

Acta Crystallographica Section E

Structure Reports

Online

ISSN 1600-5368

(R)-4-[2-(Methylsulfanyl)pyrimidin-4-yl]-1-(tetrahydrofuran-3-yl)-1H-pyrazol-5-amine

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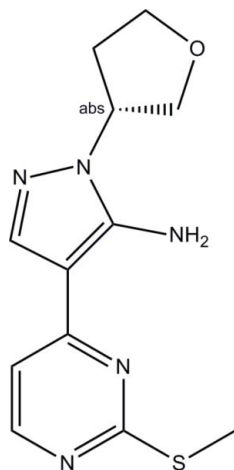
Received 26 February 2009; accepted 27 February 2009

Key indicators: single-crystal X-ray study; $T = 208$ K; mean $\sigma(\text{C}-\text{C}) = 0.002$ Å; R factor = 0.041; wR factor = 0.115; data-to-parameter ratio = 17.4.

The title compound, $\text{C}_{12}\text{H}_{15}\text{N}_5\text{OS}$, was obtained by reaction of 2-(2-(methylthio)pyrimidin-4-yl)-3-oxopropanenitrile with (tetrahydrofuran-3-yl)hydrazine dihydrochloride, and the racemic product was subsequently separated by chiral chromatography (first peak; $[\alpha]_{\text{D}}^{20} = +51.3^\circ$). The chiral center at the substituted atom of the tetrahydrofuranyl group has an *R*-configuration. The pyrimidine and pyrazolyl rings are almost coplanar, their mean planes forming a dihedral angle of $6.4(1)^\circ$. One of the H atoms of the amino group participates in an intramolecular hydrogen bond with the pyrimidine N atom in position 3. The second H atom is involved in an intermolecular hydrogen bond, which links the molecules into an infinite chain.

Related literature

For the structure of a related compound with a methyl-substituted amino group, see: Liu *et al.* (2009).



Experimental

Crystal data

$\text{C}_{12}\text{H}_{15}\text{N}_5\text{OS}$
 $M_r = 277.35$
 Orthorhombic, $P2_12_12$
 $a = 15.479(2)$ Å
 $b = 7.1217(10)$ Å
 $c = 11.7802(17)$ Å
 $V = 1298.6(3)$ Å³
 $Z = 4$
 Mo $K\alpha$ radiation
 $\mu = 0.25$ mm⁻¹
 $T = 208$ K
 $0.20 \times 0.20 \times 0.20$ mm

Data collection

Bruker D8 APEXII CCD area-detector diffractometer
 Absorption correction: multi-scan (SADABS; Bruker, 2001)
 $T_{\text{min}} = 0.844$, $T_{\text{max}} = 0.952$
 6570 measured reflections
 3025 independent reflections
 2844 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.043$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.041$
 $wR(F^2) = 0.115$
 $S = 1.07$
 3025 reflections
 174 parameters
 H-atom parameters constrained
 $\Delta\rho_{\text{max}} = 0.24$ e Å⁻³
 $\Delta\rho_{\text{min}} = -0.35$ e Å⁻³
 Absolute structure: Flack (1983),
 1180 Friedel pairs
 Flack parameter: $-0.05(8)$

Table 1

Hydrogen-bond geometry (Å, °).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$\text{N3}-\text{H3A}\cdots\text{N4}^i$	0.87	2.19	2.9731 (19)	150
$\text{N3}-\text{H3B}\cdots\text{N5}$	0.87	2.28	2.8616 (19)	124

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

Data collection: APEX2 (Bruker, 2004); cell refinement: SAINT (Bruker, 2004); data reduction: SAINT; program(s) used to solve structure: SIR2004 (Burla *et al.*, 2005); program(s) used to refine structure: SHELXL97 (Sheldrick, 2008); molecular graphics: ORTEP-32 (Farrugia, 1997); software used to prepare material for publication: WinGX (Farrugia, 1999).

Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: TK2382).

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supporting information

Acta Cryst. (2009). E65, o697 [doi:10.1107/S160053680900734X]

(R)-4-[2-(Methylsulfanyl)pyrimidin-4-yl]-1-(tetrahydrofuran-3-yl)-1H-pyrazol-5-amine

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S1. Comment

The title compound was obtained by reaction of 2-(2-(methylthio)pyrimidin-4-yl)-3-oxopropanenitrile with (tetrahydrofuran-3-yl)hydrazine dihydrochloride. The racemic product was then separated with the help of chiral chromatography; the title compound, (I), was collected as the earlier fraction, when eluted with methanol using the Chiralpak column (99% ee; $[\alpha]_D^{20} = +51.3^\circ$).

The present X-ray study unambiguously established the *R* configuration of the chiral center at the C3 atom (Fig. 1).

The pyrimidine and pyrazolyl rings lie approximately in one plane; the dihedral angle formed by their mean planes is equal to $6.4 (1)^\circ$. The orientation of the tetrahydrofurane ring can be characterized by the dihedral angle $99.6 (1)^\circ$ formed by the pyrazolyl plane with the C2—C3—C4 plane.

The molecular geometry of (I) is similar to that of related compound with a methyl substituent at the amino group (Liu *et al.*, 2009). However, the crystal packing is substantially different as (I) has one additional H atom capable of H-bond formation. Indeed, while the H3A atom forms an intramolecular H-bond with the N5 atom of the pyrimidine ring similar to that observed in methyl-substituted structure, the H3B atom is involved in intermolecular H-bonding, which links molecules into infinite chains running along the *a* axis (Fig. 2; Table 2).

S2. Experimental

To a suspension of 2-(2-(methylthio)pyrimidin-4-yl)-3-oxopropanenitrile (13.5 g, 70.0 mmol) in AcOH (100 ml) was added (tetrahydrofuran-3-yl)hydrazine dihydrochloride (12.3 g, 70.0 mmol), and the resulting orange mixture was heated at 80°C under nitrogen for 3 h. Acetic acid was removed and the orange solid residue was partitioned between aqueous Na_2CO_3 (200 ml) and EtOAc (400 ml). The mixture was refluxed for 30 min. The separated organic layer was washed with brine, dried over sodium sulfate and concentrated to give the crude product as a brown gum (16.82 g, 87%). The brown gum (8.32 g) was purified by flash chromatography using 30–70% EtOAc in hexane to afford a yellow solid (5.96 g).

The part of the product thus obtained (4.85 g) was subjected to chiral chromatography on Chiralpak AS—H 21.2 x 250 mm column with 35% MeOH in CO_2 at 140 bar as eluent (flow = 55 ml/min; UV detection at 260 nm). Two fractions corresponding to each of the enantiomers (Peak1 and Peak2) were collected and evaporated to dryness; the specific rotation $[\alpha]_D^{20}$ was measured in CH_2Cl_2 solution and yielded the values of $+51.3^\circ$ and -52.1° , respectively. The enantiomer collected as Peak 1 was recrystallized from EtOAc/hexane to yield colorless single crystals.

S3. Refinement

All H atoms were placed in geometrically calculated positions (C—H 0.94 Å, 0.97 Å, 0.98 Å, and 0.99 Å for aromatic-, methyl-, methylene- and methine-H atoms, respectively; N—H 0.87 Å) and included in the refinement in the riding model approximation. The $U_{\text{iso}}(\text{H})$ values were set to $1.2U_{\text{eq}}$ of the carrying atom except for $1.5U_{\text{eq}}$ for methyl-H atoms.

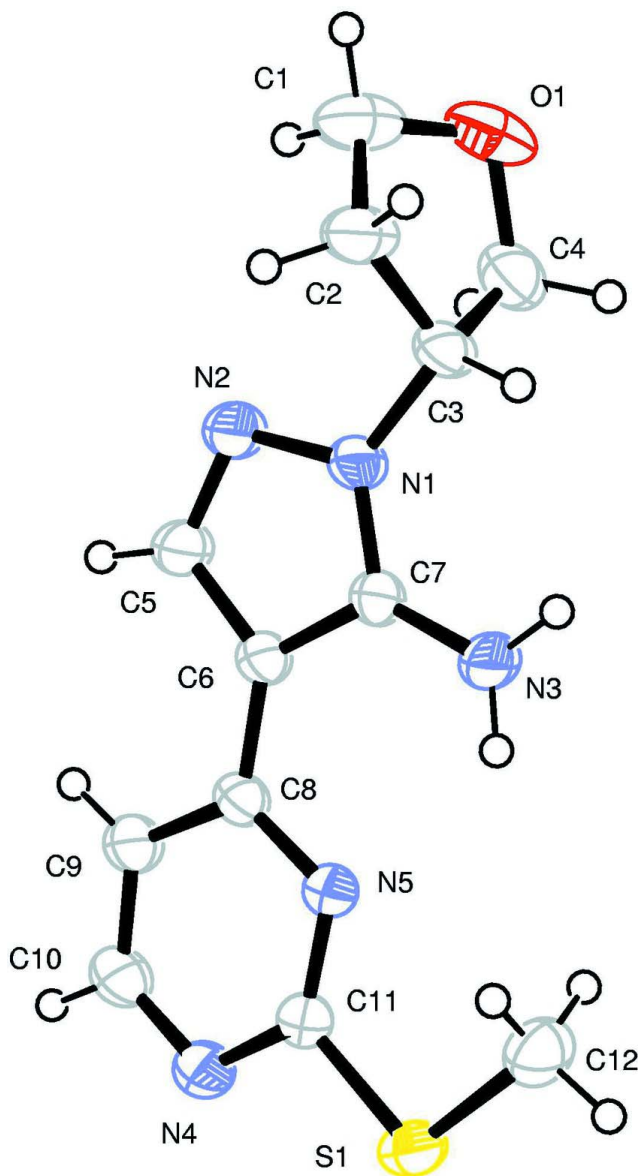
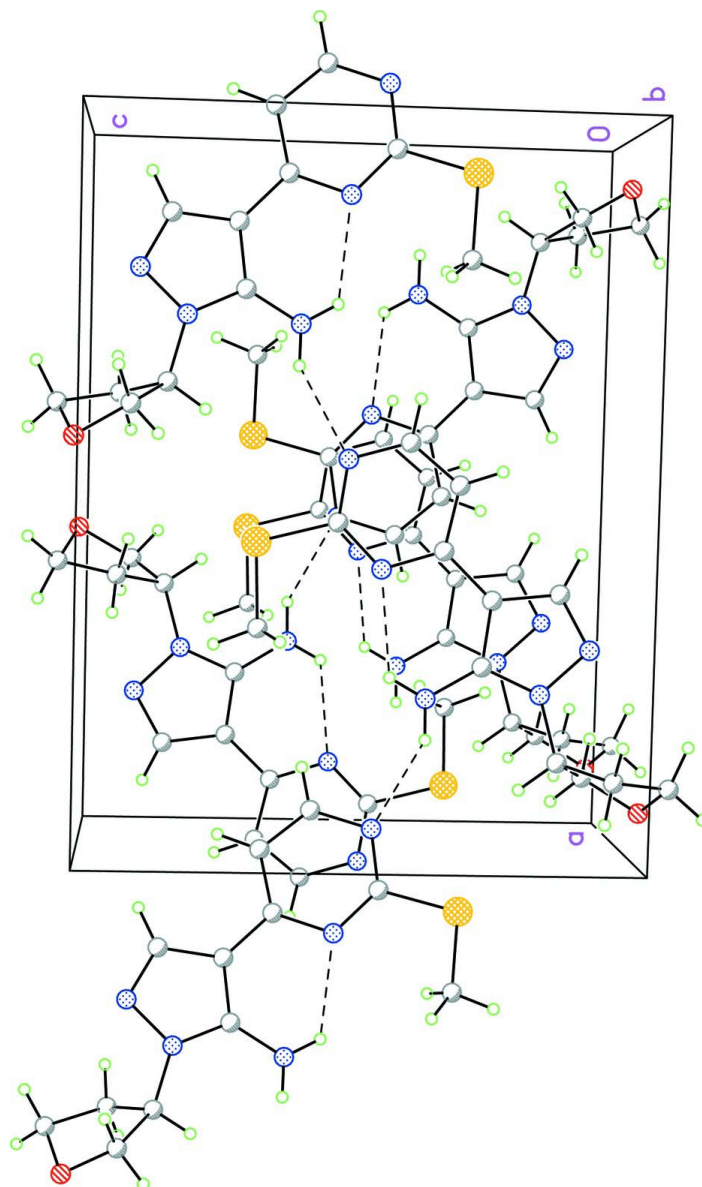


Figure 1

Molecular structure of (I), showing 50% probability displacement ellipsoids and atom numbering scheme. H atoms are drawn as circles with arbitrary small radius.

**Figure 2**

Crystal packing for (I) viewed down the *b* axis; H-bonds are shown as dashed lines.

(*R*)-4-[2-(Methylsulfonyl)pyrimidin-4-yl]-1-(tetrahydrofuran-3-yl)-1*H*-pyrazol-5-amine

Crystal data

$C_{12}H_{15}N_5OS$

$M_r = 277.35$

Orthorhombic, $P2_12_12$

Hall symbol: $P\ 2\ 2ab$

$a = 15.479\ (2)\ \text{\AA}$

$b = 7.1217\ (10)\ \text{\AA}$

$c = 11.7802\ (17)\ \text{\AA}$

$V = 1298.6\ (3)\ \text{\AA}^3$

$Z = 4$

$F(000) = 584$

$D_x = 1.419\ \text{Mg m}^{-3}$

Mo $K\alpha$ radiation, $\lambda = 0.71073\ \text{\AA}$

Cell parameters from 5004 reflections

$\theta = 2.6\text{--}28.1^\circ$

$\mu = 0.25\ \text{mm}^{-1}$

$T = 208\ \text{K}$

Block, yellow

$0.20 \times 0.20 \times 0.20\ \text{mm}$

Data collection

Bruker D8 APEXII CCD area-detector
diffractometer
Radiation source: fine-focus sealed tube
Graphite monochromator
phi and ω scans
Absorption correction: multi-scan
(*SADABS*; Bruker, 2001)
 $T_{\min} = 0.844$, $T_{\max} = 0.952$

6570 measured reflections
3025 independent reflections
2844 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.043$
 $\theta_{\text{max}} = 28.1^\circ$, $\theta_{\text{min}} = 1.7^\circ$
 $h = -20 \rightarrow 19$
 $k = -4 \rightarrow 9$
 $l = -15 \rightarrow 13$

Refinement

Refinement on F^2
Least-squares matrix: full
 $R[F^2 > 2\sigma(F^2)] = 0.041$
 $wR(F^2) = 0.115$
 $S = 1.07$
3025 reflections
174 parameters
0 restraints
Primary atom site location: structure-invariant
direct methods
Secondary atom site location: difference Fourier
map

Hydrogen site location: inferred from
neighbouring sites
H-atom parameters constrained
 $w = 1/[\sigma^2(F_o^2) + (0.0703P)^2 + 0.0815P]$
where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} = 0.001$
 $\Delta\rho_{\text{max}} = 0.24 \text{ e } \text{\AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.35 \text{ e } \text{\AA}^{-3}$
Extinction correction: *SHELXL* (Sheldrick,
2008), $F_c^* = kF_c[1 + 0.001x F_c^2 \lambda^3 / \sin(2\theta)]^{-1/4}$
Extinction coefficient: 0.058 (5)
Absolute structure: Flack (1983), 1180 Friedel
pairs
Absolute structure parameter: -0.05 (8)

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 (\AA^2)

	<i>x</i>	<i>y</i>	<i>z</i>	$U_{\text{iso}}^*/U_{\text{eq}}$
C1	0.61092 (15)	0.3862 (4)	1.04598 (18)	0.0592 (6)
H1A	0.6660	0.3550	1.0825	0.071*
H1B	0.5758	0.4600	1.0989	0.071*
C2	0.62567 (13)	0.4931 (3)	0.93597 (14)	0.0471 (4)
H2A	0.6760	0.5761	0.9418	0.057*
H2B	0.5748	0.5677	0.9154	0.057*
C3	0.64143 (10)	0.3354 (3)	0.85008 (15)	0.0414 (4)
H3	0.6054	0.3562	0.7818	0.050*
C4	0.61086 (12)	0.1571 (3)	0.91240 (18)	0.0514 (5)
H4A	0.5721	0.0835	0.8639	0.062*
H4B	0.6603	0.0785	0.9334	0.062*
C5	0.86860 (11)	0.3275 (3)	0.84766 (15)	0.0456 (4)
H5	0.9228	0.3341	0.8835	0.055*

C6	0.85782 (9)	0.3006 (3)	0.72974 (14)	0.0355 (4)
C7	0.76781 (9)	0.3006 (2)	0.71461 (13)	0.0341 (3)
C8	0.92276 (9)	0.2767 (2)	0.64376 (13)	0.0341 (3)
C9	1.01122 (10)	0.2623 (3)	0.66996 (14)	0.0427 (4)
H9	1.0308	0.2671	0.7454	0.051*
C10	1.06733 (10)	0.2412 (3)	0.58192 (16)	0.0466 (4)
H10	1.1264	0.2289	0.5987	0.056*
C11	0.95801 (10)	0.2531 (3)	0.45560 (14)	0.0371 (3)
C12	0.81445 (13)	0.2818 (3)	0.31648 (16)	0.0526 (5)
H12A	0.7888	0.1785	0.3583	0.079*
H12B	0.7917	0.2833	0.2398	0.079*
H12C	0.8006	0.3993	0.3539	0.079*
N1	0.73257 (8)	0.3241 (2)	0.81741 (12)	0.0393 (3)
N2	0.79452 (9)	0.3423 (3)	0.90197 (12)	0.0488 (4)
N3	0.72268 (9)	0.2815 (3)	0.61696 (12)	0.0493 (4)
H3A	0.6665	0.2841	0.6182	0.059*
H3B	0.7498	0.2667	0.5529	0.059*
N4	1.04322 (9)	0.2367 (3)	0.47231 (13)	0.0453 (4)
N5	0.89635 (8)	0.2704 (2)	0.53396 (11)	0.0341 (3)
O1	0.56646 (9)	0.2206 (3)	1.01145 (14)	0.0630 (5)
S1	0.92940 (3)	0.25258 (9)	0.31179 (4)	0.05191 (18)

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C1	0.0580 (12)	0.0835 (15)	0.0362 (10)	0.0152 (11)	0.0142 (8)	0.0072 (10)
C2	0.0412 (9)	0.0661 (12)	0.0340 (8)	0.0096 (8)	0.0063 (7)	0.0034 (8)
C3	0.0248 (7)	0.0669 (11)	0.0325 (8)	0.0036 (7)	0.0002 (6)	0.0017 (8)
C4	0.0343 (8)	0.0675 (12)	0.0523 (11)	-0.0037 (8)	0.0026 (7)	0.0040 (10)
C5	0.0288 (7)	0.0790 (13)	0.0290 (7)	-0.0006 (8)	-0.0025 (6)	-0.0024 (8)
C6	0.0258 (7)	0.0512 (9)	0.0293 (7)	-0.0007 (6)	-0.0009 (5)	0.0000 (7)
C7	0.0269 (7)	0.0473 (8)	0.0282 (7)	0.0005 (6)	-0.0020 (5)	-0.0004 (6)
C8	0.0262 (6)	0.0443 (8)	0.0320 (7)	-0.0002 (6)	0.0010 (5)	0.0008 (6)
C9	0.0277 (7)	0.0655 (11)	0.0350 (7)	0.0007 (7)	-0.0029 (6)	0.0006 (9)
C10	0.0259 (7)	0.0684 (11)	0.0456 (9)	0.0031 (9)	0.0023 (6)	-0.0035 (9)
C11	0.0315 (7)	0.0471 (8)	0.0327 (7)	-0.0020 (7)	0.0027 (5)	-0.0045 (8)
C12	0.0438 (9)	0.0754 (13)	0.0385 (9)	0.0067 (9)	-0.0061 (7)	-0.0041 (10)
N1	0.0254 (6)	0.0642 (9)	0.0282 (6)	0.0003 (6)	-0.0011 (5)	-0.0007 (6)
N2	0.0290 (6)	0.0884 (12)	0.0290 (7)	-0.0003 (7)	-0.0043 (5)	-0.0034 (8)
N3	0.0284 (6)	0.0917 (13)	0.0278 (6)	0.0010 (7)	-0.0043 (5)	-0.0065 (8)
N4	0.0293 (6)	0.0657 (9)	0.0408 (7)	-0.0002 (7)	0.0045 (5)	-0.0076 (9)
N5	0.0287 (6)	0.0435 (7)	0.0300 (6)	-0.0016 (5)	0.0020 (4)	-0.0026 (6)
O1	0.0460 (8)	0.0826 (11)	0.0604 (9)	0.0041 (8)	0.0233 (6)	0.0185 (8)
S1	0.0394 (2)	0.0852 (4)	0.0311 (2)	-0.0016 (2)	0.00439 (15)	-0.0075 (2)

Geometric parameters (Å, °)

C1—O1	1.425 (3)	C7—N1	1.339 (2)
C1—C2	1.520 (3)	C7—N3	1.353 (2)
C1—H1A	0.9800	C8—N5	1.357 (2)
C1—H1B	0.9800	C8—C9	1.407 (2)
C2—C3	1.531 (3)	C9—C10	1.361 (2)
C2—H2A	0.9800	C9—H9	0.9400
C2—H2B	0.9800	C10—N4	1.344 (2)
C3—N1	1.4644 (18)	C10—H10	0.9400
C3—C4	1.541 (3)	C11—N5	1.3334 (19)
C3—H3	0.9900	C11—N4	1.339 (2)
C4—O1	1.428 (3)	C11—S1	1.7510 (17)
C4—H4A	0.9800	C12—S1	1.792 (2)
C4—H4B	0.9800	C12—H12A	0.9700
C5—N2	1.317 (2)	C12—H12B	0.9700
C5—C6	1.412 (2)	C12—H12C	0.9700
C5—H5	0.9400	N1—N2	1.3888 (18)
C6—C7	1.4046 (19)	N3—H3A	0.8700
C6—C8	1.437 (2)	N3—H3B	0.8700
O1—C1—C2	104.11 (19)	N1—C7—C6	106.83 (13)
O1—C1—H1A	110.9	N3—C7—C6	128.32 (15)
C2—C1—H1A	110.9	N5—C8—C9	119.98 (14)
O1—C1—H1B	110.9	N5—C8—C6	117.70 (13)
C2—C1—H1B	110.9	C9—C8—C6	122.32 (14)
H1A—C1—H1B	109.0	C10—C9—C8	117.50 (15)
C1—C2—C3	102.70 (18)	C10—C9—H9	121.2
C1—C2—H2A	111.2	C8—C9—H9	121.2
C3—C2—H2A	111.2	N4—C10—C9	123.87 (14)
C1—C2—H2B	111.2	N4—C10—H10	118.1
C3—C2—H2B	111.2	C9—C10—H10	118.1
H2A—C2—H2B	109.1	N5—C11—N4	127.69 (15)
N1—C3—C2	111.55 (15)	N5—C11—S1	119.28 (12)
N1—C3—C4	112.07 (16)	N4—C11—S1	113.03 (12)
C2—C3—C4	103.93 (14)	S1—C12—H12A	109.5
N1—C3—H3	109.7	S1—C12—H12B	109.5
C2—C3—H3	109.7	H12A—C12—H12B	109.5
C4—C3—H3	109.7	S1—C12—H12C	109.5
O1—C4—C3	106.03 (18)	H12A—C12—H12C	109.5
O1—C4—H4A	110.5	H12B—C12—H12C	109.5
C3—C4—H4A	110.5	C7—N1—N2	112.28 (13)
O1—C4—H4B	110.5	C7—N1—C3	129.58 (14)
C3—C4—H4B	110.5	N2—N1—C3	118.13 (13)
H4A—C4—H4B	108.7	C5—N2—N1	104.20 (14)
N2—C5—C6	112.69 (15)	C7—N3—H3A	120.0
N2—C5—H5	123.7	C7—N3—H3B	120.0
C6—C5—H5	123.7	H3A—N3—H3B	120.0

C7—C6—C5	104.00 (14)	C11—N4—C10	114.37 (14)
C7—C6—C8	127.19 (14)	C11—N5—C8	116.57 (13)
C5—C6—C8	128.81 (14)	C1—O1—C4	105.25 (15)
N1—C7—N3	124.85 (14)	C11—S1—C12	102.76 (8)

Hydrogen-bond geometry (Å, °)

<i>D—H...A</i>	<i>D—H</i>	<i>H...A</i>	<i>D...A</i>	<i>D—H...A</i>
N3—H3A...N4 ⁱ	0.87	2.19	2.9731 (19)	150
N3—H3B...N5	0.87	2.28	2.8616 (19)	124

Symmetry code: (i) $x-1/2, -y+1/2, -z+1$.