organic compounds

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6-Bromo-1,3-benzothiazol-2-amine

Xing-Jun Gao,^a Shou-Wen Jin,^b* Yan-Fei Huang,^b Yong Zhou^b and Ying-Ping Zhou^b

^aFaculty of Science, ZheJiang A & F University, Lin'An 311300, People's Republic of China, and ^bTianmu College of ZheJiang A & F University, Lin'An 311300, People's Republic of China

Correspondence e-mail: shouwenjin@yahoo.cn

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Key indicators: single-crystal X-ray study; T = 298 K; mean σ (C–C) = 0.020 Å; R factor = 0.095; wR factor = 0.246; data-to-parameter ratio = 13.4.

The r.m.s. deviation from the mean plane for the non-H atoms in the title compound, $C_7H_5BrN_2S$, is 0.011 Å. In the crystal, the molecules are linked by $N-H\cdots N$ and $N-H\cdots Br$ hydrogen bonds to generate (010) sheets. Weak aromatic $\pi-\pi$ stacking [centroid-to-centroid separation = 3.884 (10) Å] and possible $C-H\cdots Br$ interactions are also observed. The crystal studied was found to be an inversion twin.

Related literature

For a related structure and background to benzothiazole derivatives, see: Jin *et al.* (2012).



Experimental

Crystal data	
$C_7H_5BrN_2S$	b = 22.487 (2) Å
$M_r = 229.10$ Orthorhombic, $Pna2_1$	c = 4.0585 (3) A $V = 787.30 (11) \text{ Å}^3$
a = 8.6268 (7) Å	Z = 4

Mo Ka radiation	
$\mu = 5.41 \text{ mm}^{-1}$	

Data collection

Bruker SMART CCD diffractometer Absorption correction: multi-scan (*SADABS*; Bruker, 2002) $T_{\rm min} = 0.215, T_{\rm max} = 0.421$

Refinement

$$\begin{split} R[F^2 > 2\sigma(F^2)] &= 0.095 & \text{H-atom parameters constrained} \\ wR(F^2) &= 0.246 & \Delta\rho_{\text{max}} = 1.13 \text{ e } \text{\AA}^{-3} \\ S &= 1.07 & \Delta\rho_{\text{min}} = -0.74 \text{ e } \text{\AA}^{-3} \\ 1340 \text{ reflections} & \text{Absolute structure: Flack (1983),} \\ 100 \text{ parameters} & 539 \text{ Friedel pairs} \\ 1 \text{ restraint} & \text{Flack parameter: } 0.42 (9) \end{split}$$

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

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots \mathbf{A}$	
$N2-H2B\cdots Br1^{i}$	0.86	3.04	3.864 (17)	160	
$N2-H2A\cdots N1^{ii}$	0.86	2.26	2.94 (2)	136	
C4−H4···Br1 ⁱⁱⁱ	0.93	2.87	3.402 (17)	118	
Symmetry codes: (i) $x - 1$, y , $z + 1$; (ii) $-x + 1$, $-y + 1$, $z + \frac{1}{2}$; (iii) $x - \frac{1}{2}$, $-y + \frac{3}{2}$, z .					

T = 298 K

 $R_{\rm int} = 0.087$

 $0.31 \times 0.25 \times 0.16 \text{ mm}$

3645 measured reflections

1340 independent reflections

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

Data collection: *SMART* (Bruker, 2002); cell refinement: *SAINT* (Bruker, 2002); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *SHELXTL* (Sheldrick, 2008); software used to prepare material for

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: HB6956).

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6-Bromo-1,3-benzothiazol-2-amine

Xing-Jun Gao, Shou-Wen Jin, Yan-Fei Huang, Yong Zhou and Ying-Ping Zhou

S1. Comment

As an extension of our study of 2-aminoheterocyclic compounds (Jin *et al.*, 2012), herein we report the crystal structure of 6-bromobenzo[*d*]thiazol-2-amine.

The single crystals of the title compound (Fig.1) with the formula $C_7H_5BrN_2S$ was obtained by slow evaporating its methanol solution.

The 6-bromobenzo[d]thiazol-2-amine molecules (Fig. 1) are linked together in head to tail fashion via the N—H···Br association to form one-dimensional chain running along the direction that made a dihedral angle of ca 30° with the a axis direction. Two neighboring chains were held together by the CH—Br interaction with C—Br distance of 3.402 Å generating one-dimensional double chain (Fig.2). The double chains were stacked along the direction that is perpendicular with its extending direction by the CH—Br interaction with C—Br distance of 3.402 Å to form two-dimensional sheet extending parallel to the ac plane. The sheets were further stacked along the b axis direction by the intersheet N—H···N hydrogen bonds to form three-dimensional ABAB layer network structure.

S2. Experimental

The 6-bromobenzo[d]thiazol-2-amine (22.9 mg, 0.1 mmol) was dissolved in a methanol solution (8 ml). The solution was filtered into a test tube. The solution was left standing at room temperature for a month, light-yellow blocks were isolated after slow evaporation of the methanol solution to ca 3 ml in air.

S3. Refinement

H atoms bonded N atoms were located in a6-Bromo-1,3-benzothiazol-2-amine difference Fourier map and refined isotropically. Other H atoms were positioned geometrically with C—H = 0.93 Å, and constrained to ride on their parent atoms with $U_{iso}(H) = 1.2Ueq(C)$.



Figure 1

The structure of the title compound, showing displacement ellipsoids drawn at the 30% probability level.



Figure 2

One-dimensional double chain structure.

6-Bromo-1,3-benzothiazol-2-amine

Crystal data C₇H₅BrN₂S $M_r = 229.10$ Orthorhombic, *Pna*2₁ a = 8.6268 (7) Å b = 22.487 (2) Å c = 4.0585 (3) Å V = 787.30 (11) Å³ Z = 4F(000) = 448

Data collection

Bruker SMART CCD diffractometer Radiation source: fine-focus sealed tube Graphite monochromator ω scans Absorption correction: multi-scan (*SADABS*; Bruker, 2002) $T_{\min} = 0.215, T_{\max} = 0.421$ $D_x = 1.933 \text{ Mg m}^{-3}$ Mo K α radiation, $\lambda = 0.71073 \text{ Å}$ Cell parameters from 868 reflections $\theta = 3.6-21.4^{\circ}$ $\mu = 5.41 \text{ mm}^{-1}$ T = 298 KBlock, colourless $0.31 \times 0.25 \times 0.16 \text{ mm}$

3645 measured reflections 1340 independent reflections 929 reflections with $I > 2\sigma(I)$ $R_{int} = 0.087$ $\theta_{max} = 25.0^{\circ}, \ \theta_{min} = 2.5^{\circ}$ $h = -6 \rightarrow 10$ $k = -26 \rightarrow 26$ $l = -4 \rightarrow 4$ Refinement

Refinement on F^2	Hydrogen site location: inferred from
Least-squares matrix: full	neighbouring sites
$R[F^2 > 2\sigma(F^2)] = 0.095$	H-atom parameters constrained
$wR(F^2) = 0.246$	$w = 1/[\sigma^2(F_o^2) + (0.067P)^2 + 14.6225P]$
S = 1.07	where $P = (F_o^2 + 2F_c^2)/3$
1340 reflections	$(\Delta/\sigma)_{\rm max} = 0.001$
100 parameters	$\Delta \rho_{\rm max} = 1.13 \text{ e } \text{\AA}^{-3}$
1 restraint	$\Delta \rho_{\min} = -0.74 \text{ e} \text{ Å}^{-3}$
Primary atom site location: structure-invariant direct methods	Absolute structure: Flack (1983), with how many Friedel pairs?
Secondary atom site location: difference Fourier map	Absolute structure parameter: 0.42 (9)

Special details

Geometry. All e.s.d.'s (except the e.s.d. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell e.s.d.'s are taken into account individually in the estimation of e.s.d.'s in distances, angles and torsion angles; correlations between e.s.d.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell e.s.d.'s is used for estimating e.s.d.'s involving l.s. planes.

Refinement. Refinement of F^2 against ALL reflections. The weighted *R*-factor *wR* and goodness of fit *S* are based on F^2 , conventional *R*-factors *R* are based on *F*, with *F* set to zero for negative F^2 . The threshold expression of $F^2 > \sigma(F^2)$ is used only for calculating *R*-factors(gt) *etc.* and is not relevant to the choice of reflections for refinement. *R*-factors based on F^2 are statistically about twice as large as those based on *F*, and *R*-factors based on ALL data will be even larger.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters $(Å^2)$

	x	У	Ζ	$U_{ m iso}$ */ $U_{ m eq}$	
Br1	1.2451 (2)	0.69710 (7)	0.3819 (16)	0.0745 (8)	
S1	0.6334 (4)	0.65747 (14)	0.8676 (16)	0.0407 (9)	
N2	0.4231 (13)	0.5675 (5)	0.884 (6)	0.051 (3)	
H2A	0.3952	0.5318	0.8379	0.061*	
H2B	0.3608	0.5908	0.9878	0.061*	
C7	0.9282 (17)	0.5595 (6)	0.404 (6)	0.044 (4)	
H7	0.9250	0.5204	0.3294	0.052*	
C6	1.0594 (18)	0.5939 (6)	0.352 (6)	0.043 (4)	
H6	1.1456	0.5786	0.2435	0.052*	
N1	0.6666 (18)	0.5508 (6)	0.627 (4)	0.047 (4)	
C1	0.5630 (19)	0.5869 (7)	0.795 (4)	0.046 (5)	
C2	0.802 (2)	0.5836 (7)	0.568 (4)	0.042 (4)	
C4	0.933 (2)	0.6779 (7)	0.634 (5)	0.046 (4)	
H4	0.9364	0.7170	0.7084	0.055*	
C3	0.804 (2)	0.6421 (8)	0.682 (4)	0.045 (4)	
C5	1.057 (2)	0.6520 (7)	0.469 (4)	0.052 (5)	

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U ²³
Br1	0.0513 (10)	0.0510 (9)	0.1212 (18)	-0.0117 (8)	0.005 (2)	0.005 (2)
S1	0.0394 (18)	0.0344 (16)	0.048 (2)	-0.0010 (15)	0.006 (3)	0.015 (3)
N2	0.041 (7)	0.041 (6)	0.071 (10)	-0.005 (5)	-0.012 (15)	-0.004 (11)

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C7	0.045 (8)	0.033 (7)	0.053 (11)	0.000 (6)	0.007 (13)	-0.012 (11)
C6	0.052 (9)	0.038 (7)	0.040 (10)	-0.002 (6)	0.014 (14)	-0.007 (11)
N1	0.054 (9)	0.040 (7)	0.047 (9)	-0.001 (7)	0.010 (8)	-0.006 (7)
C1	0.043 (9)	0.037 (8)	0.059 (15)	-0.007 (7)	0.000 (9)	-0.009 (8)
C2	0.047 (10)	0.038 (9)	0.041 (10)	-0.005 (8)	0.011 (8)	-0.004 (8)
C4	0.052 (11)	0.035 (8)	0.051 (11)	0.002 (8)	0.005 (9)	-0.008(8)
C3	0.050 (11)	0.044 (9)	0.040 (10)	-0.004 (8)	0.005 (8)	-0.001 (8)
C5	0.051 (10)	0.044 (9)	0.060 (16)	-0.001 (8)	0.004 (9)	0.002 (8)

Geometric parameters (Å, °)

Br1—C5	1.944 (18)	C6—C5	1.39 (2)
S1—C3	1.686 (19)	С6—Н6	0.9300
S1—C1	1.725 (16)	N1—C1	1.39 (2)
N2—C1	1.33 (2)	N1—C2	1.40 (2)
N2—H2A	0.8600	C2—C3	1.39 (2)
N2—H2B	0.8600	C4—C3	1.39 (3)
C7—C6	1.39 (2)	C4—C5	1.39 (2)
C7—C2	1.39 (2)	C4—H4	0.9300
С7—Н7	0.9300		
C3—S1—C1	92.4 (9)	N1—C1—S1	113.3 (12)
C1—N2—H2A	120.0	C7—C2—C3	121.1 (16)
C1—N2—H2B	120.0	C7—C2—N1	122.0 (15)
H2A—N2—H2B	120.0	C3—C2—N1	116.9 (16)
C6—C7—C2	119.7 (14)	C3—C4—C5	116.3 (15)
С6—С7—Н7	120.1	C3—C4—H4	121.8
С2—С7—Н7	120.1	C5—C4—H4	121.8
C7—C6—C5	117.5 (15)	C4—C3—C2	120.7 (17)
С7—С6—Н6	121.2	C4—C3—S1	130.0 (14)
С5—С6—Н6	121.2	C2—C3—S1	109.2 (14)
C1—N1—C2	108.1 (14)	C6—C5—C4	124.6 (16)
N2—C1—N1	121.7 (14)	C6—C5—Br1	114.7 (13)
N2—C1—S1	125.0 (13)	C4—C5—Br1	120.7 (12)
C2—C7—C6—C5	0 (3)	C7—C2—C3—C4	0 (3)
C2—N1—C1—N2	179.8 (19)	N1—C2—C3—C4	-180.0 (17)
C2—N1—C1—S1	0.3 (18)	C7—C2—C3—S1	179.8 (17)
C3—S1—C1—N2	-179.9 (18)	N1—C2—C3—S1	0 (2)
C3—S1—C1—N1	-0.4 (15)	C1—S1—C3—C4	-180 (2)
C6—C7—C2—C3	0 (3)	C1—S1—C3—C2	0.4 (15)
C6—C7—C2—N1	-179.9 (19)	C7—C6—C5—C4	0 (3)
C1—N1—C2—C7	180 (2)	C7—C6—C5—Br1	-179.5 (15)
C1—N1—C2—C3	0 (2)	C3—C4—C5—C6	0 (3)
C5—C4—C3—C2	0 (3)	C3—C4—C5—Br1	179.6 (14)
C5—C4—C3—S1	-179.7 (15)		

D—H···A *D*—Н $\mathrm{H}{\cdots}{A}$ $D \cdots A$ D—H···AN2—H2B···Br1ⁱ 0.86 3.04 3.864 (17) 160 N2—H2A···· $N1^{ii}$ 0.86 2.26 2.94 (2) 136 $C4 - \!\!-\!\!H4 \cdots Br1^{iii}$ 3.402 (17) 0.93 2.87 118

Hydrogen-bond geometry (Å, °)

Symmetry codes: (i) *x*-1, *y*, *z*+1; (ii) -*x*+1, -*y*+1, *z*+1/2; (iii) *x*-1/2, -*y*+3/2, *z*.