Acta Crystallographica Section C
Crystal Structure Communications
ISSN 0108-2701

Three 2-(methysulfanyl)nicotinamides

Ligia R. Gomes,[a] John Nicolson Low,[b]* James L. Wardell,[b,c] Alessandra C. Pinheiro,[d] Thais C. N. de Mendonça[d] and Marcus V. N. de Souza[d]

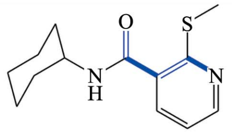
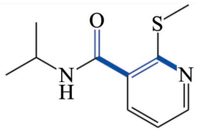
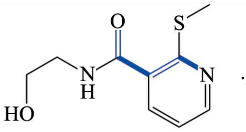
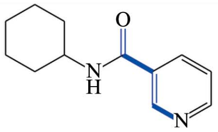
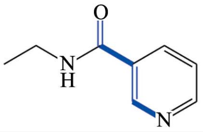
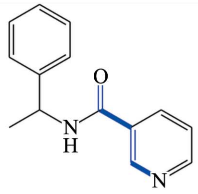
[a]REQUIMTE, Departamento de Química e Bioquímica, Faculdade de Ciências da Universidade do Porto, Rua do Campo Alegre, 687, P-4169-007 Porto, Portugal, [b]Department of Chemistry, University of Aberdeen, Meston Walk, Old Aberdeen AB24 3UE, Scotland, [c]Centro de Desenvolvimento Tecnológico em Saúde (CDTS), Fundação Oswaldo Cruz (FIOCRUZ), Casa Amarela, Campus de Manguinhos, Av. Brasil 4365, 21040-900 Rio de Janeiro, RJ, Brazil, and [d]Instituto de Tecnología em Fármacos–Farmanguinhos, FioCruz–Fundação Oswaldo Cruz, R. Sizenando Nabuco, 100, Manguinhos, 21041-250 Rio de Janeiro, RJ, Brazil
Correspondence e-mail: jnlow111@gmail.com

Received 28 January 2013
Accepted 13 February 2013
Online 16 February 2013

The molecular conformations of three *N*-alkyl-2-(methylsulfanyl)nicotinamide derivatives, namely *N*-cyclohexyl-2-(methylsulfanyl)nicotinamide, $C_{13}H_{18}N_2OS$, (I), *N*-isopropyl-2-(methylsulfanyl)nicotinamide, $C_{10}H_{14}N_2OS$, (II), in which there are two molecules in the asymmetric unit which were chosen to form a hydrogen-bonded pair, and *N*-(2-hydroxyethyl)-2-(methylsulfanyl)nicotinamide dihydrate, $C_9H_{12}N_2O_2S\cdot2H_2O$, (III), are compared with those of four unsubstituted *N*-alkylnicotinamide compounds. The substituted compounds show a higher degree of torsion of the pyridine ring with respect to the amide group than do the unsubstituted compounds, with dihedral angles in the range 40–60° for the former and 20–35° for the latter. In (I) and (II), the supramolecular structure is defined by amide-N to carbonyl-O chains. In (III), the nicotinamide molecules are linked by hydrogen bonds to two water molecules resulting in two linked chains of rings which form the three-dimensional network.

Comment

Tuberculosis (TB) is the second greatest contributor among infectious diseases to adult mortality, causing approximately 1.4 million deaths worldwide in 2010 (WHO, 2010). While heteroaromatic amides, such as nicotinamide (pyridine-3-carboxamide) and pyrazinamide (pyrazine-2-carboxamide), as well as heteroaromatic thioamides, such as thioisonicotinamide (pyridine-4-carbothioamide), are well established anti-TB agents, there is a need for new drugs in particular to combat the emergence of strains resistant to current treatments (de Souza, 2006, 2012; Gonçalves *et al.*, 2012). In continuation of our studies of amidopyridines and related compounds (de Souza *et al.*, 2005; Cuffini *et al.*, 2006; Wardell *et al.*, 2007*a*,*b*, 2008), we now report the structures of the three *N*-alkyl-2-(methylsulfanyl)nicotinamide derivatives, namely *N*-cyclohexyl-2-(methylsulfanyl)nicotinamide, (I), *N*-isopropyl-2-(methylsulfanyl)nicotinamide, (II), and *N*-(2-hydroxyethyl)-2-(methylsulfanyl)nicotinamide dihydrate, (III) (see Scheme below). The Scheme also gives details of four related compounds, (IV)–(VII), and gives details of the dihedral angles (θ) between the amide group and the heterocyclic ring, as well as highlighting their conformation with respect to each other. Compounds (I)–(III) have been synthesized for an anti-TB activity study, the results of which will be published elsewhere.

	Molecule	θ	CSD refcode (Reference)
(I)		39.20 (12)°	This work
(II)		40.8 (6)° 49.6 (6)°	This work
(III)	 ·$2H_2O$	58.79 (7)°	This work
(IV)		22.92 (15)°	YUPBUV (Li, 2010)
(V)		21.7 (2)°	JEPMAS (Srikrishnan & Parthasarathy, 1990)
(VI)		34.1°	MBNICT (Little & Morimoto, 1981)

In (I) (Fig. 1), the cyclohexyl ring adopts a chair conformation. In (II) (Fig. 2), there are two molecules (*A* and *B*) in the asymmetric unit which were chosen to form a hydrogen-bonded pair. The results of a quaternion fit of the non-H atoms with *MOLFIT* in *PLATON* (Mackay, 1984; Spek, 2009) indicate that molecule *B* inverts on to *A*, with a fit rotation angle of −166.88°, and gives r.m.s. deviations of 0.142 (unweighted) and 0.180 Å (weighted) for 14 atoms. Nicotinamide (III) (Fig. 3) crystallizes with two water molecules in the asymmetric unit.

The steric hindrance imposed by the methylsulfanyl substituent at the 2-position of the pyridine ring is reflected, as expected, by a relatively high torsion for this ring with respect to the amide group. Considering that methylsulfanyl is a soft

doi:10.1107/S0108270113004344

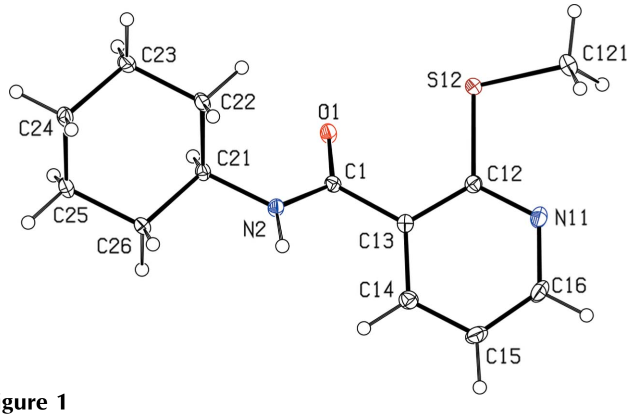


Figure 1
The molecular structure of (I), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level.

acceptor, it is reasonable to assume that conformational changes imposed by the group will be similar in solid and in aqueous environments.

The dihedral angles in compounds (I)–(III) between the mean plane of the heterocyclic ring and that of the amide group (defined by atoms C1, O1 and N2) can be compared with those of similar compounds without the methylsulfanyl substituent on C2 using data obtained from the Cambridge Structural Database (CSD, Version 5.34; Allen, 2002). Relevant compounds are *N*-cyclohexylnicotinamide, (IV) (Li, 2010), which is the nonsubstituted derivative of (I), and *N*-ethylnicotinamide, (V) (Srikrishnan & Parthasarathy, 1990), and (*S*)-*N*-(α-methylbenzyl)nicotinamide, (VI) (Little & Morimoto, 1981), which are similar to (II), as well as *N*-(pyridin-3-ylcarbonyl)glycine, (VII) (Krishnaswamy *et al.*, 1987).

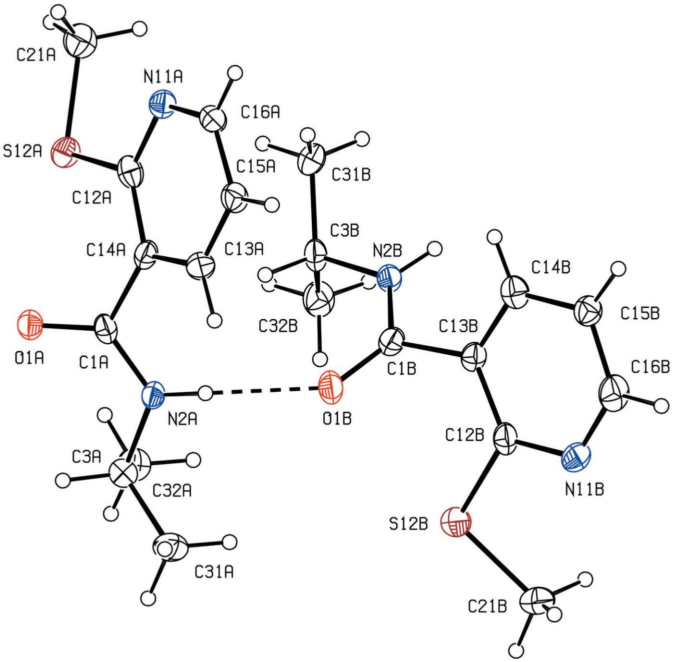


Figure 2
The molecular structure of (II), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level. The dashed bond shows the hydrogen bond linking the two molecules in the asymmetric unit.

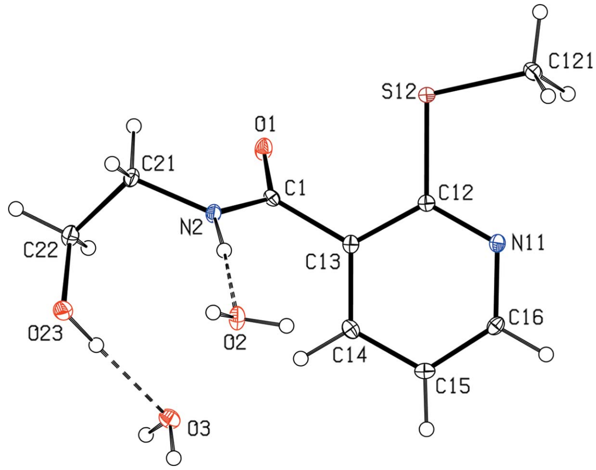


Figure 3
The molecular structure of (III), showing the atom-numbering scheme. Displacement ellipsoids are drawn at the 30% probability level. The dashed lines indicate hydrogen bonds.

Such comparisons show that the methylsulfanyl group affects the degree of twist of the pyridine ring and thus the relative position of the heteroatom with respect to the amide group. These are conformational aspects that may affect the docking to the receptor and thus the pharmacological activity of the substances described here. The values for the dihedral angles between the planes of the amide group and the pyridine rings are given in the Scheme. The dihedral angles, taken in conjunction with the values for the torsion angles about the C1—C11 bond in Tables 1 and 2, clearly indicate that the presence of the methylsulfanyl group results in changes in the orientation of the heterocyclic ring with respect to the amide group. The dihedral angles for the unsubstituted compounds are in the range 20–35°, which have smaller angular values than the range of 40–60° for compounds with the methyl-

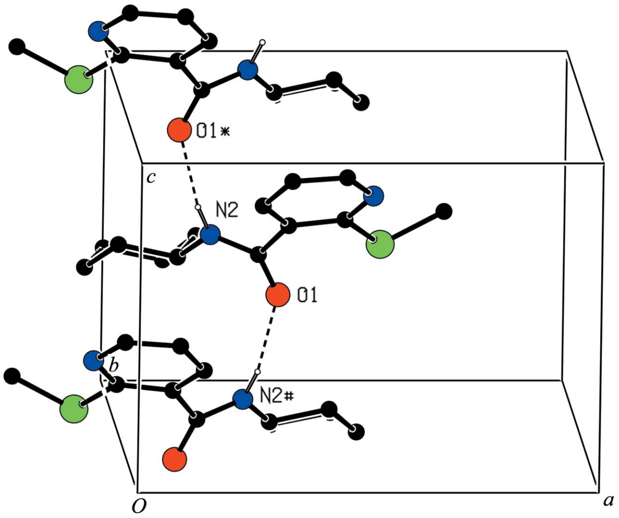


Figure 4
Part of the crystal structure of (I), showing the hydrogen-bonded chain which runs parallel to the *c* axis. Atoms labelled with an asterisk (*) and hash (#) are at the symmetry positions $(-x + \frac{1}{2}, y, z + \frac{1}{2})$ and $(-x + \frac{1}{2}, y, z - \frac{1}{2})$, respectively. H atoms not involved in the hydrogen bonding have been omitted.

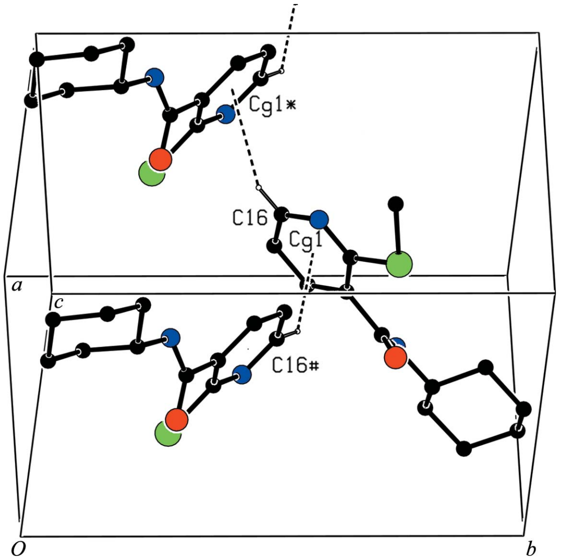


Figure 5
Part of the crystal structure of (I), showing the hydrogen-bonded chain formed by the C—H$\cdots\pi$ interaction. Atoms labelled with an asterisk (*) and hash (#) are at the symmetry positions $(-x + 1, -y + 1, z + \frac{1}{2})$ and $(-x + 1, -y + 1, z - \frac{1}{2})$, respectively. H atoms not involved in hydrogen bonding have been omitted.

sulfanyl substituent. The presence of a methylsulfanyl sustituent at the 2-position also conditions the direction of rotation of the ring. The magnitudes of the torsion angles for compounds (I)–(III) around the C1—C11 bond (Table 1) indicate that in order for the methylsulfanyl group to avoid the proximity of the amide N—H group, a clockwise rotation takes place such that the pyridine heteroatom sits in a *cis* position with respect to the carbonyl O atom. This contrasts

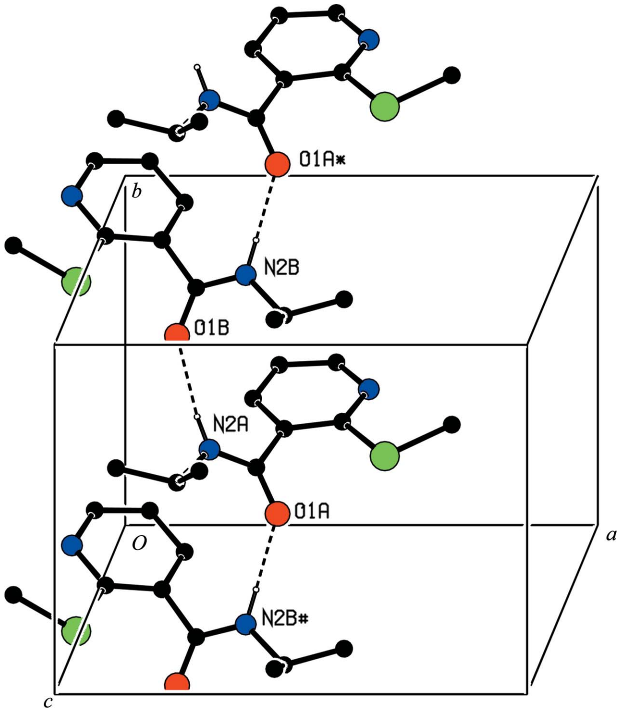


Figure 6
Part of the crystal structure of (II), showing the hydrogen-bonded chain which runs parallel to the *b* axis. Atoms labelled with an asterisk (*) and hash (#) are at the symmetry positions $(x, y + 1, z)$ and $(x, y - 1, z)$, respectively. H atoms not involved in hydrogen bonding have been omitted.

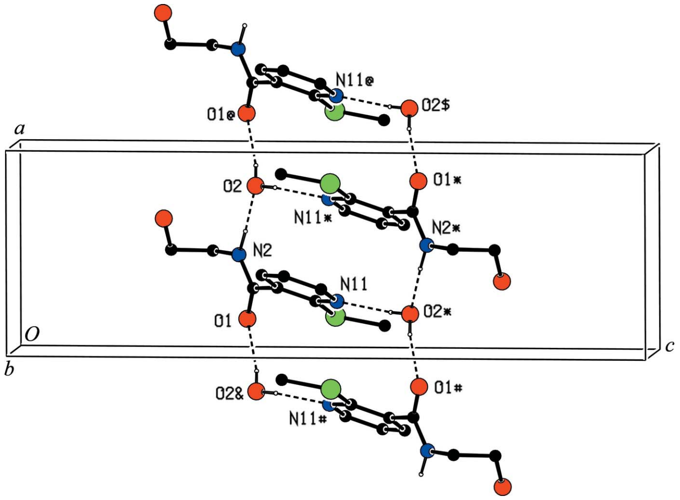


Figure 7
Part of the crystal structure of (III), showing the ladder structure formed by the linking of two centrosymmetric rings. This ladder runs parallel to the *a* axis. Atoms labelled with an asterisk (*), hash (#), dollar sign ($), ampersand (&) and 'at' symbol (@) are at the symmetry positions $(-x + 1, -y + 1, -z + 1)$, $(-x, -y + 1, -z + 1)$, $(x + 1, y, z)$, $(-x + 2, -y + 1, -z + 1)$ and $(x - 1, y, z)$, respectively. H atoms not involved in hydrogen bonding have been omitted.

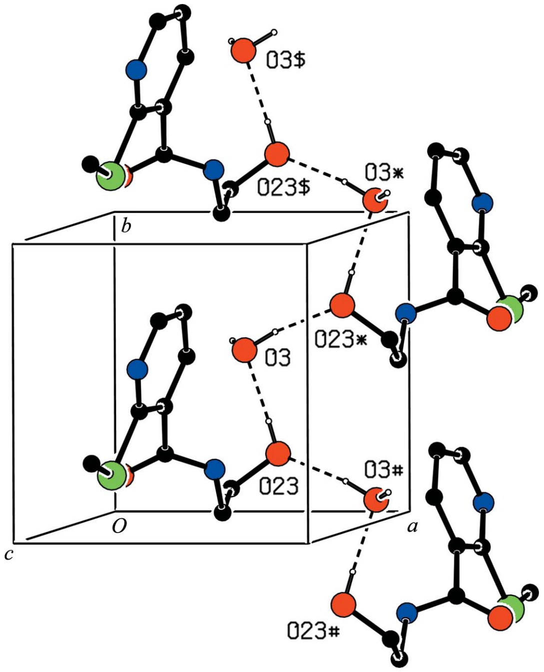


Figure 8
Part of the crystal structure of (III), showing the hydroxy–water hydrogen-bonded chain which runs parallel to the *b* axis. Atoms labelled with an asterisk (*), hash (#) and dollar sign ($) are at the symmetry positions $(-x + \frac{3}{2}, y + \frac{1}{2}, -z + \frac{1}{2})$, $(-x + \frac{3}{2}, y - \frac{1}{2}, -z + \frac{1}{2})$ and $(x, y + 1, z)$, respectively. H atoms not involved in hydrogen bonding have been omitted.

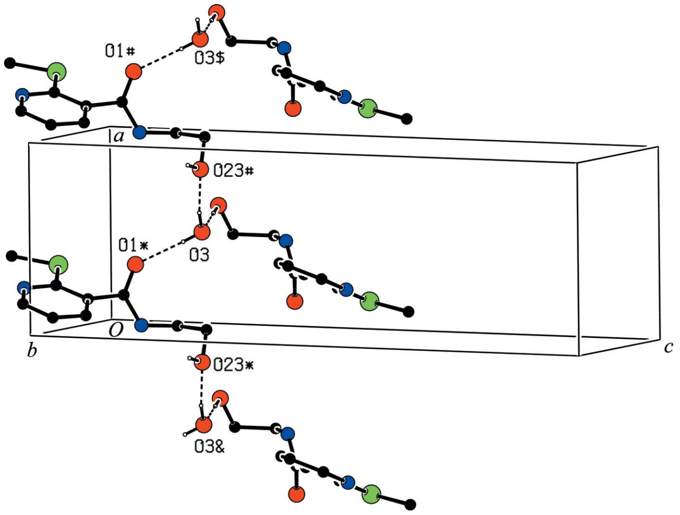


Figure 9
Part of the crystal structure of (III), showing the hydroxy–water hydrogen-bonded chain which runs parallel to the *a* axis. Atoms labelled with an asterisk (*), hash (#), dollar sign ($) and ampersand (&) are at the symmetry positions $(-x+\frac{1}{2}, y+\frac{1}{2}, -z+\frac{1}{2})$, $(-x+\frac{3}{2}, y+\frac{1}{2}, -z+\frac{1}{2})$, $(x+1, y, z)$ and $(x-1, y, z)$, respectively. The pendant molecules at (x, y, z), $(x+1, y, z)$ and $(x-1, y, z)$ are not involved in the chain. H atoms not involved in hydrogen bonding have been omitted.

with the situation in compounds with unsubstituted 2-positions, in which the amide O atom is *trans* with respect to atom C2 of the pyridine ring, as a result of the anticlockwise rotation of the pyridine ring. These differences are highlighted in the Scheme.

The S atom of the methylsulfanyl group is a very weak electron acceptor and is not expected to enter into an intramolecular interaction with the amino H atom of the amide group. Such intramolecular interactions can be observed with strong electron-acceptor substituents at the 2-position of the pyridine ring. In *N*-(2,4-difluorophenyl)-2-[3-(trifluorophenyl)-phenoxy]pyridine-3-carboxamide (CSD refcode; ZIKXEW; Pèpe *et al.*, 1995), there is an intramolecular hydrogen bond between the amide N atom and the phenoxy O atom [N—H = 0.93 (4) Å, H⋯O = 1.76 (4) Å, N⋯O = 2.649 (4) Å and N—H⋯O = 160 (3)°]; the dihedral angle between the mean planes of the pyridine ring and the amide group is 4.6 (4)°.

The main factor affecting the conformation of molecules containing an amide group is the presence of intra- and intermolecular hydrogen bonding. One common supramolecular structure found in compounds with amide groups is the formation of *C*4 chains (Bernstein *et al.*, 1995) *via* intermolecular N—H⋯O═C—NH⋯ hydrogen bonds. Another common supramolecular structure, mentioned below, involves the formation of intermolecular amide–pyridine N—H⋯N hydrogen bonds. While these supramolecular structures are common, they may not occur in the presence of other strong acceptors, *e.g.* the water molecules in (III). All the other structures discussed above contain these *C*4 chains.

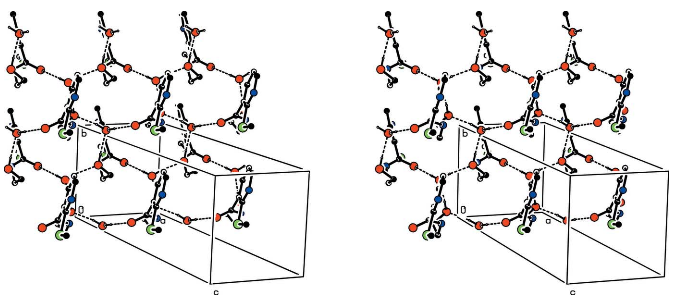


Figure 10
A stereoview showing the structure formed by the combination of the two hydroxy–water hydrogen-bonded chains in (III). This lies in the *ab* plane.

In (I), molecules are linked by N—H⋯O hydrogen bonds to form *C*(4) chains, generated by the glide-plane axis at $x = \frac{1}{4}$ and with translations parallel to the *c* axis (Fig. 4 and Table 3). C16—H16⋯$Cg1^{\rm ii}$ interactions (symmetry code as in Table 3; *Cg*1 is the centroid of the pyridine ring) link these chains into a two-dimensional sheet (Fig. 5). There are no other intermolecular interactions.

In (II), molecules *A* and *B* are linked by N—H⋯O hydrogen bonds within the selected asymmetric unit (Table 4). These pairs are then linked to further pairs of molecules by unit-cell translation along the *b* axis to form a $C_2^2(8)$ chain (Fig. 6). There are no other intermolecular interactions.

In (III), the asymmetric unit was selected so that the N—H and O—H donors formed hydrogen bonds with the water molecules *via* N2—H2⋯O2 and O23—H23⋯O3 hydrogen bonds within that unit (Table 5). Having so many donors and acceptors available leads to a complex supramolecular structure which is best described by considering the several substructures.

In (III), nicotinamide molecules and hydrate atom O2 form two centrosymmetric $R_2^2(16)$ rings (Bernstein *et al.*, 1995), one centred on the centre of symmetry at $(\frac{1}{2}, \frac{1}{2}, \frac{1}{2})$ and the other at $(0, \frac{1}{2}, \frac{1}{2})$. In the first of these, the O2—H2*A*⋯$N11^{\rm iii}$ hydrogen bond links the asymmetric unit and its centrosymmetric counterpart at $(-x+1, -y+1, -z+1)$ to form the ring. In the second, the water molecules at $(-x+1, -y+1, -z+1)$ and $(x-1, y, z)$ act as hydrogen-bond donors *via* H2*A* to atom N11 at (x, y, z) and $(-x+1, -y+1, -z+1)$, respectively, and *via* H2*B* to atom O1 at $(-x+1, -y+1, -z+1)$ and (x, y, z), respectively, to form the ring. These rings alternate within a ladder structure which runs parallel to the *a* axis (Fig. 7). There is a π–π interaction between the pyridine rings in the first of these rings, in which the centroid–centroid distance between these pyridine rings which lie across the centre of symmetry at $(\frac{1}{2}, \frac{1}{2}, \frac{1}{2})$ is 3.5839 (16) Å, the perpendicular distance between the rings is 3.3083 (5) Å and the slippage is 1.378 Å, so supplementing this substructure. Water molecule O3 is hydrogen bonded to atom O23 *via* atom H23 in the asymmetric unit, as mentioned above. The action of the screw axis at $(\frac{3}{4}, y, \frac{1}{4})$ produces a zigzag $C_2^2(4)$ chain, which runs parallel to the *b* axis. Atom O3 acts as a donor *via* H3*A* to atom O23 at $(-x+\frac{3}{2}, y+\frac{1}{2}, -z+\frac{1}{2})$ and this links *via* H23 to atom O3 in the same asymmetric residue unit, so forming the chain (Fig. 8). This water molecule also acts as a hydrogen-bond donor to atoms O1 and O23. $C_2^2(9)$ chains are thus produced along the *a* axis linking molecules at $(-x+\frac{1}{2}, y+\frac{1}{2}, -z+\frac{1}{2})$, $(-x+\frac{3}{2}, y+\frac{1}{2}, -z+\frac{1}{2})$ *etc. via* water molecules at (*x*, *y*,

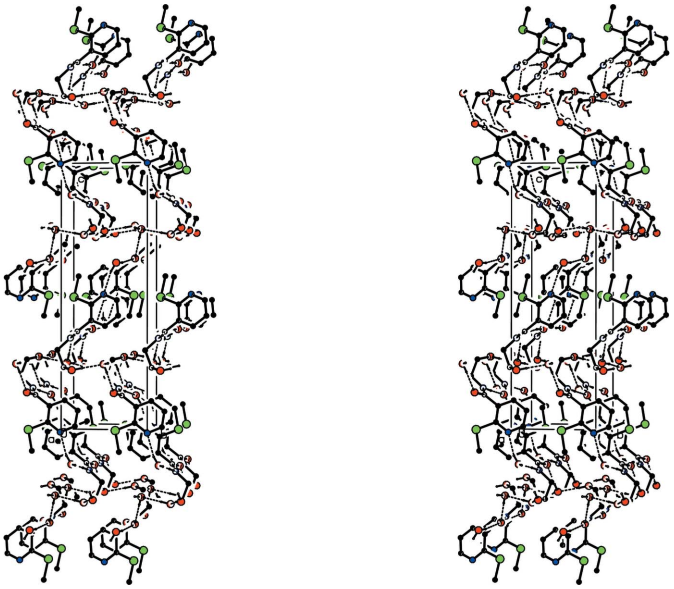


Figure 11
A stereoview of the packing for (III).

z) and at unit-cell translations along the a axis (Fig. 9). These two interactions combine to form a sheet of $R_6^6(20)$ rings (Fig. 10). A packing diagram involving all these substructures is shown in Fig. 11. All potential strong hydrogen-bond donors and acceptors are utilized in the building of the supramolecular structure.

Experimental

The following is a general procedure for the synthesis of *N*-substituted 2-(methylsulfanyl)nicotinamides. A stirred solution of methyl 2-(methylsulfanyl)nicotinate (1 mmol), prepared from 2-mercaptonicotinic acid, methyl iodide and K_2CO_3, and an amine (20 mmol) was refluxed for 24 h. The reaction was concentrated under reduced pressure and the residue was diluted with ethyl acetate, washed with brine, dried over Na_2SO_4, filtered and evaporated. The crude product was purified by column chromatography on silica gel (0–50% ethyl acetate in hexane) affording the *N*-substituted 2-(methylsulfanyl)-nicotinamide derivatives in 60–88% yield. For *N*-cyclohexyl-2-(methylsulfanyl)nicotinamide, (I) (yield: 60%), the crystals used in the structure determination were grown from an ethanol solution. For *N*-isopropyl-2-(methylsulfanyl)nicotinamide (II) (yield: 65%), the crystals used in the structure determination were grown from a methanol solution. For *N*-(2-hydroxyethyl)-2-(methylsulfanyl)nicotinamide, (III) (yield: 88%), the crystals used in the structure determination were grown from a moist ethyl acetate solution.

Compound (I)

Crystal data

$C_{13}H_{18}N_2OS$
$M_r = 250.35$
Orthorhombic, $Pca2_1$
$a = 11.5273\ (9)$ Å
$b = 13.4634\ (10)$ Å
$c = 8.3956\ (6)$ Å
$V = 1302.97\ (17)$ Å^3
$Z = 4$
Mo $K\alpha$ radiation
$\mu = 0.24$ mm^{-1}
$T = 100$ K
$0.26 \times 0.19 \times 0.04$ mm

Table 1
Selected torsion angles (°).

The angles are the equivalent torsion angles for each molecule. In (II), the corresponding atom labels for the two independent molecules end in *A* and *B*.

	(I)	(II*A*)	(II*B*)	(III)
O1—C1—C13—C14	−139.12 (13)	138.7 (6)	−128.7 (7)	−120.22 (14)
N2—C1—C13—C14	39.88 (17)	−40.7 (8)	50.7 (8)	59.14 (16)
O1—C1—C13—C12	38.15 (17)	−40.9 (8)	47.7 (8)	57.58 (17)
N2—C1—C13—C12	−142.85 (11)	139.7 (6)	−132.9 (6)	−123.06 (13)

Table 2
Selected torsion angles (°) for (IV), (V), (VI) and (VII).

The angles are the equivalent torsion angles for each molecule as for the current compounds.

	(IV)	(V)	(VI)	(VII)
O1—C1—C13—C14	22.27 (19)	19.7 (2)	−30.87	−148.37 (18)
N2—C1—C13—C14	−157.12 (12)	−158.21 (16)	149.63	29.5 (3)
O1—C1—C13—C12	−156.49 (13)	−158.93 (18)	146.37	26.6 (3)
N2—C1—C13—C12	−142.85 (18)	23.2 (2)	−36.12	−155.55 (18)

Data collection

Rigaku Saturn724+ (2x2 bin mode) diffractometer
Absorption correction: multi-scan (*CrystalClear-SM Expert*; Rigaku, 2011)
$T_{\min} = 0.942$, $T_{\max} = 0.991$
11531 measured reflections
2731 independent reflections
2657 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.026$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.024$
$wR(F^2) = 0.064$
$S = 1.06$
2731 reflections
156 parameters
1 restraint
H-atom parameters constrained
$\Delta\rho_{\max} = 0.25$ e Å^{-3}
$\Delta\rho_{\min} = -0.15$ e Å^{-3}
Absolute structure: Flack (1983), 1133 Friedel pairs
Flack parameter: 0.06 (5)

Compound (II)

Crystal data

$C_{10}H_{14}N_2OS$
$M_r = 210.29$
Monoclinic, $P2_1/c$
$a = 11.42\ (2)$ Å
$b = 8.580\ (19)$ Å
$c = 23.61\ (5)$ Å
$\beta = 94.15\ (3)°$
$V = 2307\ (8)$ Å^3
$Z = 8$
Synchrotron radiation
$\lambda = 0.68890$ Å
$\mu = 0.25$ mm^{-1}
$T = 100$ K
$0.10 \times 0.03 \times 0.01$ mm

Data collection

CrystalLogic diffractometer
Absorption correction: multi-scan (*CrystalClear-SM Expert*; Rigaku, 2011)
$T_{\min} = 0.975$, $T_{\max} = 0.998$
10806 measured reflections
4493 independent reflections
2445 reflections with $I > 2\sigma(I)$
$R_{\rm int} = 0.150$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.119$
$wR(F^2) = 0.366$
$S = 1.06$
4493 reflections
259 parameters
H-atom parameters constrained
$\Delta\rho_{\max} = 0.67$ e Å^{-3}
$\Delta\rho_{\min} = -0.67$ e Å^{-3}

Table 3
Hydrogen-bond geometry (Å, °) for (I).

*Cg*1 is the centroid of the pyridine ring.

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N2—H2···O1^{i}	0.88	2.01	2.8399 (15)	157
C16—H16···*Cg*1^{ii}	0.95	2.97	3.7489 (18)	141

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

Table 4
Hydrogen-bond geometry (Å, °) for (II).

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N2*A*—H2*A*···O1*B*	0.88	2.02	2.862 (9)	160
N2*B*—H2*B*···O1*A*^{i}	0.88	2.03	2.869 (9)	159

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

Table 5
Hydrogen-bond geometry (Å, °) for (III).

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N2—H2···O2	0.98	1.83	2.8096 (16)	176
O23—H23···O3	0.84	1.85	2.6906 (17)	177
O3—H3*B*···O1^{i}	0.80	2.00	2.7966 (15)	178
O3—H3*A*···O23^{ii}	0.89	1.84	2.7200 (15)	170
O2—H2*A*···N11^{iii}	0.83	2.04	2.8449 (17)	164
C14—H14···O3	0.95	2.37	3.3122 (19)	174
C21—H21*A*···O1	0.99	2.48	2.8208 (17)	100

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

Compound (III)

Crystal data

$C_9H_{12}N_2O_2S\cdot 2H_2O$
$M_r = 248.30$
Monoclinic, $P2_1/n$
$a = 7.194$ (2) Å
$b = 7.285$ (3) Å
$c = 22.388$ (8) Å
$\beta = 90.341$ (5)°
$V = 1173.3$ (7) Å^3
$Z = 4$
Mo $K\alpha$ radiation
$\mu = 0.28$ mm^{-1}
$T = 100$ K
0.26 × 0.12 × 0.05 mm

Data collection

Rigaku Saturn724+ (2x2 bin mode) diffractometer
Absorption correction: multi-scan (*CrystalClear-SM Expert*; Rigaku, 2011)
$T_{min} = 0.931$, $T_{max} = 0.986$
6865 measured reflections
2063 independent reflections
1977 reflections with $I > 2\sigma(I)$
$R_{int} = 0.016$

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.027$
$wR(F^2) = 0.071$
$S = 1.07$
2063 reflections
146 parameters
H-atom parameters constrained
$\Delta\rho_{max} = 0.25$ e Å^{-3}
$\Delta\rho_{min} = -0.24$ e Å^{-3}

In (I) and (II), H atoms were treated as riding atoms, with aromatic C—H = 0.95 Å and N—H = 0.88 Å, with $U_{iso}(H) = 1.2U_{eq}$(C,N), and methyl C—H = 0.98 Å, with $U_{iso}(H) = 1.5U_{eq}$(C). In (III), H atoms were treated as riding atoms, with aromatic C—H = 0.95 Å and $U_{iso}(H) = 1.2U_{eq}$(C), and methyl C—H = 0.98 Å and $U_{iso}(H) = 1.5U_{eq}$(C). The positions of the H atoms attached to N, hydroxy O and the water O atoms were located in difference maps and allowed to ride at these positions, with $U_{iso}(H) = 1.2U_{eq}$(N) and $1.5U_{eq}$(O).

The positions of the H atoms attached to N atoms, methyl groups, hydroxy groups and water molecules were checked in difference maps during and after the refinement was complete.

The crystals of (II) were very small (0.10 × 0.03 × 0.01 mm) and even though data were collected by synchrotron radiation it was not possible to collect a complete observable data set.

For all compounds, data collection: *CrystalClear-SM Expert* (Rigaku, 2011); cell refinement: *CrystalClear-SM Expert*; data reduction: *CrystalClear-SM Expert*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 2008); program(s) used to refine structure: *OSCAIL* (McArdle *et al.*, 2004) and *SHELXL97* (Sheldrick, 2008); molecular graphics: *PLATON* (Spek, 2009); software used to prepare material for publication: *OSCAIL* and *SHELXL97*.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: SK3475). Services for accessing these data are described at the back of the journal.

References

Allen, F. H. (2002). *Acta Cryst.* B**58**, 380–388.
Bernstein, J., Davis, R. E., Shimoni, I. & Chang, N.-L. (1995). *Angew. Chem. Int. Ed. Engl.* **34**, 1555–1573.
Cuffini, S., Glidewell, C., Low, J. N., de Oliveira, A. G., de Souza, M. V. N., Vasconcelos, T. R. A., Wardell, S. M. S. V. & Wardell, J. L. (2006). *Acta Cryst.* B**62**, 651–665.
Flack, H. D. (1983). *Acta Cryst.* A**39**, 876–881.
Gonçalves, R. S. B., Kaiser, C. R., Lourenço, M. C. S., Bezerra, F. A. F. M., de Souza, M. N., Wardell, J. L., Wardell, S. M. S. V., Henriques, M., das, G. M. de O. & Costa, T. (2012). *Bioorg. Med. Chem.* **20**, 243–248.
Krishnaswamy, S., Pattabhi, V. & Guru Row, T. N. (1987). *Acta Cryst.* C**43**, 728–729.
Li, N. (2010). *Acta Cryst.* E**66**, o1759.
Little, R. G. & Morimoto, C. (1981). *Acta Cryst.* B**37**, 1637–1640.
Mackay, A. L. (1984). *Acta Cryst.* A**40**, 165–166.
McArdle, P., Gilligan, K., Cunningham, D., Dark, R. & Mahon, M. (2004). *CrystEngComm*, **6**, 303–309.
Pèpe, G., Pfefer, G., Boistelle, R. & Marchal, P. (1995). *Acta Cryst.* C**51**, 2671–2672.
Rigaku (2011). *CrystalClear-SM Expert*. Rigaku Corporation, Tokyo, Japan.
Sheldrick, G. M. (2008). *Acta Cryst.* A**64**, 112–122.
Souza, M. V. N. de (2006). *Recent Pat. Antiinfect. Drug Discov.* **1**, 33–44.
Souza, M. V. N. de (2012). *Mycobact. Diseases*, **2**, e107. doi:10.4172/2161-1068.1000e107.
Souza, M. V. N. de, Vasconcelos, T. R. A., Wardell, S. M. S. V., Wardell, J. L., Low, J. N. & Glidewell, C. (2005). *Acta Cryst.* C**61**, o204–o208.
Spek, A. L. (2009). *Acta Cryst.* D**65**, 148–155.
Srikrishnan, T. & Parthasarathy, R. (1990). *Acta Cryst.* C**46**, 1723–1725.
Wardell, S. M. S. V., de Souza, M. V. N., Vasconcelos, T. R. A., Ferreira, M. L., Wardell, J. L., Low, J. N. & Glidewell, C. (2008). *Acta Cryst.* B**64**, 84–100.
Wardell, S. M. S. V., de Souza, M. V. N., Wardell, J. L., Low, J. N. & Glidewell, C. (2007*a*). *Acta Cryst.* B**63**, 879–895.
Wardell, S. M. S. V., de Souza, M. V. N., Wardell, J. L., Low, J. N. & Glidewell, C. (2007*b*). *Acta Cryst.* B**63**, 101–110.
WHO (2010). *Global Tuberculosis Control*. Report. Geneva: World Health Organization.

supplementary materials

Acta Cryst. (2013). C**69**, 293-298   [doi:10.1107/S0108270113004344]

Three 2-(methysulfanyl)nicotinamides

Ligia R. Gomes, John Nicolson Low, James L. Wardell, Alessandra C. Pinheiro, Thais C. N. de Mendonça and Marcus V. N. de Souza

(I) *N*-Cyclohexyl-2-(methylsulfanyl)nicotinamide

Crystal data

$C_{13}H_{18}N_2OS$
$M_r = 250.35$
Orthorhombic, $Pca2_1$
Hall symbol: P 2c -2ac
$a = 11.5273$ (9) Å
$b = 13.4634$ (10) Å
$c = 8.3956$ (6) Å
$V = 1302.97$ (17) Å^3
$Z = 4$

$F(000) = 536$
$D_x = 1.276$ Mg m^{-3}
Mo $K\alpha$ radiation, $\lambda = 0.71075$ Å
Cell parameters from 11307 reflections
$\theta = 3.0–27.6°$
$\mu = 0.24$ mm^{-1}
$T = 100$ K
Plate, colourless
0.26 × 0.19 × 0.04 mm

Data collection

Rigaku Saturn724+ (2x2 bin mode) diffractometer
Radiation source: Rotating Anode
Confocal monochromator
Detector resolution: 28.5714 pixels mm^{-1}
profile data from ω–scans
Absorption correction: multi-scan (*CrystalClear-SM Expert*; Rigaku, 2011)
$T_{min} = 0.942$, $T_{max} = 0.991$

11531 measured reflections
2731 independent reflections
2657 reflections with $I > 2\sigma(I)$
$R_{int} = 0.026$
$\theta_{max} = 27.5°$, $\theta_{min} = 3.0°$
$h = -14 \rightarrow 14$
$k = -17 \rightarrow 16$
$l = -10 \rightarrow 9$

Refinement

Refinement on F^2
Least-squares matrix: full
$R[F^2 > 2\sigma(F^2)] = 0.024$
$wR(F^2) = 0.064$
$S = 1.06$
2731 reflections
156 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-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0369P)^2 + 0.1954P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} = 0.001$
$\Delta\rho_{max} = 0.25$ e Å^{-3}
$\Delta\rho_{min} = -0.15$ e Å^{-3}
Absolute structure: Flack, (1983)
Flack parameter: 0.06 (5)

Special details

Experimental. N-Cyclohexyl-2-(methylsulfanyl)nicotinamide (I). NMR^{1}H (400MHz, DMSO-d$_6$) δ (ppm): 8.50 (1H, dd; J = 4.8 and J = 1.7, H6), 8.27 (1H, d, J = 7.7 Hz, NH), 7.68 (1H, dd, J = 7.5 and J = 1.7 Hz, H4), 7.16 (1H, dd, J = 7.5 and J = 4.8Hz, H5), 3.70 (1H, m; CHNH), 2.43 (3H, s; (CH$_3$)S), 1.8-1.2 (10H, m, Cy).
NMR ^{13}C (100MHz, DMSO-d$_6$) δ (ppm): 165.2,157.2, 149.6, 134.8, 130.6, 118.6, 48.1, 32.2, 25.2, 24.6, 12.9. IR (cm^{-1}; KBr): 3231 (NH), 1643 (CON) MS/ESI: [M+Na]: 273.1

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	*y*	*z*	$U_{\rm iso}$*/$U_{\rm eq}$
S12	0.57915 (2)	0.73272 (2)	0.50452 (5)	0.01785 (8)
O1	0.35932 (8)	0.73433 (7)	0.35091 (12)	0.0187 (2)
N2	0.21218 (8)	0.75002 (7)	0.52819 (14)	0.0164 (2)
H2	0.1828	0.7291	0.6189	0.020*
N11	0.55072 (9)	0.58148 (10)	0.70269 (16)	0.0249 (3)
C1	0.31404 (10)	0.71397 (9)	0.47992 (16)	0.0144 (2)
C12	0.49487 (10)	0.64461 (9)	0.60905 (16)	0.0162 (3)
C13	0.37295 (10)	0.64360 (9)	0.59140 (15)	0.0152 (2)
C14	0.31125 (11)	0.57267 (9)	0.67571 (17)	0.0200 (3)
H14	0.2292	0.5698	0.6669	0.024*
C15	0.36892 (13)	0.50619 (11)	0.7725 (2)	0.0274 (3)
H15	0.3280	0.4570	0.8310	0.033*
C16	0.48803 (14)	0.51356 (12)	0.7814 (2)	0.0314 (4)
H16	0.5281	0.4677	0.8474	0.038*
C121	0.71530 (12)	0.72066 (11)	0.6085 (2)	0.0292 (3)
H12A	0.7017	0.7247	0.7235	0.044*
H12B	0.7676	0.7743	0.5757	0.044*
H12C	0.7505	0.6564	0.5827	0.044*
C21	0.14793 (10)	0.82314 (9)	0.43501 (16)	0.0149 (2)
H21	0.1579	0.8071	0.3195	0.018*
C22	0.19572 (10)	0.92726 (9)	0.46497 (18)	0.0198 (3)
H22A	0.1877	0.9440	0.5793	0.024*
H22B	0.2792	0.9290	0.4376	0.024*
C23	0.13070 (11)	1.00374 (10)	0.36499 (19)	0.0216 (3)
H23A	0.1615	1.0709	0.3876	0.026*
H23B	0.1429	0.9896	0.2505	0.026*
C24	0.00155 (11)	1.00077 (10)	0.40255 (17)	0.0187 (3)
H24A	−0.0400	1.0478	0.3321	0.022*
H24B	−0.0112	1.0219	0.5141	0.022*
C25	−0.04705 (10)	0.89657 (10)	0.37903 (18)	0.0203 (3)
H25A	−0.0435	0.8793	0.2645	0.024*
H25B	−0.1296	0.8958	0.4117	0.024*

C26	0.01919 (10)	0.81846 (9)	0.47470 (17)	0.0190 (3)
H26A	0.0078	0.8304	0.5900	0.023*
H26B	−0.0112	0.7515	0.4493	0.023*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S12	0.01405 (13)	0.01819 (14)	0.02131 (17)	−0.00011 (9)	0.00024 (15)	0.00287 (15)
O1	0.0153 (4)	0.0281 (5)	0.0128 (5)	0.0022 (3)	0.0006 (4)	0.0030 (4)
N2	0.0152 (5)	0.0206 (5)	0.0133 (6)	0.0026 (3)	0.0016 (4)	0.0032 (4)
N11	0.0199 (5)	0.0276 (6)	0.0272 (7)	0.0055 (4)	−0.0005 (5)	0.0090 (5)
C1	0.0141 (5)	0.0168 (5)	0.0122 (7)	−0.0016 (4)	−0.0013 (4)	−0.0010 (5)
C12	0.0163 (6)	0.0163 (6)	0.0161 (6)	0.0019 (4)	0.0018 (5)	−0.0005 (5)
C13	0.0159 (5)	0.0158 (6)	0.0140 (7)	0.0018 (4)	−0.0005 (5)	−0.0023 (5)
C14	0.0194 (6)	0.0203 (6)	0.0203 (7)	0.0004 (5)	0.0026 (5)	0.0006 (6)
C15	0.0280 (7)	0.0225 (7)	0.0316 (9)	0.0016 (5)	0.0072 (6)	0.0120 (6)
C16	0.0279 (8)	0.0319 (9)	0.0344 (9)	0.0081 (6)	0.0007 (6)	0.0189 (7)
C121	0.0161 (6)	0.0332 (8)	0.0383 (10)	−0.0020 (5)	−0.0055 (6)	0.0065 (7)
C21	0.0129 (5)	0.0185 (6)	0.0131 (6)	0.0018 (4)	0.0002 (4)	−0.0001 (5)
C22	0.0118 (5)	0.0209 (6)	0.0267 (8)	−0.0002 (4)	−0.0020 (5)	−0.0010 (5)
C23	0.0143 (6)	0.0198 (6)	0.0306 (8)	0.0001 (5)	0.0028 (5)	0.0021 (6)
C24	0.0137 (5)	0.0214 (6)	0.0210 (7)	0.0039 (4)	0.0018 (5)	0.0001 (5)
C25	0.0121 (5)	0.0244 (6)	0.0243 (7)	0.0009 (5)	−0.0023 (5)	0.0002 (5)
C26	0.0121 (5)	0.0206 (6)	0.0244 (8)	−0.0012 (4)	0.0004 (5)	0.0024 (5)

Geometric parameters (Å, º)

S12—C12	1.7668 (13)	C121—H12C	0.9800
S12—C121	1.8030 (15)	C21—C26	1.5222 (15)
O1—C1	1.2332 (16)	C21—C22	1.5271 (17)
N2—C1	1.3336 (15)	C21—H21	1.0000
N2—C21	1.4593 (16)	C22—C23	1.5253 (18)
N2—H2	0.8800	C22—H22A	0.9900
N11—C12	1.3247 (17)	C22—H22B	0.9900
N11—C16	1.340 (2)	C23—C24	1.5223 (17)
C1—C13	1.4949 (17)	C23—H23A	0.9900
C12—C13	1.4132 (16)	C23—H23B	0.9900
C13—C14	1.3853 (18)	C24—C25	1.5234 (19)
C14—C15	1.379 (2)	C24—H24A	0.9900
C14—H14	0.9500	C24—H24B	0.9900
C15—C16	1.379 (2)	C25—C26	1.5278 (18)
C15—H15	0.9500	C25—H25A	0.9900
C16—H16	0.9500	C25—H25B	0.9900
C121—H12A	0.9800	C26—H26A	0.9900
C121—H12B	0.9800	C26—H26B	0.9900
C12—S12—C121	100.24 (7)	C26—C21—H21	108.4
C1—N2—C21	121.97 (11)	C22—C21—H21	108.4
C1—N2—H2	119.0	C23—C22—C21	110.60 (10)
C21—N2—H2	119.0	C23—C22—H22A	109.5

C12—N11—C16	117.93 (12)	C21—C22—H22A	109.5
O1—C1—N2	123.96 (12)	C23—C22—H22B	109.5
O1—C1—C13	119.91 (11)	C21—C22—H22B	109.5
N2—C1—C13	116.13 (11)	H22A—C22—H22B	108.1
N11—C12—C13	122.64 (11)	C24—C23—C22	110.41 (11)
N11—C12—S12	117.28 (9)	C24—C23—H23A	109.6
C13—C12—S12	120.08 (9)	C22—C23—H23A	109.6
C14—C13—C12	117.62 (11)	C24—C23—H23B	109.6
C14—C13—C1	121.57 (11)	C22—C23—H23B	109.6
C12—C13—C1	120.75 (11)	H23A—C23—H23B	108.1
C15—C14—C13	120.05 (12)	C23—C24—C25	110.92 (10)
C15—C14—H14	120.0	C23—C24—H24A	109.5
C13—C14—H14	120.0	C25—C24—H24A	109.5
C16—C15—C14	117.72 (13)	C23—C24—H24B	109.5
C16—C15—H15	121.1	C25—C24—H24B	109.5
C14—C15—H15	121.1	H24A—C24—H24B	108.0
N11—C16—C15	124.03 (13)	C24—C25—C26	112.45 (11)
N11—C16—H16	118.0	C24—C25—H25A	109.1
C15—C16—H16	118.0	C26—C25—H25A	109.1
S12—C121—H12A	109.5	C24—C25—H25B	109.1
S12—C121—H12B	109.5	C26—C25—H25B	109.1
H12A—C121—H12B	109.5	H25A—C25—H25B	107.8
S12—C121—H12C	109.5	C21—C26—C25	110.10 (10)
H12A—C121—H12C	109.5	C21—C26—H26A	109.6
H12B—C121—H12C	109.5	C25—C26—H26A	109.6
N2—C21—C26	110.46 (10)	C21—C26—H26B	109.6
N2—C21—C22	110.36 (10)	C25—C26—H26B	109.6
C26—C21—C22	110.71 (10)	H26A—C26—H26B	108.2
N2—C21—H21	108.4		

C21—N2—C1—O1	−4.14 (18)	C1—C13—C14—C15	177.27 (13)
C21—N2—C1—C13	176.90 (10)	C13—C14—C15—C16	0.1 (2)
C16—N11—C12—C13	0.9 (2)	C12—N11—C16—C15	−0.9 (3)
C16—N11—C12—S12	−179.30 (12)	C14—C15—C16—N11	0.4 (3)
C121—S12—C12—N11	−13.77 (13)	C1—N2—C21—C26	155.76 (11)
C121—S12—C12—C13	166.03 (11)	C1—N2—C21—C22	−81.49 (14)
N11—C12—C13—C14	−0.45 (19)	N2—C21—C22—C23	178.71 (10)
S12—C12—C13—C14	179.76 (10)	C26—C21—C22—C23	−58.69 (14)
N11—C12—C13—C1	−177.82 (12)	C21—C22—C23—C24	57.95 (15)
S12—C12—C13—C1	2.39 (16)	C22—C23—C24—C25	−55.64 (15)
O1—C1—C13—C14	−139.12 (13)	C23—C24—C25—C26	54.76 (16)
N2—C1—C13—C14	39.88 (17)	N2—C21—C26—C25	178.91 (11)
O1—C1—C13—C12	38.15 (17)	C22—C21—C26—C25	56.37 (14)
N2—C1—C13—C12	−142.85 (11)	C24—C25—C26—C21	−54.86 (15)
C12—C13—C14—C15	−0.08 (19)		

Hydrogen-bond geometry (Å, º)

Cg1 is the centroid of the pyridine ring.

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N2—H2···O1[i]	0.88	2.01	2.8399 (15)	157
C16—H16···*Cg*1[ii]	0.95	2.97	3.7489 (18)	141

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

(II) *N*-Isopropyl-2-(methylsulfanyl)nicotinamide

Crystal data

$C_{10}H_{14}N_2OS$	$F(000) = 896$
$M_r = 210.29$	$D_x = 1.211$ Mg m^{-3}
Monoclinic, $P2_1/c$	Synchrotron radiation, $\lambda = 0.68890$ Å
Hall symbol: -P 2ybc	Cell parameters from 3067 reflections
$a = 11.42$ (2) Å	$\theta = 1.7$–$26.9°$
$b = 8.580$ (19) Å	$\mu = 0.25$ mm^{-1}
$c = 23.61$ (5) Å	$T = 100$ K
$\beta = 94.15$ (3)°	Plate, colourless
$V = 2307$ (8) Å^3	0.10 × 0.03 × 0.01 mm
$Z = 8$	

Data collection

CrystalLogic diffractometer	$T_{\min} = 0.975$, $T_{\max} = 0.998$
Radiation source: synchrotron, DLS beamline I19	10806 measured reflections
Double crystal silicon monochromator	4493 independent reflections
Detector resolution: 28.5714 pixels mm^{-1}	2445 reflections with $I > 2\sigma(I)$
profile data from ω–scans	$R_{\text{int}} = 0.150$
Absorption correction: multi-scan (*CrystalClear-SM Expert*; Rigaku, 2011)	$\theta_{\max} = 26.4°$, $\theta_{\min} = 1.7°$
	$h = -14 \rightarrow 7$
	$k = -9 \rightarrow 11$
	$l = -30 \rightarrow 24$

Refinement

Refinement on F^2	Secondary atom site location: difference Fourier map
Least-squares matrix: full	Hydrogen site location: inferred from neighbouring sites
$R[F^2 > 2\sigma(F^2)] = 0.119$	H-atom parameters constrained
$wR(F^2) = 0.366$	$w = 1/[\sigma^2(F_o^2) + (0.1896P)^2 + 2.8333P]$ where $P = (F_o^2 + 2F_c^2)/3$
$S = 1.06$	$(\Delta/\sigma)_{\max} < 0.001$
4493 reflections	$\Delta\rho_{\max} = 0.67$ e Å^{-3}
259 parameters	$\Delta\rho_{\min} = -0.67$ e Å^{-3}
0 restraints	
Primary atom site location: structure-invariant direct methods	

Special details

Experimental. N-iso-Propyl-2-(methylsulfanyl)nicotinamide (II). NMR ^{1}H (400MHz, DMSO-d$_6$) δ (ppm): 8.51 (1H, dd; J = 4.8 and J = 1.7 Hz, H6), 8.28 (1H, d, J = 7.5Hz, NH), 7.70 (1H, dd; J = 7.5 and J = 1.7 Hz, H4), 7.16 (1H, dd, J = 7.5 and J = 4.8 Hz, H5), 4.02 (1H, dq, J = 7.5 and J = 6.5 Hz, CH), 2.43 (3H, s, (CH3)S), 1.14 (6H, d, J= 6.5 Hz, (CH3)2C). (ppm): 165.2, 157.3, 149.6, 134.8, 130.5, 118.5, 40.9, 22.1, 12.9. IR (cm^{-1}; KBr): 3234 (NH), 1628 (CON) MS/ESI: [M-H]: 209.2

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 (Å²)

	x	y	z	$U_{\rm iso}$*/$U_{\rm eq}$
S12A	0.60559 (16)	0.3799 (2)	0.37711 (6)	0.0381 (5)
O1A	0.3807 (4)	0.2214 (5)	0.39115 (18)	0.0376 (11)
N2A	0.2371 (5)	0.4063 (6)	0.3933 (2)	0.0327 (12)
H2A	0.2086	0.4931	0.3780	0.039*
N11A	0.5566 (5)	0.5227 (6)	0.2767 (2)	0.0348 (13)
C1A	0.3330 (6)	0.3455 (7)	0.3729 (2)	0.0325 (15)
C3A	0.1751 (6)	0.3348 (8)	0.4410 (3)	0.0406 (16)
H3A	0.1850	0.2191	0.4398	0.049*
C12A	0.5072 (6)	0.4513 (7)	0.3210 (2)	0.0358 (16)
C13A	0.3849 (6)	0.4327 (7)	0.3244 (3)	0.0333 (15)
C14A	0.3125 (6)	0.4980 (8)	0.2806 (3)	0.0367 (15)
H14A	0.2296	0.4918	0.2816	0.044*
C15A	0.3611 (6)	0.5724 (8)	0.2352 (3)	0.0375 (16)
H15A	0.3122	0.6172	0.2052	0.045*
C16A	0.4819 (6)	0.5794 (7)	0.2350 (3)	0.0362 (15)
H16A	0.5143	0.6274	0.2034	0.043*
C21A	0.7443 (7)	0.4600 (10)	0.3566 (3)	0.0506 (19)
H21A	0.7634	0.4142	0.3204	0.076*
H22A	0.8067	0.4355	0.3859	0.076*
H23A	0.7372	0.5733	0.3525	0.076*
C31A	0.0452 (6)	0.3729 (9)	0.4337 (3)	0.0462 (18)
H31A	0.0343	0.4857	0.4370	0.069*
H32A	0.0042	0.3197	0.4632	0.069*
H33A	0.0133	0.3378	0.3962	0.069*
C32A	0.2312 (7)	0.3956 (9)	0.4979 (3)	0.0475 (18)
H34A	0.3156	0.3735	0.5004	0.071*
H35A	0.1950	0.3436	0.5292	0.071*
H36A	0.2187	0.5083	0.5003	0.071*
S12B	−0.04296 (18)	0.8929 (2)	0.40668 (8)	0.0484 (6)
O1B	0.1648 (4)	0.7202 (5)	0.3693 (2)	0.0451 (12)
N2B	0.3119 (5)	0.9004 (6)	0.3819 (2)	0.0339 (12)
H2B	0.3328	0.9970	0.3751	0.041*
N11B	−0.0650 (5)	1.0966 (7)	0.3200 (2)	0.0421 (14)
C1B	0.2044 (6)	0.8554 (7)	0.3633 (3)	0.0346 (15)
C3B	0.3975 (6)	0.7991 (7)	0.4128 (3)	0.0371 (16)
H3B	0.3786	0.6885	0.4024	0.044*
C12B	0.0103 (6)	0.9958 (7)	0.3477 (3)	0.0376 (16)
C13B	0.1274 (6)	0.9771 (7)	0.3327 (3)	0.0328 (15)

C14B	0.1687 (7)	1.0629 (8)	0.2883 (3)	0.0391 (16)
H14B	0.2475	1.0522	0.2784	0.047*
C15B	0.0905 (7)	1.1664 (8)	0.2583 (3)	0.0393 (16)
H15B	0.1150	1.2278	0.2278	0.047*
C16B	−0.0235 (7)	1.1754 (9)	0.2749 (3)	0.048 (2)
H16B	−0.0769	1.2411	0.2534	0.058*
C21B	−0.1738 (8)	1.0040 (11)	0.4210 (4)	0.063 (2)
H21B	−0.2127	0.9546	0.4520	0.094*
H22B	−0.2278	1.0065	0.3867	0.094*
H23B	−0.1513	1.1107	0.4318	0.094*
C31B	0.5220 (6)	0.8371 (8)	0.3944 (3)	0.0443 (18)
H31B	0.5404	0.9467	0.4026	0.066*
H32B	0.5245	0.8182	0.3535	0.066*
H33B	0.5798	0.7704	0.4153	0.066*
C32B	0.3868 (7)	0.8189 (9)	0.4767 (3)	0.0505 (19)
H34B	0.3070	0.7916	0.4859	0.076*
H35B	0.4032	0.9275	0.4875	0.076*
H36B	0.4433	0.7503	0.4976	0.076*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S12A	0.0347 (12)	0.0414 (9)	0.0374 (8)	0.0036 (7)	−0.0040 (7)	0.0016 (6)
O1A	0.036 (3)	0.030 (2)	0.046 (2)	0.002 (2)	−0.0012 (19)	0.0024 (18)
N2A	0.030 (4)	0.026 (2)	0.041 (3)	0.004 (2)	0.000 (2)	0.002 (2)
N11A	0.031 (4)	0.033 (3)	0.041 (3)	−0.001 (2)	−0.002 (2)	−0.002 (2)
C1A	0.036 (4)	0.022 (3)	0.038 (3)	−0.002 (3)	−0.006 (3)	0.002 (2)
C3A	0.040 (5)	0.036 (3)	0.046 (4)	−0.001 (3)	0.007 (3)	0.004 (3)
C12A	0.049 (5)	0.027 (3)	0.030 (3)	−0.002 (3)	−0.003 (3)	−0.003 (2)
C13A	0.029 (4)	0.027 (3)	0.043 (3)	0.005 (3)	−0.005 (3)	−0.003 (2)
C14A	0.031 (4)	0.037 (3)	0.042 (3)	−0.001 (3)	0.000 (3)	0.001 (3)
C15A	0.038 (5)	0.036 (3)	0.037 (3)	0.003 (3)	−0.003 (3)	0.008 (3)
C16A	0.035 (5)	0.032 (3)	0.041 (3)	−0.002 (3)	0.003 (3)	0.005 (3)
C21A	0.049 (5)	0.054 (4)	0.047 (4)	0.002 (4)	−0.005 (3)	0.008 (3)
C31A	0.034 (5)	0.054 (4)	0.051 (4)	−0.009 (3)	0.001 (3)	0.002 (3)
C32A	0.046 (5)	0.054 (4)	0.041 (3)	0.000 (4)	−0.004 (3)	0.005 (3)
S12B	0.0406 (13)	0.0465 (10)	0.0590 (11)	0.0049 (8)	0.0088 (9)	0.0150 (8)
O1B	0.040 (3)	0.026 (2)	0.069 (3)	0.001 (2)	−0.006 (2)	0.003 (2)
N2B	0.026 (3)	0.027 (2)	0.048 (3)	−0.001 (2)	−0.006 (2)	0.003 (2)
N11B	0.024 (4)	0.044 (3)	0.057 (3)	0.005 (3)	−0.007 (2)	0.006 (3)
C1B	0.032 (4)	0.033 (3)	0.039 (3)	0.006 (3)	0.001 (3)	−0.001 (2)
C3B	0.039 (5)	0.024 (3)	0.046 (3)	0.003 (3)	−0.009 (3)	0.002 (2)
C12B	0.037 (5)	0.025 (3)	0.049 (4)	0.001 (3)	−0.008 (3)	−0.001 (3)
C13B	0.027 (4)	0.029 (3)	0.040 (3)	0.000 (3)	−0.008 (3)	−0.003 (2)
C14B	0.044 (5)	0.034 (3)	0.038 (3)	−0.002 (3)	−0.006 (3)	−0.001 (3)
C15B	0.039 (5)	0.038 (3)	0.040 (3)	0.004 (3)	−0.001 (3)	0.004 (3)
C16B	0.043 (5)	0.046 (4)	0.052 (4)	0.005 (3)	−0.017 (3)	0.006 (3)
C21B	0.046 (6)	0.063 (5)	0.083 (6)	0.007 (4)	0.027 (4)	0.020 (4)
C31B	0.036 (5)	0.043 (4)	0.052 (4)	0.011 (3)	−0.001 (3)	0.006 (3)
C32B	0.048 (5)	0.048 (4)	0.054 (4)	0.003 (4)	−0.009 (3)	0.007 (3)

Geometric parameters (Å, º)

S12A—C12A	1.783 (7)	S12B—C12B	1.791 (7)
S12A—C21A	1.823 (8)	S12B—C21B	1.824 (9)
O1A—C1A	1.257 (7)	O1B—C1B	1.257 (8)
N2A—C1A	1.333 (8)	N2B—C1B	1.331 (8)
N2A—C3A	1.504 (8)	N2B—C3B	1.464 (8)
N2A—H2A	0.8800	N2B—H2B	0.8800
N11A—C16A	1.346 (8)	N11B—C12B	1.354 (8)
N11A—C12A	1.369 (8)	N11B—C16B	1.374 (10)
C1A—C13A	1.524 (9)	C1B—C13B	1.514 (9)
C3A—C31A	1.516 (10)	C3B—C32B	1.532 (10)
C3A—C32A	1.536 (9)	C3B—C31B	1.552 (11)
C3A—H3A	1.0000	C3B—H3B	1.0000
C12A—C13A	1.413 (10)	C12B—C13B	1.417 (10)
C13A—C14A	1.395 (9)	C13B—C14B	1.391 (10)
C14A—C15A	1.396 (9)	C14B—C15B	1.413 (9)
C14A—H14A	0.9500	C14B—H14B	0.9500
C15A—C16A	1.381 (10)	C15B—C16B	1.389 (11)
C15A—H15A	0.9500	C15B—H15B	0.9500
C16A—H16A	0.9500	C16B—H16B	0.9500
C21A—H21A	0.9800	C21B—H21B	0.9800
C21A—H22A	0.9800	C21B—H22B	0.9800
C21A—H23A	0.9800	C21B—H23B	0.9800
C31A—H31A	0.9800	C31B—H31B	0.9800
C31A—H32A	0.9800	C31B—H32B	0.9800
C31A—H33A	0.9800	C31B—H33B	0.9800
C32A—H34A	0.9800	C32B—H34B	0.9800
C32A—H35A	0.9800	C32B—H35B	0.9800
C32A—H36A	0.9800	C32B—H36B	0.9800
C12A—S12A—C21A	100.7 (3)	C12B—S12B—C21B	102.4 (4)
C1A—N2A—C3A	123.6 (5)	C1B—N2B—C3B	124.0 (5)
C1A—N2A—H2A	118.2	C1B—N2B—H2B	118.0
C3A—N2A—H2A	118.2	C3B—N2B—H2B	118.0
C16A—N11A—C12A	116.5 (6)	C12B—N11B—C16B	116.5 (6)
O1A—C1A—N2A	123.7 (6)	O1B—C1B—N2B	124.1 (6)
O1A—C1A—C13A	119.3 (6)	O1B—C1B—C13B	119.3 (6)
N2A—C1A—C13A	117.0 (5)	N2B—C1B—C13B	116.6 (6)
N2A—C3A—C31A	109.7 (5)	N2B—C3B—C32B	109.1 (6)
N2A—C3A—C32A	109.1 (6)	N2B—C3B—C31B	109.1 (5)
C31A—C3A—C32A	111.6 (6)	C32B—C3B—C31B	113.1 (6)
N2A—C3A—H3A	108.8	N2B—C3B—H3B	108.4
C31A—C3A—H3A	108.8	C32B—C3B—H3B	108.4
C32A—C3A—H3A	108.8	C31B—C3B—H3B	108.4
N11A—C12A—C13A	123.9 (6)	N11B—C12B—C13B	121.9 (6)
N11A—C12A—S12A	116.7 (5)	N11B—C12B—S12B	116.8 (6)
C13A—C12A—S12A	119.4 (5)	C13B—C12B—S12B	121.2 (5)
C14A—C13A—C12A	116.6 (6)	C14B—C13B—C12B	120.5 (6)
C14A—C13A—C1A	120.8 (6)	C14B—C13B—C1B	120.5 (6)

C12A—C13A—C1A	122.6 (5)	C12B—C13B—C1B	119.0 (6)
C13A—C14A—C15A	120.4 (7)	C13B—C14B—C15B	118.2 (7)
C13A—C14A—H14A	119.8	C13B—C14B—H14B	120.9
C15A—C14A—H14A	119.8	C15B—C14B—H14B	120.9
C16A—C15A—C14A	118.4 (6)	C16B—C15B—C14B	117.7 (6)
C16A—C15A—H15A	120.8	C16B—C15B—H15B	121.1
C14A—C15A—H15A	120.8	C14B—C15B—H15B	121.1
N11A—C16A—C15A	124.2 (6)	N11B—C16B—C15B	125.0 (6)
N11A—C16A—H16A	117.9	N11B—C16B—H16B	117.5
C15A—C16A—H16A	117.9	C15B—C16B—H16B	117.5
S12A—C21A—H21A	109.5	S12B—C21B—H21B	109.5
S12A—C21A—H22A	109.5	S12B—C21B—H22B	109.5
H21A—C21A—H22A	109.5	H21B—C21B—H22B	109.5
S12A—C21A—H23A	109.5	S12B—C21B—H23B	109.5
H21A—C21A—H23A	109.5	H21B—C21B—H23B	109.5
H22A—C21A—H23A	109.5	H22B—C21B—H23B	109.5
C3A—C31A—H31A	109.5	C3B—C31B—H31B	109.5
C3A—C31A—H32A	109.5	C3B—C31B—H32B	109.5
H31A—C31A—H32A	109.5	H31B—C31B—H32B	109.5
C3A—C31A—H33A	109.5	C3B—C31B—H33B	109.5
H31A—C31A—H33A	109.5	H31B—C31B—H33B	109.5
H32A—C31A—H33A	109.5	H32B—C31B—H33B	109.5
C3A—C32A—H34A	109.5	C3B—C32B—H34B	109.5
C3A—C32A—H35A	109.5	C3B—C32B—H35B	109.5
H34A—C32A—H35A	109.5	H34B—C32B—H35B	109.5
C3A—C32A—H36A	109.5	C3B—C32B—H36B	109.5
H34A—C32A—H36A	109.5	H34B—C32B—H36B	109.5
H35A—C32A—H36A	109.5	H35B—C32B—H36B	109.5

C3A—N2A—C1A—O1A	0.6 (9)	C3B—N2B—C1B—O1B	−1.4 (10)
C3A—N2A—C1A—C13A	180.0 (5)	C3B—N2B—C1B—C13B	179.2 (6)
C1A—N2A—C3A—C31A	−149.9 (6)	C1B—N2B—C3B—C32B	−92.6 (7)
C1A—N2A—C3A—C32A	87.5 (7)	C1B—N2B—C3B—C31B	143.3 (6)
C16A—N11A—C12A—C13A	1.0 (9)	C16B—N11B—C12B—C13B	2.6 (9)
C16A—N11A—C12A—S12A	−178.6 (4)	C16B—N11B—C12B—S12B	179.8 (5)
C21A—S12A—C12A—N11A	8.1 (6)	C21B—S12B—C12B—N11B	−15.3 (6)
C21A—S12A—C12A—C13A	−171.6 (5)	C21B—S12B—C12B—C13B	162.0 (6)
N11A—C12A—C13A—C14A	−2.8 (9)	N11B—C12B—C13B—C14B	−0.1 (9)
S12A—C12A—C13A—C14A	176.9 (5)	S12B—C12B—C13B—C14B	−177.2 (5)
N11A—C12A—C13A—C1A	176.9 (5)	N11B—C12B—C13B—C1B	−176.4 (6)
S12A—C12A—C13A—C1A	−3.5 (8)	S12B—C12B—C13B—C1B	6.4 (8)
O1A—C1A—C13A—C14A	138.7 (6)	O1B—C1B—C13B—C14B	−128.7 (7)
N2A—C1A—C13A—C14A	−40.7 (8)	N2B—C1B—C13B—C14B	50.7 (8)
O1A—C1A—C13A—C12A	−40.9 (8)	O1B—C1B—C13B—C12B	47.7 (8)
N2A—C1A—C13A—C12A	139.7 (6)	N2B—C1B—C13B—C12B	−132.9 (6)
C12A—C13A—C14A—C15A	2.1 (9)	C12B—C13B—C14B—C15B	−1.1 (9)
C1A—C13A—C14A—C15A	−177.5 (6)	C1B—C13B—C14B—C15B	175.2 (5)
C13A—C14A—C15A—C16A	0.0 (10)	C13B—C14B—C15B—C16B	−0.3 (9)
C12A—N11A—C16A—C15A	1.4 (9)	C12B—N11B—C16B—C15B	−4.2 (10)

C14A—C15A—C16A—N11A	−2.0 (10)	C14B—C15B—C16B—N11B	3.1 (11)

Hydrogen-bond geometry (Å, º)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N2*A*—H2*A*···O1*B*	0.88	2.02	2.862 (9)	160
N2*B*—H2*B*···O1*A*^{i}	0.88	2.03	2.869 (9)	159

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

(III) *N*-(2-Hydroxyethyl)-2-(methylsulfanyl)nicotinamide dihydrate

Crystal data

$C_9H_{12}N_2O_2S\cdot 2H_2O$
$M_r = 248.30$
Monoclinic, $P2_1/n$
Hall symbol: -P 2yn
$a = 7.194$ (2) Å
$b = 7.285$ (3) Å
$c = 22.388$ (8) Å
$\beta = 90.341$ (5)°
$V = 1173.3$ (7) Å^3
$Z = 4$
$F(000) = 528$
$D_x = 1.406$ Mg m^{-3}
Mo $K\alpha$ radiation, $\lambda = 0.71075$ Å
Cell parameters from 11307 reflections
$\theta = 3.0–27.6°$
$\mu = 0.28$ mm^{-1}
$T = 100$ K
Plate, colourless
0.26 × 0.12 × 0.05 mm

Data collection

Rigaku Saturn724+ (2x2 bin mode) diffractometer
Radiation source: Rotating Anode
Confocal monochromator
Detector resolution: 28.5714 pixels mm^{-1}
profile data from ω–scans
Absorption correction: multi-scan (*CrystalClear-SM Expert*; Rigaku, 2011)
$T_{min} = 0.931$, $T_{max} = 0.986$
6865 measured reflections
2063 independent reflections
1977 reflections with $I > 2\sigma(I)$
$R_{int} = 0.016$
$\theta_{max} = 25.0°$, $\theta_{min} = 2.9°$
$h = -8\rightarrow 8$
$k = -8\rightarrow 8$
$l = -26\rightarrow 25$

Refinement

Refinement on F^2
Least-squares matrix: full
$R[F^2 > 2\sigma(F^2)] = 0.027$
$wR(F^2) = 0.071$
$S = 1.07$
2063 reflections
146 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
$w = 1/[\sigma^2(F_o^2) + (0.0367P)^2 + 0.579P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max} = 0.25$ e Å^{-3}
$\Delta\rho_{min} = -0.24$ e Å^{-3}

Special details

Experimental. N-(2-Hydroxyethyl)-2-(methylsulfanyl)nicotinamide (III)′ NMR ^{1}H (400MHz, DMSO-d$_6$) δ (ppm): 8.51 (1H, dd, J = 4.8 and J = 1.6 Hz, H6), 8.37 (1H, s, NH), 7.77 (1H, dd, J = 7.6 and J = 1.6Hz, H4) 7.16 (1H, dd, J = 7.6 and J = 4.8 Hz, H5), 3.50 (2H, t, J = 6.2 Hz, CH_2OH), 3.30 (2H, t, J = 6.2 Hz, CH_2NH), 2.42 (3H, s, (CH_3)S). NMR ^{13}C (100MHz, DMSO-d$_6$) δ (ppm): 166.1; 157.7; 149.8; 135.0; 129.8; 118.4; 59.6; 41.9; 12.9. IR (cm^{-1}; KBr): 3258 (NH, OH); 1643 (CON) MS/ESI: [M+Na]: 235.1

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 (Å²)

	x	y	z	$U_{\rm iso}$*/$U_{\rm eq}$
S12	0.16008 (5)	0.17288 (4)	0.496490 (14)	0.01456 (12)
O1	0.14465 (13)	0.15851 (13)	0.35800 (4)	0.0178 (2)
O23	0.63288 (13)	0.21703 (14)	0.22908 (4)	0.0189 (2)
H23	0.6034	0.3265	0.2359	0.028*
N2	0.45696 (15)	0.17664 (14)	0.34545 (5)	0.0139 (2)
H2	0.5746	0.2354	0.3572	0.017*
N11	0.25158 (14)	0.52793 (15)	0.50671 (5)	0.0126 (2)
C1	0.29727 (17)	0.23204 (18)	0.36899 (6)	0.0125 (3)
C12	0.24506 (17)	0.38431 (18)	0.46972 (6)	0.0115 (3)
C13	0.30932 (17)	0.39415 (18)	0.41033 (6)	0.0120 (3)
C14	0.37886 (17)	0.55973 (18)	0.38990 (6)	0.0140 (3)
H14	0.4243	0.5702	0.3503	0.017*
C15	0.38137 (18)	0.71039 (18)	0.42798 (6)	0.0143 (3)
H15	0.4257	0.8262	0.4147	0.017*
C16	0.31791 (18)	0.68745 (18)	0.48552 (6)	0.0135 (3)
H16	0.3213	0.7902	0.5116	0.016*
C21	0.46845 (19)	0.02847 (18)	0.30153 (6)	0.0159 (3)
H21A	0.3589	−0.0527	0.3057	0.019*
H21B	0.5811	−0.0457	0.3096	0.019*
C22	0.47580 (19)	0.10174 (19)	0.23793 (6)	0.0177 (3)
H22A	0.4812	−0.0026	0.2097	0.021*
H22B	0.3609	0.1720	0.2293	0.021*
C121	0.11816 (19)	0.2207 (2)	0.57439 (6)	0.0173 (3)
H12A	0.2350	0.2567	0.5938	0.026*
H12B	0.0689	0.1105	0.5938	0.026*
H12C	0.0278	0.3208	0.5778	0.026*
O2	0.80120 (13)	0.33454 (13)	0.37567 (4)	0.0185 (2)
H2A	0.7959	0.3934	0.4074	0.028*
H2B	0.8969	0.2784	0.3749	0.028*
O3	0.52737 (13)	0.56527 (13)	0.25016 (4)	0.0185 (2)
H3A	0.6327	0.6270	0.2546	0.028*
H3B	0.4761	0.5936	0.2199	0.028*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
S12	0.01866 (19)	0.01151 (18)	0.01353 (19)	−0.00259 (12)	0.00296 (13)	−0.00031 (12)
O1	0.0135 (5)	0.0220 (5)	0.0179 (5)	−0.0025 (4)	0.0007 (4)	−0.0069 (4)

O23	0.0196 (5)	0.0173 (5)	0.0198 (5)	0.0005 (4)	0.0046 (4)	0.0003 (4)
N2	0.0135 (5)	0.0146 (6)	0.0136 (6)	−0.0010 (4)	0.0020 (4)	−0.0037 (4)
N11	0.0117 (5)	0.0133 (5)	0.0126 (5)	0.0017 (4)	−0.0003 (4)	−0.0010 (4)
C1	0.0141 (6)	0.0139 (6)	0.0096 (6)	0.0000 (5)	0.0004 (5)	0.0018 (5)
C12	0.0087 (6)	0.0125 (6)	0.0132 (6)	0.0007 (5)	−0.0006 (5)	0.0004 (5)
C13	0.0091 (6)	0.0144 (6)	0.0124 (6)	0.0016 (5)	−0.0010 (5)	−0.0010 (5)
C14	0.0119 (6)	0.0181 (7)	0.0120 (6)	0.0015 (5)	0.0002 (5)	0.0019 (5)
C15	0.0127 (6)	0.0123 (6)	0.0178 (7)	−0.0009 (5)	−0.0009 (5)	0.0029 (5)
C16	0.0119 (6)	0.0121 (6)	0.0165 (7)	0.0015 (5)	−0.0016 (5)	−0.0024 (5)
C21	0.0175 (7)	0.0133 (6)	0.0169 (7)	0.0003 (5)	0.0038 (5)	−0.0043 (5)
C22	0.0183 (7)	0.0181 (7)	0.0166 (7)	0.0002 (6)	0.0001 (5)	−0.0041 (5)
C121	0.0193 (7)	0.0191 (7)	0.0134 (7)	−0.0032 (6)	0.0022 (5)	0.0013 (5)
O2	0.0152 (5)	0.0243 (5)	0.0161 (5)	0.0004 (4)	0.0013 (4)	−0.0070 (4)
O3	0.0186 (5)	0.0206 (5)	0.0163 (5)	−0.0007 (4)	−0.0005 (4)	0.0037 (4)

Geometric parameters (Å, º)

S12—C12	1.7635 (14)	C15—C16	1.379 (2)
S12—C121	1.8055 (15)	C15—H15	0.9500
O1—C1	1.2449 (16)	C16—H16	0.9500
O23—C22	1.4228 (17)	C21—C22	1.5219 (19)
O23—H23	0.8397	C21—H21A	0.9900
N2—C1	1.3295 (17)	C21—H21B	0.9900
N2—C21	1.4628 (17)	C22—H22A	0.9900
N2—H2	0.9827	C22—H22B	0.9900
N11—C12	1.3351 (17)	C121—H12A	0.9800
N11—C16	1.3439 (18)	C121—H12B	0.9800
C1—C13	1.5026 (18)	C121—H12C	0.9800
C12—C13	1.4121 (19)	O2—H2A	0.8308
C13—C14	1.3846 (19)	O2—H2B	0.8012
C14—C15	1.390 (2)	O3—H3A	0.8865
C14—H14	0.9500	O3—H3B	0.7957

C12—S12—C121	102.71 (6)	N11—C16—H16	118.2
C22—O23—H23	109.5	C15—C16—H16	118.2
C1—N2—C21	122.88 (11)	N2—C21—C22	111.87 (11)
C1—N2—H2	120.4	N2—C21—H21A	109.2
C21—N2—H2	116.7	C22—C21—H21A	109.2
C12—N11—C16	118.03 (11)	N2—C21—H21B	109.2
O1—C1—N2	123.66 (12)	C22—C21—H21B	109.2
O1—C1—C13	120.49 (11)	H21A—C21—H21B	107.9
N2—C1—C13	115.84 (11)	O23—C22—C21	111.68 (11)
N11—C12—C13	122.27 (12)	O23—C22—H22A	109.3
N11—C12—S12	118.99 (10)	C21—C22—H22A	109.3
C13—C12—S12	118.72 (10)	O23—C22—H22B	109.3
C14—C13—C12	118.44 (12)	C21—C22—H22B	109.3
C14—C13—C1	120.06 (11)	H22A—C22—H22B	107.9
C12—C13—C1	121.47 (12)	S12—C121—H12A	109.5
C13—C14—C15	119.26 (12)	S12—C121—H12B	109.5
C13—C14—H14	120.4	H12A—C121—H12B	109.5

C15—C14—H14	120.4	S12—C121—H12C	109.5
C16—C15—C14	118.29 (12)	H12A—C121—H12C	109.5
C16—C15—H15	120.9	H12B—C121—H12C	109.5
C14—C15—H15	120.9	H2A—O2—H2B	109.0
N11—C16—C15	123.69 (12)	H3A—O3—H3B	110.9

C21—N2—C1—O1	3.3 (2)	N2—C1—C13—C14	59.14 (16)
C21—N2—C1—C13	−176.08 (11)	O1—C1—C13—C12	57.58 (17)
C16—N11—C12—C13	1.62 (18)	N2—C1—C13—C12	−123.06 (13)
C16—N11—C12—S12	179.59 (9)	C12—C13—C14—C15	−0.68 (18)
C121—S12—C12—N11	−3.62 (12)	C1—C13—C14—C15	177.19 (11)
C121—S12—C12—C13	174.42 (10)	C13—C14—C15—C16	1.50 (19)
N11—C12—C13—C14	−0.92 (18)	C12—N11—C16—C15	−0.74 (19)
S12—C12—C13—C14	−178.90 (9)	C14—C15—C16—N11	−0.8 (2)
N11—C12—C13—C1	−178.76 (11)	C1—N2—C21—C22	97.15 (14)
S12—C12—C13—C1	3.27 (16)	N2—C21—C22—O23	59.98 (14)
O1—C1—C13—C14	−120.22 (14)		

Hydrogen-bond geometry (Å, º)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N2—H2···O2	0.98	1.83	2.8096 (16)	176
O23—H23···O3	0.84	1.85	2.6906 (17)	177
O3—H3*B*···O1^{i}	0.80	2.00	2.7966 (15)	178
O3—H3*A*···O23^{ii}	0.89	1.84	2.7200 (15)	170
O2—H2*A*···N11^{iii}	0.83	2.04	2.8449 (17)	164
C14—H14···O3	0.95	2.37	3.3122 (19)	174
C21—H21*A*···O1	0.99	2.48	2.8208 (17)	100

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

Selected torsion angles (°)

	(I)	(IIA)	(IIB)	(III)
O1—C1—C13—C14	-139.12 (13)	138.7 (6)	-128.7 (7)	-120.22 (14)
N2—C1—C13—C14	39.88 (17)	-40.7 (8)	50.7 (8)	59.14 (16)
O1—C1—C13—C12	38.15 (17)	-40.9 (8)	47.7 (8)	57.58 (17)
N2—C1—C13—C12	-142.85 (11)	139.7 (6)	-132.9 (6)	-123.06 (13)

The angles are the equivalent torsion angles for each molecule. In (IIA) and (IIB), C21 is labelled as C3A and C3B, respectively.

Selected torsion angles (°) for (IV), (V), (VI) and (VII)

	(IV)	(V)	(VI)	(VII)
O1—C1—C13—C14	22.27 (19)	19.7 (2)	-30.87	-148.37 (18)
N2—C1—C13—C14	-157.12 (12)	-158.21 (16)	149.63′	29.5 (3)
O1—C1—C13—C12	-156.49 (13)	-158.93 (18)	146.37	26.6 (3)
N2—C1—C13—C12	-142.85 (18)	23.2 (2)	-36.12′	-155.55 (18)

The angles are the equivalent torsion angles for each molecule as for the current compounds.