104.314$  (1)°  
 $V = 1125.08$  (7) Å<sup>3</sup>  
 $Z = 4$   
 Mo  $K\alpha$  radiation  
 $\mu = 0.09$  mm<sup>-1</sup>  
 $T = 293$  K  
 $0.21 \times 0.19 \times 0.16$  mm

## Data collection

Bruker X8 APEXII diffractometer  
 14670 measured reflections  
 3095 independent reflections  
 1823 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.034$

## Refinement

$R[F^2 > 2\sigma(F^2)] = 0.049$   
 $wR(F^2) = 0.157$   
 $S = 1.01$   
 3095 reflections  
 160 parameters  
 1 restraint  
 H atoms treated by a mixture of independent and constrained refinement  
 $\Delta\rho_{\text{max}} = 0.24$  e Å<sup>-3</sup>  
 $\Delta\rho_{\text{min}} = -0.19$  e Å<sup>-3</sup>

Table 1

Hydrogen-bond geometry (Å, °).

$D-\text{H}\cdots A$	$D-\text{H}$	$\text{H}\cdots A$	$D\cdots A$	$D-\text{H}\cdots A$
$\text{N1}-\text{H1}\cdots\text{N4}^i$	0.86 (1)	2.01 (1)	2.867 (2)	174 (2)

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

Data collection: APEX2 (Bruker, 2008); cell refinement: SAINT (Bruker, 2008); data reduction: SAINT; 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).

We thank Université Mohammed V-Agdal and the University of Malaya for supporting this study.

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: SI2255).

## References

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 Romano, C., De la Cuesta, E., Avendano, C., Florencio, F. & Sainz-Aparicio, J. (1988). *Tetrahedron*, **44**, 7185–7192.  
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 Westrip, S. P. (2010). *publCIF*. In preparation.

## supporting information

*Acta Cryst.* (2010). E66, o1093 [https://doi.org/10.1107/S1600536810013498]

**3,4-Dimethyl-1*H*-1,2,4-triazepino[2,3-*a*]benzimidazol-2(3*H*)-one**

**Asmae Saber, Abdusalam Al Subari, Hafid Zouihri, El Mokhtar Essassi and Seik Weng Ng**

**S1. Comment**

1,2-Diaminobenzimidazoles react with  $\beta$ -dicarbonyl compounds to form 1,2,4-triazepino[2,3-*a*]benzimidazoles (Romano *et al.*, 1988), a class of compounds used in the treatment of neuronal disorders. The title compound (Scheme I, Fig. 1) was synthesized from 2-aminobenzimidazole and ethyl 2-methylacetoacetate. A carbon atom and a nitrogen atom of the benzimidazole fused-ring portion are part of a seven-membered ring; this ring adopts a boat-shaped conformation (with the fused-ring atoms representing the stern and the  $sp^3$ -hybridized carbon atom the prow). Its methyl substituent occupies a quasi-equatorial position. The amino group is hydrogen-bond donor to the imidazole group (Table 1) of an inversion-related molecule, the pair of N—H $\cdots$ N hydrogen bonds (Fig. 1) giving rise to a hydrogen-bonded dimer.

**S2. Experimental**

2-Aminobenzimidazole (1 g, 6.75 mmol) and a slight excess of ethyl 2-methylacetoacetate (1.69 ml) were refluxed in xylene (10 ml) and acetic acid (0.5 ml) for 3 hours. The mixture was concentrated under reduced pressure and the resulting residue was recrystallized from ethanol. Brown crystals were isolated when the solvent was allowed to evaporate.

**S3. Refinement**

Carbon-bound H-atoms were placed in calculated positions (C—H 0.93–0.98 Å) and were included in the refinement in the riding model approximation, with  $U_{\text{iso}}(\text{H})$  set to  $1.2U_{\text{eq}}(\text{C})$ . The amino H-atom was located in a difference Fourier map, and was refined with a distance restraint of N—H 0.86 (1) Å.

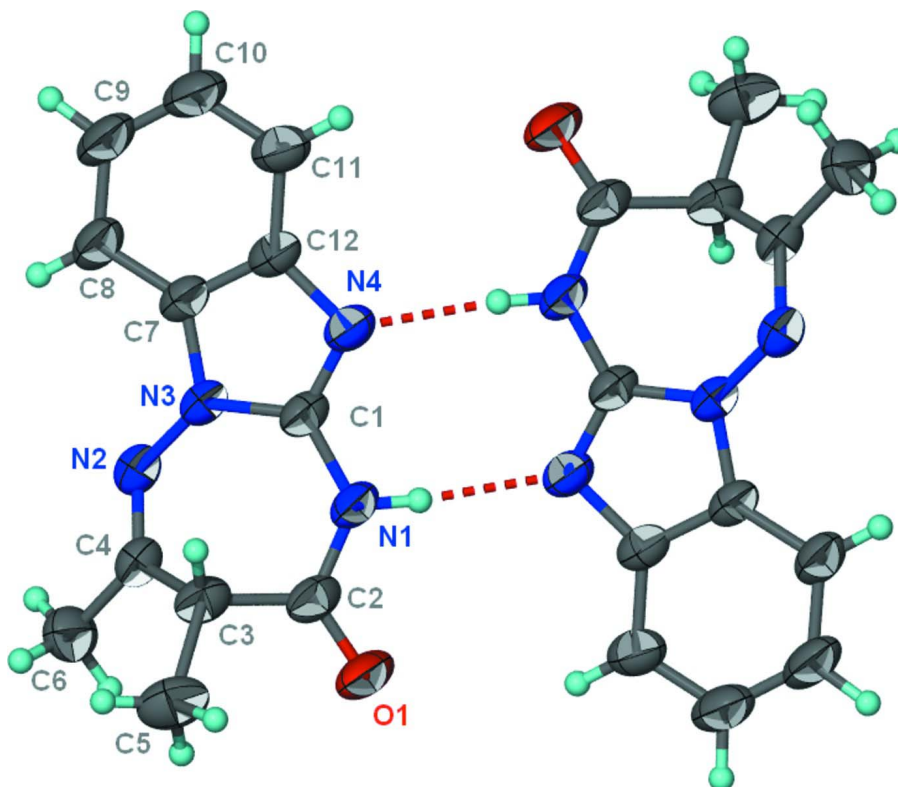


Figure 1

Thermal ellipsoid plot (Barbour, 2001) of the hydrogen-bonded dimeric structure of  $C_{12}H_{12}N_4O$  at the 50% probability level; hydrogen atoms are drawn as arbitrary radius. Symmetry code for the inversion related molecule:  $1 - x, 1 - y, 1 - z$ .

### 3,4-Dimethyl-1H-1,2,4-triazepino[2,3-a]benzimidazol- 2(3H)-one

#### Crystal data

$C_{12}H_{12}N_4O$

$M_r = 228.26$

Monoclinic,  $P2_1/c$

Hall symbol:  $-P 2ybc$

$a = 7.2899$  (3) Å

$b = 14.4888$  (5) Å

$c = 10.9932$  (4) Å

$\beta = 104.314$  (1)°

$V = 1125.08$  (7) Å<sup>3</sup>

$Z = 4$

$F(000) = 480$

$D_x = 1.348$  Mg m<sup>-3</sup>

Mo  $K\alpha$  radiation,  $\lambda = 0.71073$  Å

Cell parameters from 3188 reflections

$\theta = 2.4$ – $24.8$ °

$\mu = 0.09$  mm<sup>-1</sup>

$T = 293$  K

Prism, brown

$0.21 \times 0.19 \times 0.16$  mm

#### Data collection

Bruker X8 APEXII  
diffractometer

Radiation source: fine-focus sealed tube

Graphite monochromator

$\varphi$  and  $\omega$  scans

14670 measured reflections

3095 independent reflections

1823 reflections with  $I > 2\sigma(I)$

$R_{int} = 0.034$

$\theta_{max} = 29.4$ °,  $\theta_{min} = 2.4$ °

$h = -9 \rightarrow 10$

$k = -20 \rightarrow 19$

$l = -15 \rightarrow 13$

Refinement

Refinement on  $F^2$

Least-squares matrix: full

$R[F^2 > 2\sigma(F^2)] = 0.049$

$wR(F^2) = 0.157$

$S = 1.01$

3095 reflections

160 parameters

1 restraint

Primary atom site location: structure-invariant  
direct methods

Secondary atom site location: difference Fourier  
map

Hydrogen site location: inferred from  
neighbouring sites

H atoms treated by a mixture of independent  
and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0742P)^2 + 0.1838P]$

where  $P = (F_o^2 + 2F_c^2)/3$

$(\Delta/\sigma)_{\max} < 0.001$

$\Delta\rho_{\max} = 0.24 \text{ e } \text{\AA}^{-3}$

$\Delta\rho_{\min} = -0.19 \text{ e } \text{\AA}^{-3}$

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters ( $\text{\AA}^2$ )

	x	y	z	$U_{\text{iso}}^*/U_{\text{eq}}$
O1	0.40956 (19)	0.51793 (12)	0.14398 (13)	0.0762 (5)
N1	0.5626 (2)	0.53766 (12)	0.34574 (15)	0.0574 (4)
H1	0.486 (3)	0.5002 (13)	0.3696 (19)	0.075 (7)*
N2	0.95622 (19)	0.59291 (9)	0.32932 (14)	0.0508 (4)
N3	0.86966 (19)	0.60627 (9)	0.42759 (13)	0.0475 (4)
N4	0.6799 (2)	0.58224 (10)	0.55706 (13)	0.0552 (4)
C1	0.6977 (2)	0.57641 (11)	0.44172 (16)	0.0488 (4)
C2	0.5294 (2)	0.55903 (14)	0.22125 (17)	0.0569 (5)
C3	0.6491 (2)	0.63705 (13)	0.18892 (16)	0.0551 (5)
H3	0.6428	0.6886	0.2454	0.066*
C4	0.8529 (2)	0.60475 (11)	0.21815 (17)	0.0498 (4)
C5	0.5699 (3)	0.67076 (16)	0.05638 (19)	0.0797 (7)
H5A	0.6472	0.7202	0.0387	0.120*
H5B	0.4429	0.6926	0.0475	0.120*
H5C	0.5692	0.6210	-0.0014	0.120*
C6	0.9446 (3)	0.58710 (16)	0.11287 (19)	0.0694 (6)
H6A	1.0719	0.5659	0.1463	0.104*
H6B	0.9466	0.6432	0.0667	0.104*
H6C	0.8742	0.5409	0.0580	0.104*
C7	0.9748 (2)	0.62947 (10)	0.54769 (16)	0.0486 (4)
C8	1.1602 (3)	0.65870 (13)	0.59037 (19)	0.0636 (5)
H8	1.2399	0.6664	0.5369	0.076*
C9	1.2194 (3)	0.67573 (16)	0.7180 (2)	0.0790 (7)
H9	1.3432	0.6950	0.7517	0.095*
C10	1.0993 (4)	0.66492 (16)	0.7969 (2)	0.0780 (7)
H10	1.1444	0.6782	0.8819	0.094*
C11	0.9147 (3)	0.63502 (14)	0.75350 (18)	0.0653 (5)
H11	0.8348	0.6279	0.8070	0.078*
C12	0.8542 (3)	0.61603 (11)	0.62561 (16)	0.0516 (4)

Atomic displacement parameters ( $\text{\AA}^2$ )

	$U^{11}$	$U^{22}$	$U^{33}$	$U^{12}$	$U^{13}$	$U^{23}$
O1	0.0480 (8)	0.1131 (12)	0.0627 (9)	-0.0193 (7)	0.0049 (6)	-0.0313 (8)

N1	0.0401 (8)	0.0756 (10)	0.0538 (9)	-0.0152 (7)	0.0068 (7)	-0.0171 (7)
N2	0.0385 (7)	0.0536 (8)	0.0580 (9)	-0.0022 (6)	0.0074 (7)	-0.0016 (6)
N3	0.0368 (7)	0.0521 (8)	0.0487 (8)	-0.0038 (6)	0.0012 (6)	-0.0036 (6)
N4	0.0461 (8)	0.0639 (9)	0.0520 (9)	-0.0080 (7)	0.0055 (7)	-0.0121 (7)
C1	0.0378 (8)	0.0540 (9)	0.0505 (9)	-0.0027 (7)	0.0035 (7)	-0.0103 (7)
C2	0.0349 (9)	0.0763 (12)	0.0565 (10)	0.0011 (8)	0.0056 (8)	-0.0202 (9)
C3	0.0468 (10)	0.0591 (10)	0.0536 (10)	0.0051 (8)	0.0014 (8)	-0.0080 (8)
C4	0.0404 (9)	0.0497 (9)	0.0563 (10)	-0.0035 (7)	0.0066 (8)	-0.0038 (7)
C5	0.0758 (15)	0.0797 (14)	0.0688 (13)	0.0114 (11)	-0.0103 (11)	-0.0030 (11)
C6	0.0578 (12)	0.0891 (15)	0.0640 (12)	-0.0009 (10)	0.0202 (10)	-0.0015 (10)
C7	0.0439 (9)	0.0417 (8)	0.0517 (9)	-0.0036 (7)	-0.0045 (8)	0.0010 (7)
C8	0.0482 (10)	0.0662 (11)	0.0657 (11)	-0.0128 (8)	-0.0065 (9)	0.0088 (9)
C9	0.0628 (13)	0.0825 (14)	0.0724 (14)	-0.0247 (11)	-0.0200 (11)	0.0067 (11)
C10	0.0816 (16)	0.0786 (14)	0.0575 (12)	-0.0199 (11)	-0.0137 (11)	-0.0014 (10)
C11	0.0708 (13)	0.0655 (11)	0.0521 (10)	-0.0082 (10)	0.0009 (9)	-0.0061 (8)
C12	0.0501 (10)	0.0467 (9)	0.0507 (9)	-0.0036 (7)	-0.0012 (8)	-0.0047 (7)

*Geometric parameters (Å, °)*

O1—C2	1.213 (2)	C5—H5B	0.9600
N1—C2	1.365 (2)	C5—H5C	0.9600
N1—C1	1.373 (2)	C6—H6A	0.9600
N1—H1	0.864 (9)	C6—H6B	0.9600
N2—C4	1.279 (2)	C6—H6C	0.9600
N2—N3	1.393 (2)	C7—C8	1.383 (2)
N3—C1	1.371 (2)	C7—C12	1.385 (3)
N3—C7	1.394 (2)	C8—C9	1.384 (3)
N4—C1	1.309 (2)	C8—H8	0.9300
N4—C12	1.396 (2)	C9—C10	1.386 (3)
C2—C3	1.523 (3)	C9—H9	0.9300
C3—C5	1.510 (3)	C10—C11	1.382 (3)
C3—C4	1.515 (2)	C10—H10	0.9300
C3—H3	0.9800	C11—C12	1.393 (2)
C4—C6	1.495 (3)	C11—H11	0.9300
C5—H5A	0.9600		
C2—N1—C1	126.41 (17)	H5A—C5—H5C	109.5
C2—N1—H1	118.6 (14)	H5B—C5—H5C	109.5
C1—N1—H1	114.7 (14)	C4—C6—H6A	109.5
C4—N2—N3	116.74 (14)	C4—C6—H6B	109.5
C1—N3—N2	130.27 (13)	H6A—C6—H6B	109.5
C1—N3—C7	105.84 (14)	C4—C6—H6C	109.5
N2—N3—C7	121.30 (14)	H6A—C6—H6C	109.5
C1—N4—C12	104.53 (15)	H6B—C6—H6C	109.5
N4—C1—N3	113.68 (14)	C8—C7—C12	123.37 (17)
N4—C1—N1	123.18 (16)	C8—C7—N3	131.12 (19)
N3—C1—N1	122.98 (16)	C12—C7—N3	105.50 (14)
O1—C2—N1	120.60 (19)	C7—C8—C9	115.6 (2)

O1—C2—C3	123.76 (18)	C7—C8—H8	122.2
N1—C2—C3	115.63 (14)	C9—C8—H8	122.2
C5—C3—C4	115.20 (18)	C8—C9—C10	121.89 (19)
C5—C3—C2	111.16 (15)	C8—C9—H9	119.1
C4—C3—C2	108.05 (14)	C10—C9—H9	119.1
C5—C3—H3	107.4	C11—C10—C9	122.06 (19)
C4—C3—H3	107.4	C11—C10—H10	119.0
C2—C3—H3	107.4	C9—C10—H10	119.0
N2—C4—C6	116.53 (16)	C10—C11—C12	116.7 (2)
N2—C4—C3	124.01 (16)	C10—C11—H11	121.7
C6—C4—C3	119.45 (16)	C12—C11—H11	121.7
C3—C5—H5A	109.5	C7—C12—C11	120.37 (17)
C3—C5—H5B	109.5	C7—C12—N4	110.36 (15)
H5A—C5—H5B	109.5	C11—C12—N4	129.27 (19)
C3—C5—H5C	109.5		
C4—N2—N3—C1	45.3 (2)	C5—C3—C4—C6	-14.2 (2)
C4—N2—N3—C7	-155.63 (15)	C2—C3—C4—C6	110.73 (19)
C12—N4—C1—N3	-1.68 (19)	C1—N3—C7—C8	176.13 (18)
C12—N4—C1—N1	173.69 (17)	N2—N3—C7—C8	12.6 (3)
N2—N3—C1—N4	164.44 (16)	C1—N3—C7—C12	-2.84 (17)
C7—N3—C1—N4	2.94 (19)	N2—N3—C7—C12	-166.39 (14)
N2—N3—C1—N1	-10.9 (3)	C12—C7—C8—C9	-1.1 (3)
C7—N3—C1—N1	-172.44 (16)	N3—C7—C8—C9	-179.90 (18)
C2—N1—C1—N4	152.30 (18)	C7—C8—C9—C10	-0.6 (3)
C2—N1—C1—N3	-32.8 (3)	C8—C9—C10—C11	1.2 (4)
C1—N1—C2—O1	177.59 (18)	C9—C10—C11—C12	0.0 (3)
C1—N1—C2—C3	-3.3 (3)	C8—C7—C12—C11	2.3 (3)
O1—C2—C3—C5	13.2 (3)	N3—C7—C12—C11	-178.66 (16)
N1—C2—C3—C5	-165.91 (17)	C8—C7—C12—N4	-177.09 (16)
O1—C2—C3—C4	-114.2 (2)	N3—C7—C12—N4	1.99 (18)
N1—C2—C3—C4	66.8 (2)	C10—C11—C12—C7	-1.6 (3)
N3—N2—C4—C6	-177.91 (15)	C10—C11—C12—N4	177.58 (18)
N3—N2—C4—C3	3.5 (2)	C1—N4—C12—C7	-0.27 (19)
C5—C3—C4—N2	164.30 (17)	C1—N4—C12—C11	-179.55 (19)
C2—C3—C4—N2	-70.7 (2)		

*Hydrogen-bond geometry (Å, °)*

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
N1—H1...N4 <sup>i</sup>	0.86 (1)	2.01 (1)	2.867 (2)	174 (2)

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