organic compounds

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N-Methylpyrrolidine-1-carbothioamide

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Key indicators: single-crystal X-ray study; T = 296 K; mean σ (C–C) = 0.011 Å; R factor = 0.079; wR factor = 0.262; data-to-parameter ratio = 16.4.

There are two independent molecules in the asymmetric unit of the title compound, $C_6H_{12}N_2S$, in which the *N*-methylthioformamide unit and the pyrrolidine ring mean plane are oriented at dihedral angles of 5.9 (5) and 5.9 (4)°. In the crystal, zigzag C(4) chains extending along the *a* axis are formed due to N-H···S hydrogen bonds between alternate arrangements of molecules. The chains are interlinked by C-H···S hydrogen bonds.

Related literature

For a related structure, see: Jiang (2009). For graph-set notation, see: Bernstein *et al.* (1995).



Experimental

 $\begin{array}{l} Crystal \ data \\ {\rm C_6H_{12}N_2S} \\ M_r = 144.25 \\ {\rm Triclinic}, \ P\overline{1} \\ a = 8.616 \ (2) \ {\rm \AA} \\ b = 9.077 \ (2) \ {\rm \AA} \\ c = 10.796 \ (3) \ {\rm \AA} \\ \alpha = 73.725 \ (14)^\circ \\ \beta = 86.656 \ (15)^\circ \end{array}$

 $\gamma = 76.177 \ (16)^{\circ}$ $V = 787.0 \ (3) \ \text{Å}^3$ Z = 4Mo K α radiation $\mu = 0.33 \ \text{mm}^{-1}$ $T = 296 \ \text{K}$ $0.30 \times 0.25 \times 0.20 \ \text{mm}$

Data collection

Bruker Kappa APEXII CCD diffractometer

Absorption correction: multi-scan (SADABS; Bruker, 2005) $T_{\min} = 0.957, T_{\max} = 0.966$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.079$	165 parameters
$wR(F^2) = 0.262$	H-atom parameters constrained
S = 1.04	$\Delta \rho_{\rm max} = 0.43 \text{ e } \text{\AA}^{-3}$
2699 reflections	$\Delta \rho_{\rm min} = -0.33 \ {\rm e} \ {\rm \AA}^{-3}$

9119 measured reflections

 $R_{\rm int} = 0.067$

2699 independent reflections

1385 reflections with $I > 2\sigma(I)$

Table 1

Hydrogen-bond geometry (Å, °).

$D-\mathrm{H}\cdots A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$N1 - H1 \cdot \cdot \cdot S2^{i}$	0.86	2.73	3.472 (5)	145
$N3-H4\cdots S1^{ii}$	0.86	2.64	3.410 (5)	150
$C12-H12B\cdots S1^{iii}$	0.97	2.84	3.765 (5)	159

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

Data collection: *APEX2* (Bruker, 2007); cell refinement: *SAINT* (Bruker, 2007); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *SHELXL97* (Sheldrick, 2008); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997) and *PLATON* (Spek, 2009); software used to prepare material for publication: *WinGX* (Farrugia, 1999) and *PLATON*.

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: BQ2355).

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N-Methylpyrrolidine-1-carbothioamide

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S1. Comment

The title compound (I), (Fig. 1) has been synthesized as a derivative. The crystal structure of *N*-phenylpyrrolidine-1carbothioamide related to this structure (I) has been published previously (Jiang, 2009). In (I), two molecules in the asymmetric unit are present, which differ slightly from each other geometrically. In one molecule, the *N*-methylthioformamide moiety A (C1/N1/C2/S1) and the pyrrolidine ring B (N2/C3–C6) are planar with r.m.s. deviation of 0.0010 Å and 0.0360 Å, respectively. The dihedral angle between A/B is 5.88 (46)°. In second molecule, the similar groups C (C7/N3/C8/S2) and D (N4/C9–C12) are also planar with r.m.s. deviation of 0.0032 Å and 0.0839 Å, respectively and the dihedral angle between C/D is 5.92 (39)°. Both molecules are interlinked through classical intramolecular H–bonding of N–H···S type (Table 1, Fig. 2) with *C*(4) chains (Bernstein *et al.*, 1995) to form zigzag infinite one-dimensional polymeric chains extending along the *a*-axis. The polymeric chains are interlinked due to C–H···S type of H–bonding (Table 1, Fig. 2).

S2. Experimental

A solution of pyrrolidine (0.36 g, 5.00 mmol) in CH₃CN (3 ml) was added dropwise to a stirred solution of methyl isothiocyanate (0.47 ml, 5.50 mmol) in CH₃CN (10 ml, anhydrous) under cooling in an ice-bath to keep the reaction temperature below 283 K. The ice-bath was removed and stirring was continued at room temperature for 2 h to furnish a yellow-colored solution. The reaction mixture was extracted with ethylacetate and subjected to column chromatography to get the colorless product in 67% yield and then recrystalized with methanol to get colorless prisms of (I).

S3. Refinement

The H-atoms were positioned geometrically (C–H = 0.96–0.97 Å, N—H = 0.86 Å) and refined as riding with $U_{iso}(H) = xU_{eq}(C, N)$, where x = 1.5 for methyl and x = 1.2 for all other H-atoms.



Figure 1

View of the title compound with the atom numbering scheme. The thermal ellipsoids are drawn at the 50% probability level.



Figure 2

The partial packing (*PLATON*; Spek, 2009) which shows that molecules are interlinked to form polymeric chains along the *a*-axis. The H-atoms not involved in H-bonding are omitted for clarity.

N-Methylpyrrolidine-1-carbothioamide

Crystal data
$C_6H_{12}N_2S$
$M_r = 144.25$
Triclinic, P1
Hall symbol: -P 1
<i>a</i> = 8.616 (2) Å
<i>b</i> = 9.077 (2) Å
c = 10.796 (3) Å
$\alpha = 73.725 \ (14)^{\circ}$
$\beta = 86.656 \ (15)^{\circ}$
$\gamma = 76.177 \ (16)^{\circ}$
V = 787.0 (3) Å ³

Z = 4 F(000) = 312 $D_x = 1.217 \text{ Mg m}^{-3}$ Mo K α radiation, $\lambda = 0.71073 \text{ Å}$ Cell parameters from 1204 reflections $\theta = 2.4-26.0^{\circ}$ $\mu = 0.33 \text{ mm}^{-1}$ T = 296 KPrism, colorless $0.30 \times 0.25 \times 0.20 \text{ mm}$ Data collection

Bruker Kappa APEXII CCD diffractometer Radiation source: fine-focus sealed tube Graphite monochromator Detector resolution: 8.10 pixels mm ⁻¹ ω scans Absorption correction: multi-scan (<i>SADABS</i> ; Bruker, 2005) $T_{\min} = 0.957, T_{\max} = 0.966$	9119 measured reflections 2699 independent reflections 1385 reflections with $I > 3\sigma(I)$ $R_{int} = 0.067$ $\theta_{max} = 25.0^{\circ}, \theta_{min} = 2.4^{\circ}$ $h = -10 \rightarrow 10$ $k = -11 \rightarrow 11$ $l = -13 \rightarrow 13$
Refinement	
Refinement on F^2 Least-squares matrix: full $R[F^2 > 2\sigma(F^2)] = 0.079$ $wR(F^2) = 0.262$ S = 1.04 2699 reflections 165 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 $w = 1/[\sigma^2(F_o^2) + (0.1268P)^2 + 0.3916P]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 0.43$ e Å ⁻³ $\Delta\rho_{min} = -0.33$ e Å ⁻³

Special details

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds 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	$U_{ m iso}$ */ $U_{ m eq}$	
C1	0.4239 (8)	0.1340 (7)	0.3083 (6)	0.101 (2)	
H1A	0.3186	0.1209	0.3350	0.151*	
H1B	0.4965	0.0862	0.3803	0.151*	
H1C	0.4586	0.0844	0.2406	0.151*	
C2	0.3360 (6)	0.3972 (7)	0.1594 (5)	0.0699 (14)	
C3	0.2574 (7)	0.6685 (8)	0.0191 (5)	0.0913 (18)	
H3A	0.2961	0.6484	-0.0622	0.110*	
H3B	0.1437	0.6732	0.0248	0.110*	
C4	0.2906 (12)	0.8143 (10)	0.0304 (9)	0.153 (3)	
H4A	0.3452	0.8611	-0.0463	0.184*	
H4B	0.1906	0.8885	0.0365	0.184*	
C5	0.3868 (11)	0.7860 (8)	0.1411 (7)	0.123 (3)	
H5A	0.3265	0.8361	0.2030	0.148*	
H5B	0.4801	0.8297	0.1166	0.148*	
C6	0.4365 (7)	0.6143 (7)	0.1987 (5)	0.0846 (17)	
H6A	0.4123	0.5869	0.2900	0.101*	

H6B	0.5503	0.5764	0.1880	0.101*
C7	0.0612 (8)	0.8849 (7)	0.7020 (6)	0.0905 (18)
H7A	0.1661	0.8968	0.7156	0.136*
H7B	-0.0082	0.9109	0.7695	0.136*
H7C	0.0199	0.9542	0.6202	0.136*
C8	0.1664 (6)	0.6492 (6)	0.6253 (4)	0.0668 (14)
C9	0.2534 (7)	0.4014 (7)	0.5615 (5)	0.0791 (15)
H9A	0.3672	0.3846	0.5754	0.095*
H9B	0.2292	0.4497	0.4704	0.095*
C10	0.2012 (10)	0.2515 (9)	0.6076 (8)	0.126 (3)
H10A	0.1297	0.2437	0.5447	0.151*
H10B	0.2930	0.1627	0.6193	0.151*
C11	0.1210(11)	0.2487 (8)	0.7269 (7)	0.125 (3)
H11A	0.1933	0.1864	0.7980	0.150*
H11B	0.0307	0.2009	0.7314	0.150*
C12	0.0651 (7)	0.4120 (6)	0.7365 (5)	0.0768 (15)
H12A	-0.0481	0.4515	0.7165	0.092*
H12B	0.0846	0.4183	0.8222	0.092*
N1	0.4210 (5)	0.2971 (5)	0.2626 (4)	0.0771 (13)
H1	0.4775	0.3348	0.3037	0.093*
N2	0.3437 (5)	0.5463 (6)	0.1280 (4)	0.0739 (12)
N3	0.0697 (5)	0.7250 (5)	0.7032 (4)	0.0746 (12)
H4	0.0100	0.6740	0.7564	0.089*
N4	0.1603 (5)	0.5002 (5)	0.6404 (4)	0.0677 (11)
S1	0.22218 (19)	0.3304 (2)	0.07310 (14)	0.0932 (6)
S2	0.28575 (19)	0.74016 (18)	0.51593 (13)	0.0881 (6)

Atomic displacement parameters $(Å^2)$

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
C1	0.122 (5)	0.099 (5)	0.083 (4)	-0.026 (4)	-0.013 (4)	-0.024 (4)
C2	0.071 (3)	0.102 (4)	0.040 (3)	-0.018 (3)	0.003 (2)	-0.027 (3)
C3	0.087 (4)	0.116 (5)	0.060 (3)	-0.020 (4)	-0.009 (3)	-0.007 (3)
C4	0.202 (10)	0.116 (6)	0.127 (7)	-0.046 (6)	-0.058 (7)	0.007 (5)
C5	0.180 (8)	0.100 (5)	0.095 (5)	-0.040 (5)	-0.017 (5)	-0.025 (4)
C6	0.102 (4)	0.107 (5)	0.052 (3)	-0.030 (4)	-0.004 (3)	-0.027 (3)
C7	0.115 (5)	0.085 (4)	0.078 (4)	-0.024 (3)	0.000 (3)	-0.032 (3)
C8	0.071 (3)	0.088 (4)	0.042 (3)	-0.018 (3)	-0.014 (2)	-0.016 (3)
C9	0.081 (4)	0.100 (4)	0.061 (3)	-0.013 (3)	-0.001 (3)	-0.035 (3)
C10	0.154 (7)	0.104 (5)	0.136 (7)	-0.036 (5)	0.023 (6)	-0.061 (5)
C11	0.187 (8)	0.088 (5)	0.109 (6)	-0.044 (5)	0.038 (5)	-0.036 (4)
C12	0.093 (4)	0.096 (4)	0.050 (3)	-0.038 (3)	0.000 (3)	-0.021 (3)
N1	0.088 (3)	0.093 (3)	0.054 (3)	-0.023 (3)	-0.011 (2)	-0.022 (2)
N2	0.081 (3)	0.098 (3)	0.041 (2)	-0.020 (3)	-0.009(2)	-0.017 (2)
N3	0.090 (3)	0.086 (3)	0.055 (3)	-0.031 (2)	0.008 (2)	-0.023 (2)
N4	0.083 (3)	0.080(3)	0.045 (2)	-0.021 (2)	-0.001 (2)	-0.023 (2)
S 1	0.0962 (12)	0.1408 (15)	0.0594 (9)	-0.0374 (10)	-0.0056 (8)	-0.0447 (9)
S2	0.0935 (12)	0.1108 (13)	0.0601 (9)	-0.0357 (9)	0.0018 (8)	-0.0135 (8)

Geometric parameters (Å, °)

C1—N1	1.418 (7)	C7—H7A	0.9600
C1—H1A	0.9600	С7—Н7В	0.9600
C1—H1B	0.9600	C7—H7C	0.9600
C1—H1C	0.9600	C8—N4	1.330 (6)
C2—N2	1.316(6)	C8—N3	1.358 (6)
C2—N1	1.346 (6)	C8—S2	1.688 (5)
C2—S1	1.705 (5)	C9—N4	1.475 (6)
C3—C4	1.457 (9)	C9—C10	1.480 (9)
C3—N2	1.464 (7)	С9—Н9А	0.9700
С3—НЗА	0.9700	С9—Н9В	0.9700
С3—Н3В	0.9700	C10—C11	1.422 (10)
C4—C5	1.423 (10)	C10—H10A	0.9700
C4—H4A	0.9700	C10—H10B	0.9700
C4—H4B	0.9700	C11—C12	1.476 (8)
С5—С6	1.473 (8)	C11—H11A	0.9700
C5—H5A	0.9700	C11—H11B	0.9700
С5—Н5В	0.9700	C12—N4	1.462 (6)
C6—N2	1.474 (6)	C12—H12A	0.9700
С6—Н6А	0.9700	C12—H12B	0.9700
C6—H6B	0.9700	N1—H1	0.8600
C7—N3	1.432 (6)	N3—H4	0.8600
	100 5		115 0 (5)
NI-CI-HIA	109.5	N4 - C8 - N3	115.8 (5)
NI-CI-HIB	109.5	N4 - C8 - S2	122.6 (4)
HIA—CI—HIB	109.5	N3 - C8 - S2	121.6 (4)
NI-CI-HIC	109.5	N4—C9—C10	103.7 (5)
HIA—CI—HIC	109.5	N4—C9—H9A	111.0
HIB—CI—HIC	109.5	C10—C9—H9A	111.0
N2—C2—N1	118.2 (4)	N4—C9—H9B	111.0
N2—C2—S1	121.6 (4)	C10—C9—H9B	111.0
NI-C2-SI	120.2 (4)	H9A—C9—H9B	109.0
C4 - C3 - N2	104.4 (5)	C11—C10—C9	108.4 (6)
C4—C3—H3A	110.9	C11— $C10$ — $H10A$	110.0
N2—C3—H3A	110.9	C9—C10—H10A	110.0
C4—C3—H3B	110.9	C11—C10—H10B	110.0
N2—C3—H3B	110.9	C9—C10—H10B	110.0
H3A—C3—H3B	108.9	HI0A—CI0—HI0B	108.4
C5—C4—C3	111.2 (6)	C10-C11-C12	108.9 (6)
C5—C4—H4A	109.4	C10—C11—H11A	109.9
C3—C4—H4A	109.4	C12—C11—H11A	109.9
C3—C4—H4B	109.4	CIO-CII-HIIB	109.9
C3—C4—H4B	109.4	C12—C11—H11B	109.9
H4A—C4—H4B	108.0	HIIA—CII—HIIB	108.3
C4—C5—C6	108.3 (6)	N4—C12—C11	103.6 (5)
C4—C5—H5A	110.0	N4—C12—H12A	111.0
C6-C5-H5A	110.0	C11—C12—H12A	111.0

C4—C5—H5B	110.0	N4—C12—H12B	111.0
С6—С5—Н5В	110.0	C11—C12—H12B	111.0
H5A—C5—H5B	108.4	H12A—C12—H12B	109.0
C5—C6—N2	104.9 (5)	C2—N1—C1	124.6 (5)
С5—С6—Н6А	110.8	C2—N1—H1	117.7
N2—C6—H6A	110.8	C1—N1—H1	117.7
С5—С6—Н6В	110.8	C2—N2—C3	124.3 (5)
N2—C6—H6B	110.8	C2—N2—C6	125.1 (4)
H6A—C6—H6B	108.8	C3—N2—C6	110.6 (5)
N3—C7—H7A	109.5	C8—N3—C7	123.9 (5)
N3—C7—H7B	109.5	C8—N3—H4	118.0
H7A—C7—H7B	109.5	C7—N3—H4	118.0
N3—C7—H7C	109.5	C8—N4—C12	125.5 (4)
H7A—C7—H7C	109.5	C8—N4—C9	123.2 (4)
H7B—C7—H7C	109.5	C12—N4—C9	111.3 (4)
N2-C3-C4-C5	-1.7 (10)	C4—C3—N2—C6	-4.0 (7)
C3—C4—C5—C6	6.6 (11)	C5—C6—N2—C2	-170.9 (6)
C4—C5—C6—N2	-8.6 (8)	C5—C6—N2—C3	7.8 (6)
N4—C9—C10—C11	-15.4 (8)	N4—C8—N3—C7	179.3 (5)
C9—C10—C11—C12	21.4 (10)	S2—C8—N3—C7	-1.0 (7)
C10-C11-C12-N4	-17.9 (8)	N3—C8—N4—C12	-3.0 (7)
N2-C2-N1-C1	179.6 (5)	S2—C8—N4—C12	177.3 (4)
S1—C2—N1—C1	-0.3 (7)	N3—C8—N4—C9	178.1 (4)
N1—C2—N2—C3	-179.7 (5)	S2—C8—N4—C9	-1.6 (6)
S1—C2—N2—C3	0.3 (7)	C11—C12—N4—C8	-170.9 (5)
N1-C2-N2-C6	-1.1 (8)	C11—C12—N4—C9	8.1 (6)
S1—C2—N2—C6	178.8 (4)	C10—C9—N4—C8	-176.9 (5)
C4—C3—N2—C2	174.7 (6)	C10-C9-N4-C12	4.1 (6)

Hydrogen-bond geometry (Å, °)

<i>D</i> —H··· <i>A</i>	D—H	Н…А	D··· A	D—H··· A	
N1— $H1$ ···S2 ⁱ	0.86	2.73	3.472 (5)	145	
N3—H4···S1 ⁱⁱ	0.86	2.64	3.410 (5)	150	
C12—H12 <i>B</i> ····S1 ⁱⁱⁱ	0.97	2.84	3.765 (5)	159	

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