organic compounds

N-(2-Amino-5-chlorophenyl)-2-bromo-benzenesulfonamide

Maria Altamura,[a] Valentina Fedi,[a] Rossano Nannicini,[a] Paola Paoli[b]* and Patrizia Rossi[b]

[a]Chemistry Department, Menarini Ricerche S.p.A., Via dei Sette Santi 3, I-50131 Firenze, Italy, and [b]Dipartimento Energetica "Sergio Stecco", University of Firenze, Via S. Marta 3, I-50139 Firenze, Italy

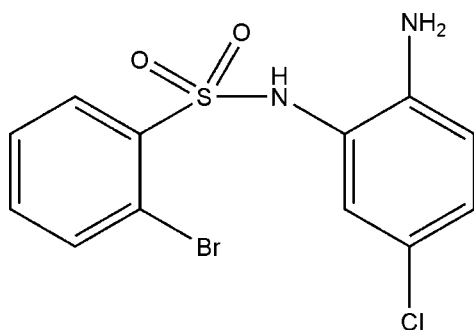Correspondence e-mail: paolapaoli@unifi.it

In the title compound, $C_{12}H_{10}BrClN_2O_2S$, the sulfonamide group adopts a staggered conformation about the N—S bond [the C—S—N—H torsion angle is 97 (3)°] with the N-atom lone pair bisecting the O=S=O angle. For the C(Ar)—S bond, the *ortho*-substituted C atom bisects one of O=S–N angles [the C—C—S—N torsion angle is −57.7 (3)°]. The mean planes of the aromatic rings form a dihedral angle of 75.1 (1)°. In the crystal, molecules form inversion dimers through pairs of N—H···NH₂ hydrogen bonds. The molecules are further consolidated into layers along the bc plane by weaker N—H···O interactions.

Related literature

For the synthesis of the title compound, see: Altamura *et al.* (2009). For the biological activity of sulfa drugs, see: Chegwidden *et al.* (2000); Lu & Tucker (2007); Tappe *et al.* (2008); Purushottamachar *et al.* (2008). For structural studies of molecules having the sulfonamide –SO₂—NH group, see: Parkin *et al.* (2008); Perlovich *et al.* (2009, 2011); Vega-Hissi *et al.* (2011); Altamura *et al.* (2009, 2012).

Experimental

Crystal data

$C_{12}H_{10}BrClN_2O_2S$	V = 1364.8 (3) Å³
M_r = 361.64	Z = 4
Monoclinic, $P2_1/c$	Mo $K\alpha$ radiation
a = 13.657 (1) Å	μ = 3.36 mm⁻¹
b = 14.361 (2) Å	T = 298 K
c = 7.0829 (9) Å	0.32 × 0.26 × 0.22 mm
β = 100.75 (1)°	

Data collection

Oxford Diffraction Xcalibur3 CCD diffractometer	6647 measured reflections
	2533 independent reflections
Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)	1629 reflections with $I > 2\sigma(I)$
T_{min} = 0.365, T_{max} = 0.447	R_{int} = 0.028

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.038	H atoms treated by a mixture of independent and constrained refinement
$wR(F^2)$ = 0.082	
S = 0.94	
2533 reflections	$\Delta\rho_{max}$ = 0.32 e Å⁻³
181 parameters	$\Delta\rho_{min}$ = −0.38 e Å⁻³

Table 1
Selected torsion angles (°).

HN1—N1—S1—C1	97 (3)	C6—C1—S1—N1	−57.7 (3)
HN1—N1—S1—O1	−19 (3)	C6—C1—S1—O1	57.8 (3)
C7—N1—S1—O2	50.2 (3)		

Table 2
Hydrogen-bond geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
N1—HN1···N2[i]	0.78 (3)	2.26 (3)	3.022 (4)	166 (3)
N2—HN2A···O1[ii]	0.87 (3)	2.45 (3)	3.258 (4)	154 (3)

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

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2006); cell refinement: *CrysAlis CCD*; data reduction: *CrysAlis RED* (Oxford Diffraction, 2006); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *PARST* (Nardelli, 1995).

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: LD2080).

References

Altamura, M., Fedi, V., Giannotti, D., Paoli, P. & Rossi, P. (2009). *New J. Chem.* **33**, 2219–2231.

Altamura, M., Fedi, V., Nannicini, R., Paoli, P. & Rossi, P. (2012). *Acta Cryst.* E**68**, o3144–o3145.

Altomare, A., Burla, M. C., Camalli, M., Cascarano, G. L., Giacovazzo, C., Guagliardi, A., Moliterni, A. G. G., Polidori, G. & Spagna, R. (1999). *J. Appl. Cryst.* **32**, 115–119.

Chegwidden, W. R., Carter, N. D. & Edwards, Y. H. (2000). In *The Carbonic Anhydrases New Horizons*. Basel: Birkhauser Verlag.

Farrugia, L. J. (1997). *J. Appl. Cryst.* **30**, 565.

Lu, R. J. & Tucker, J. A. (2007). *J. Med. Chem.* **50**, 6535–6544.

Nardelli, M. (1995). *J. Appl. Cryst.* **28**, 659.

Oxford Diffraction (2006). *CrysAlis CCD* and *CrysAlis RED.* Oxford Diffraction Ltd, Abingdon, England.

Parkin, A., Collins, A., Gilmore, C. J. & Wilson, C. C. (2008). *Acta Cryst.* B**64**, 66–71.

Perlovich, G. L., Ryzhakov, A. M., Tkachev, T. T. & Hansen, L. K. (2011). *Cryst. Growth Des.* **11**, 1067–1081.

Perlovich, G. L., Tkachev, V. V., Strakhova, N. N., Kazachenko, V. P., Volkova, T. V., Surov, O. V., Schaper, K.-J. & Raevsky, O. A. (2009). *J. Pharm. Sci.* **98**, 4738–4755.

Purushottamachar, P., Khandelwal, A., Vasaitis, T. S., Bruno, R. D., Gediya, L. K. & Njar, V. C. O. (2008). *Bioorg. Med. Chem.* **16**, 3519–3529.

Sheldrick, G. M. (1996). *SADABS*. University of Göttingen, Germany.

Sheldrick, G. M. (2008). *Acta Cryst.* A**64**, 112–122.

Tappe, W., Zarfl, C., Kummer, S., Burauel, P., Vereecken, H. & Groeneweg, J. (2008). *Chemosphere*, **72**, 836–843.

Vega-Hissi, E. G., Andrada, M. F., Zamarbide, G. N., Estrada, M. R. & Tomas-Vert, F. (2011). *J. Mol. Model.* **17**, 1317–1323.

N-(2-Amino-5-chlorophenyl)-2-bromobenzenesulfonamide

Maria Altamura, Valentina Fedi, Rossano Nannicini, Paola Paoli and Patrizia Rossi

Comment

The study of the structural and conformational properties of the sulfonamide group (R—SO$_2$—NR_2) is essential to the comprehension of the "sulfa drugs" action. They found applications as HIV inhibitors (Lu & Tucker, 2007), antimicrobial drugs (Tappe *et al.*, 2008), carbonic anhydrase inhibitors (Chegwidden *et al.*, 2000), anti-tumor agents (Purushottamachar *et al.*, 2008), just to name a few. In this respect a lot of publications have appeared reporting structural data of compounds containing the sulfonamide function (Parkin *et al.*, 2008, Altamura *et al.*, 2009, Perlovich *et al.*, 2009, Perlovich *et al.*, 2011,Vega-Hissi *et al.*, 2011, Altamura *et al.*, 2012). The molecule, as expected, has a staggered conformation about the N—S bond, with the N lone pair bisecting the OŜO angle (Table 1, Fig. 1). The value of the dihedral angle C6—C1—S1 —O1 (Table 1) is also in the range observed for arylsulfonamides bearing a non-hydrogen atom in *ortho* position (a bromine atom in this case). The sulfonamide nitrogen atom is almost planar- trigonal (Σ<N=357 (3)°). The aromatic rings are almost perpendicular to each other with a dihedral angle of 75.1 (1)°. In the crystal, dimers are formed by a couple of complementary hydrogen bonds involving the nitrogen atom of the sulfonamide grouping as a donor and amino nitrogen as an acceptor (Table 2). Dimers form layers along bc plane through weaker NH$_2$···SO$_2$ H-bonds between the amino group and an oxygen atom of the sulfonamide moiety (Table 2). The remaining amine H atom (HN2B) appears to be involved in bifurcated intra-molecular contacts with the oxygen and the nitrogen atoms of the sulfonamide group (HN2B···O2 = 2.72 (3) Å, N2—HN2B···O2 = 132 (3)°; HN2B···N1 = 2.58 (4) Å, N2—HN2B···N1 = 98 (3)°), which could contribute in stabilization of the observed molecular conformation.

Experimental

For the synthesis of the title compound, see: Altamura *et al.* (2009). Crystals of the title compound suitable for single-crystal X-ray diffraction analysis were obtained by slow evaporation of an ethyl acetate/hexane solution of *N*-(2-amino-5-chlorophenyl)-2-bromobenzenesulfonamide.

Refinement

The N—H H atoms were located in the Fourier difference map and their coordinates were refined with U(H) = 1.2U_{eq}(N). All other H atoms were positioned using idealized geometry and refined using a riding model with U(H) 1.2 times U_{eq}(C).

Computing details

Data collection: *CrysAlis CCD* (Oxford Diffraction, 2006); cell refinement: *CrysAlis CCD* (Oxford Diffraction, 2006); data reduction: *CrysAlis RED* (Oxford Diffraction, 2006); program(s) used to solve structure: *SIR97* (Altomare *et al.*, 1999); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *PARST* (Nardelli, 1995).
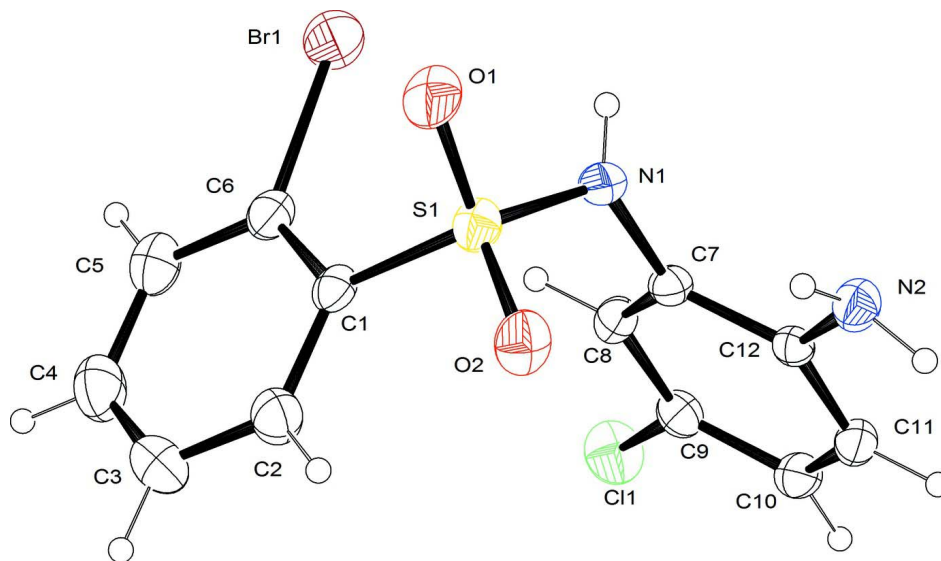
Figure 1

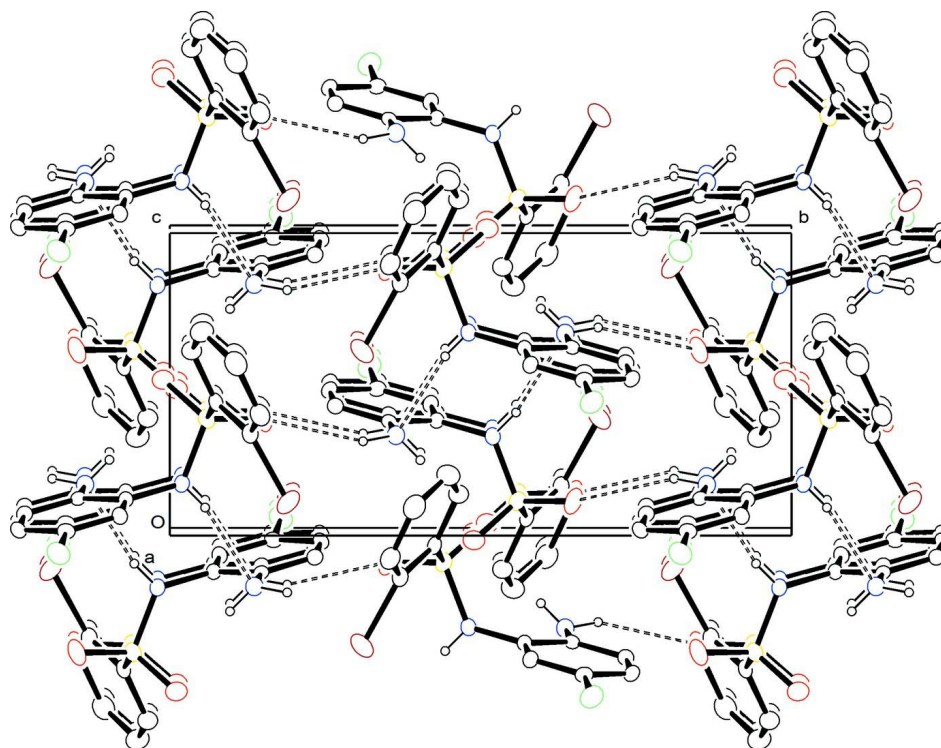The structure of the title compound showing labelling and displacement ellipsoids drawn at the 30% probability level.

Figure 2

Crystal structure of the title compound as viewed along the a axis. Hydrogen bonds are shown as dashed lines.

N-(2-Amino-5-chlorophenyl)-2-bromobenzenesulfonamide

Crystal data

$C_{12}H_{10}BrClN_2O_2S$	$Z = 4$
$M_r = 361.64$	$F(000) = 720$
Monoclinic, $P2_1/c$	$D_x = 1.760$ Mg m^{-3}
$a = 13.657$ (1) Å	Mo $K\alpha$ radiation, $\lambda = 0.71069$ Å
$b = 14.361$ (2) Å	$\mu = 3.36$ mm^{-1}
$c = 7.0829$ (9) Å	$T = 298$ K
$\beta = 100.75$ (1)°	Prismatic, colourless
$V = 1364.8$ (3) Å^3	$0.32 \times 0.26 \times 0.22$ mm

Data collection

Oxford Diffraction Xcalibur3 CCD diffractometer	6647 measured reflections
	2533 independent reflections
Radiation source: Enhance (Mo) X-ray Source	1629 reflections with $I > 2\sigma(I)$
Graphite monochromator	$R_{int} = 0.028$
Detector resolution: 16.4547 pixels mm^{-1}	$\theta_{max} = 27.3°$, $\theta_{min} = 4.5°$
ω scans	$h = -16\rightarrow16$
Absorption correction: multi-scan	$k = -17\rightarrow18$
(*SADABS*; Sheldrick, 1996)	$l = -8\rightarrow8$
$T_{min} = 0.365$, $T_{max} = 0.447$	

Refinement

Refinement on F^2	Secondary atom site location: difference Fourier map
Least-squares matrix: full	
$R[F^2 > 2\sigma(F^2)] = 0.038$	Hydrogen site location: inferred from neighbouring sites
$wR(F^2) = 0.082$	
$S = 0.94$	H atoms treated by a mixture of independent and constrained refinement
2533 reflections	
181 parameters	$w = 1/[\sigma^2(F_o^2) + (0.0371P)^2]$
0 restraints	where $P = (F_o^2 + 2F_c^2)/3$
Primary atom site location: structure-invariant direct methods	$(\Delta/\sigma)_{max} < 0.001$
	$\Delta\rho_{max} = 0.32$ e Å^{-3}
	$\Delta\rho_{min} = -0.38$ e Å^{-3}

Special details

Geometry. All s.u.'s (except the s.u. in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell s.u.'s are taken into account individually in the estimation of s.u.'s in distances, angles and torsion angles; correlations between s.u.'s in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell s.u.'s is used for estimating s.u.'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 $F^2 > 2\sigma(F^2)$ 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	*y*	*z*	U_{iso}*/U_{eq}
O1	0.09409 (17)	0.35073 (16)	0.8889 (4)	0.0597 (7)
O2	0.11627 (17)	0.51070 (16)	1.0184 (3)	0.0530 (6)
S1	0.13873 (6)	0.44073 (6)	0.88946 (13)	0.0402 (2)
Cl1	0.37936 (7)	0.67877 (7)	0.45078 (14)	0.0597 (3)
Br1	0.26467 (3)	0.30924 (3)	0.61701 (6)	0.0772 (2)

C1	0.2700 (2)	0.4257 (2)	0.9480 (5)	0.0353 (8)
C2	0.3192 (3)	0.4646 (2)	1.1197 (5)	0.0501 (9)
H2	0.2842	0.5022	1.1912	0.060*
C3	0.4190 (3)	0.4482 (3)	1.1847 (6)	0.0648 (11)
H3	0.4509	0.4743	1.3000	0.078*
C4	0.4715 (3)	0.3937 (3)	1.0807 (6)	0.0626 (11)
H4	0.5389	0.3829	1.1258	0.075*
C5	0.4252 (3)	0.3548 (2)	0.9097 (6)	0.0527 (10)
H5	0.4611	0.3183	0.8380	0.063*
C6	0.3248 (2)	0.3706 (2)	0.8458 (5)	0.0419 (8)
C7	0.1417 (2)	0.5706 (2)	0.6229 (4)	0.0313 (7)
C8	0.2332 (2)	0.5803 (2)	0.5710 (4)	0.0362 (8)
H8	0.2742	0.5286	0.5697	0.043*
C9	0.2643 (2)	0.6666 (2)	0.5209 (5)	0.0373 (8)
C10	0.2038 (3)	0.7433 (2)	0.5235 (4)	0.0398 (8)
H10	0.2252	0.8016	0.4911	0.048*
C11	0.1118 (2)	0.7335 (2)	0.5742 (4)	0.0391 (8)
H11	0.0712	0.7854	0.5745	0.047*
C12	0.0789 (2)	0.6470 (2)	0.6248 (4)	0.0292 (7)
N1	0.1089 (2)	0.48048 (18)	0.6746 (4)	0.0380 (7)
HN1	0.091 (2)	0.443 (2)	0.595 (5)	0.046*
N2	−0.0166 (2)	0.6362 (2)	0.6676 (4)	0.0428 (8)
HN2A	−0.045 (3)	0.689 (2)	0.687 (5)	0.051*
HN2B	−0.021 (3)	0.597 (2)	0.750 (5)	0.051*

Atomic displacement parameters (Å^2)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
O1	0.0480 (14)	0.0428 (15)	0.088 (2)	−0.0138 (13)	0.0117 (13)	0.0216 (13)
O2	0.0536 (15)	0.0621 (16)	0.0470 (15)	0.0154 (13)	0.0193 (12)	−0.0013 (12)
S1	0.0373 (5)	0.0376 (5)	0.0473 (5)	−0.0003 (4)	0.0122 (4)	0.0064 (4)
Cl1	0.0463 (6)	0.0695 (7)	0.0655 (7)	−0.0078 (5)	0.0160 (5)	0.0115 (5)
Br1	0.0876 (4)	0.0665 (3)	0.0700 (3)	0.0282 (2)	−0.0049 (2)	−0.0302 (2)
C1	0.0377 (19)	0.0259 (18)	0.043 (2)	−0.0002 (15)	0.0094 (16)	0.0059 (14)
C2	0.053 (2)	0.052 (2)	0.044 (2)	0.008 (2)	0.0050 (18)	−0.0004 (17)
C3	0.062 (3)	0.071 (3)	0.054 (3)	0.001 (2)	−0.009 (2)	−0.006 (2)
C4	0.042 (2)	0.065 (3)	0.077 (3)	0.006 (2)	0.003 (2)	0.012 (2)
C5	0.048 (2)	0.051 (2)	0.062 (3)	0.009 (2)	0.016 (2)	0.0096 (19)
C6	0.044 (2)	0.033 (2)	0.049 (2)	0.0027 (17)	0.0091 (17)	0.0018 (15)
C7	0.0335 (19)	0.0278 (18)	0.0318 (18)	−0.0037 (16)	0.0040 (14)	0.0002 (13)
C8	0.040 (2)	0.0309 (19)	0.038 (2)	0.0035 (16)	0.0072 (15)	0.0028 (14)
C9	0.0369 (19)	0.043 (2)	0.0308 (19)	−0.0014 (17)	0.0046 (14)	0.0013 (14)
C10	0.052 (2)	0.032 (2)	0.034 (2)	−0.0057 (18)	0.0023 (17)	0.0065 (14)
C11	0.048 (2)	0.034 (2)	0.0329 (19)	0.0083 (18)	0.0013 (16)	−0.0009 (14)
C12	0.0305 (18)	0.0313 (18)	0.0250 (17)	0.0009 (16)	0.0029 (13)	−0.0030 (13)
N1	0.0424 (17)	0.0304 (16)	0.0391 (17)	−0.0034 (14)	0.0021 (13)	−0.0018 (12)
N2	0.0429 (19)	0.040 (2)	0.046 (2)	0.0065 (16)	0.0081 (15)	−0.0001 (14)

Geometric parameters (Å, º)

O1—S1	1.429 (2)	C5—H5	0.9300
O2—S1	1.429 (2)	C7—C8	1.375 (4)
S1—N1	1.605 (3)	C7—C12	1.395 (4)
S1—C1	1.776 (3)	C7—N1	1.438 (4)
Cl1—C9	1.743 (3)	C8—C9	1.377 (4)
Br1—C6	1.892 (3)	C8—H8	0.9300
C1—C6	1.383 (4)	C9—C10	1.379 (4)
C1—C2	1.392 (4)	C10—C11	1.376 (4)
C2—C3	1.375 (5)	C10—H10	0.9300
C2—H2	0.9300	C11—C12	1.390 (4)
C3—C4	1.366 (5)	C11—H11	0.9300
C3—H3	0.9300	C12—N2	1.402 (4)
C4—C5	1.377 (5)	N1—HN1	0.78 (3)
C4—H4	0.9300	N2—HN2A	0.87 (3)
C5—C6	1.380 (4)	N2—HN2B	0.82 (3)
O1—S1—O2	119.70 (16)	C8—C7—C12	121.0 (3)
O1—S1—N1	106.66 (16)	C8—C7—N1	120.0 (3)
O2—S1—N1	108.00 (14)	C12—C7—N1	119.0 (3)
O1—S1—C1	107.58 (14)	C7—C8—C9	119.9 (3)
O2—S1—C1	105.30 (15)	C7—C8—H8	120.0
N1—S1—C1	109.34 (15)	C9—C8—H8	120.0
C6—C1—C2	117.8 (3)	C8—C9—C10	120.1 (3)
C6—C1—S1	124.6 (3)	C8—C9—Cl1	120.1 (3)
C2—C1—S1	117.2 (3)	C10—C9—Cl1	119.8 (3)
C3—C2—C1	120.7 (3)	C11—C10—C9	120.0 (3)
C3—C2—H2	119.7	C11—C10—H10	120.0
C1—C2—H2	119.7	C9—C10—H10	120.0
C4—C3—C2	120.4 (4)	C10—C11—C12	120.9 (3)
C4—C3—H3	119.8	C10—C11—H11	119.6
C2—C3—H3	119.8	C12—C11—H11	119.6
C3—C4—C5	120.4 (4)	C11—C12—C7	118.1 (3)
C3—C4—H4	119.8	C11—C12—N2	120.9 (3)
C5—C4—H4	119.8	C7—C12—N2	120.9 (3)
C4—C5—C6	119.1 (3)	C7—N1—S1	121.7 (2)
C4—C5—H5	120.4	C7—N1—HN1	120 (3)
C6—C5—H5	120.4	S1—N1—HN1	115 (3)
C5—C6—C1	121.6 (3)	C12—N2—HN2A	114 (2)
C5—C6—Br1	116.7 (3)	C12—N2—HN2B	116 (3)
C1—C6—Br1	121.6 (2)	HN2A—N2—HN2B	112 (3)
HN1—N1—S1—C1	97 (3)	C6—C1—S1—N1	−57.7 (3)
HN1—N1—S1—O1	−19 (3)	C6—C1—S1—O1	57.8 (3)
C7—N1—S1—O2	50.2 (3)		

Hydrogen-bond geometry (Å, º)

D—H⋯A	D—H	H⋯A	D⋯A	D—H⋯A
N1—H*N*1⋯N2[i]	0.78 (3)	2.26 (3)	3.022 (4)	166 (3)
N2—H*N*2*A*⋯O1[ii]	0.87 (3)	2.45 (3)	3.258 (4)	154 (3)

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