Data collection: $P2_1$ diffractometer software. Cell refinement: $P2_1$ diffractometer software. Data reduction: *XP*21 (Pavelčík, 1987). Program(s) used to solve structure: *SHELXS*86 (Sheldrick, 1985). Program(s) used to refine structure: *SHELXL*93 (Sheldrick, 1993). Molecular graphics: *ORTEP*II (Johnson, 1976). Software used to prepare material for publication: *SHELXL*93.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: GS1022). Services for accessing these data are described at the back of the journal.

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# 4,6,7,8,8a,9-Hexahydrothieno[3,2-*f*]-indolizine-6,9-dione


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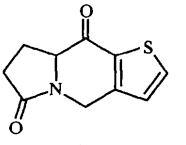
## Abstract

The title compound, $C_{10}H_9NO_2S$, belongs to a series of new heterocyclic compounds and was selected for structure determination in order to study some aspects of the relationship between conformational and electronic properties. The conformation of the individual rings and the bonding pattern of the molecule are analysed in detail and compared with those of analogous compounds.


## Comment

As part of our on-going study of the relationship between the molecular and electronic structures of new heterocyclic compounds, we report here on the crystal structure of the title compound, (I).




(I)

The molecular structure of (I) is shown in Fig. 1. The ring system of the molecule consists of an oxo-substituted tetrahydrothienopyridine moiety joined to an oxo-pyrrolidine ring. The thiophene ring is exactly planar, with an average deviation of the ring atoms from the least-squares plane of 0.006 (2) Å. Bond lengths and angles within the thiophene ring agree well with the corresponding values in other compounds containing this molecular fragment (Gilmore *et al.*, 1983; Bak *et al.*, 1961).

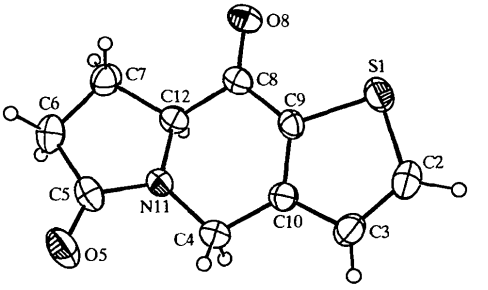



Fig. 1. *ORTEP*II (Johnson, 1976) view of the title molecule, showing the labelling of the non-H atoms. Displacement ellipsoids are shown at the 35% probability level and H atoms are drawn as small spheres of an arbitrary radius.

The central six-membered ring is not planar. A calculation of the least-squares planes has shown that this ring is puckered in such a manner that the four atoms C8, C9, C10 and C4 are planar to within 0.010 (3) Å, while atoms N11 and C12 are unequally displaced from this plane on opposite sides, with out-of-plane displacements of −0.356 (2) and 0.168 (2) Å, respectively. Using the terminology of Cremer & Pople (1975), the conformation of the ring can be described as intermediate between an envelope form, $^{N}E$, with N11 as the out-of-plane atom, and a half-chair form, $^{12}H_N$, with C12 and N11 as the out-of-plane atoms [$Q$ =

0.350 (3) Å, $\theta$ = 53.0 (4), $\varphi$ = 18.5 (5)°; calculated for the sequence N11,C12,C8,C9,C10,C4]. The oxopyrrolidine ring adopts a flat-envelope conformation, with C7 on the flap; the deviation of the out-of-plane atom from the best plane of the remaining four atoms [r.m.s. deviation 0.001 (1) Å] is 0.341 (3) Å. As shown in Table 1, the N11—C4 and N11—C12 bonds are equivalent and both are much longer than the N11—C5 bond. Moreover, the N11 atom is $sp^2$ hybridized, as evidenced by the sum of the valence angles around this atom [359.6 (2)°]. These data are consistent with conjugation of the lone-pair electrons on N11 with the adjacent carbonyl function, similar to what is observed for amides. Indeed, the N—C bond lengths at N11 are in good agreement with the comparable bond lengths found in cyclic amino acids (Benedetti *et al.*, 1983). As a result of the relatively severe puckering of the central ring, the molecule as a whole is nonplanar but consists of two approximately planar segments, C4,C10,C3,C2,S1,C9,C8,O8,C12 [r.m.s. deviation 0.069 (3) Å] and C4,N11,C5,O5,C6,C7,C12 [r.m.s. deviation 0.087 (3) Å], folded about the C4···C12 line [dihedral angle 30.3 (3)°].

A search of the Cambridge Structural Database (Allen *et al.*, 1983) for structures incorporating the tetrahydrothienopyridine fragment has revealed that the present structure, (I), is directly comparable with that reported by Luger & Schnorrenberg (1987), (II), which is a deoxo analogue of (I). The only difference between the two structures concerns the C8—C9 and C9—C10 bond lengths, the former being shorter and the latter longer in (I) as compared with (II). This might be caused by some degree of conjugation between the C9═C10 and C8═O8 double bonds in molecule (I).

## Experimental

The title compound was synthesized in several steps, starting from 5-oxoproline methyl ester and halogenomethylthiophene, as described by Marchalin *et al.* (1993). The final product was crystallized from ethanol.

*Crystal data*

$C_{10}H_9NO_2S$
$M_r$ = 207.24
Monoclinic
$P2_1/c$
$a$ = 8.067 (3) Å
$b$ = 9.699 (4) Å
$c$ = 12.191 (4) Å
$\beta$ = 100.19 (3)°
$V$ = 938.8 (6) Å$^3$
$Z$ = 4
$D_x$ = 1.459 Mg m$^{-3}$
$D_m$ = 1.45 (1) Mg m$^{-3}$
$D_m$ measured by flotation in bromoform–hexane
Mo $K\alpha$ radiation
$\lambda$ = 0.71073 Å
Cell parameters from 15 reflections
$\theta$ = 8–19°
$\mu$ = 0.314 mm$^{-1}$
$T$ = 293 (2) K
Prism
0.40 × 0.25 × 0.20 mm
Light yellow

*Data collection*

Syntex $P2_1$ diffractometer
$\theta/2\theta$ scans
Absorption correction: none
2389 measured reflections
2177 independent reflections
1143 reflections with $I > 2\sigma(I)$
$R_{int}$ = 0.035
$\theta_{max}$ = 27.59°
$h = -10 \rightarrow 0$
$k = 0 \rightarrow 12$
$l = -15 \rightarrow 15$
2 standard reflections
frequency: 100 min
intensity decay: none

*Refinement*

Refinement on $F^2$
$R$ = 0.048
$wR$ = 0.091
$S$ = 1.105
2177 reflections
128 parameters
H-atom parameters not refined
$w = 1/[\sigma^2(F_o^2) + (0.0776P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max}$ = −0.002
$\Delta\rho_{max}$ = 0.282 e Å$^{-3}$
$\Delta\rho_{min}$ = −0.221 e Å$^{-3}$
Extinction correction: *SHELXL*93 (Sheldrick, 1993)
Extinction coefficient: 0.001 (3)
Scattering factors from *International Tables for Crystallography* (Vol. C)

Table 1. *Selected geometric parameters (Å, °)*

| | | | |
|---|---|---|---|
| S1—C2 | 1.688 (3) | C5—C6 | 1.490 (4) |
| S1—C9 | 1.721 (2) | C6—C7 | 1.515 (4) |
| C2—C3 | 1.360 (4) | C7—C12 | 1.525 (3) |
| C3—C10 | 1.406 (3) | C8—O8 | 1.222 (3) |
| C4—N11 | 1.436 (3) | C8—C9 | 1.436 (3) |
| C4—C10 | 1.490 (4) | C8—C12 | 1.518 (3) |
| C5—O5 | 1.218 (3) | C9—C10 | 1.369 (3) |
| C5—N11 | 1.346 (3) | N11—C12 | 1.449 (3) |
| C2—S1—C9 | 91.00 (13) | C5—N11—C12 | 114.0 (2) |
| C5—N11—C4 | 124.0 (2) | C4—N11—C12 | 121.6 (2) |
| N11—C5—C6—C7 | −13.4 (3) | C10—C4—N11—C12 | 41.0 (3) |
| C5—C6—C7—C12 | 20.8 (3) | C4—N11—C12—C8 | −49.0 (3) |
| C12—C8—C9—C10 | −5.1 (3) | C5—N11—C12—C7 | 13.4 (3) |
| C8—C9—C10—C4 | −2.4 (4) | C9—C8—C12—N11 | 27.8 (3) |
| N11—C4—C10—C9 | −13.6 (3) | C6—C7—C12—N11 | −20.5 (2) |
| C6—C5—N11—C12 | −0.1 (3) | | |

All H atoms were located in a difference map and fixed at these positions, with $U_{iso}$ set to 1.2$U_{eq}$ of the associated atom.

Data collection: $P2_1$ *Diffractometer Software* (Syntex, 1974). Cell refinement: $P2_1$ *Diffractometer Software*. Data reduction: *XP*21 (Pavelčík, 1987). Program(s) used to solve structure: *SHELXS*86 (Sheldrick, 1985). Program(s) used to refine structure: *SHELXL*93 (Sheldrick, 1993). Molecular graphics: *ORTEP*II (Johnson, 1976). Software used to prepare material for publication: *SHELXL*93.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: GS1027). Services for accessing these data are described at the back of the journal.

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# Molecular aggregation in selected crystalline 1:1 complexes of hydrophobic D- and L-amino acids. II.† The D-norleucine series

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## Abstract

The amino acid D-norleucine has been co-crystallized with selected L-amino acids with linear side chains including L-norvaline [D-norleucine–L-norvaline (1/1), $C_6H_{13}NO_2{\cdot}C_5H_{11}NO_2$, amino-acid side chain $R$ = $CH_2CH_2CH_3$] and L-methionine [D-norleucine–L-methionine, $C_6H_{13}NO_2{\cdot}C_5H_{11}NO_2S$ (1/1), $R = CH_2CH_2SCH_3$], as well as amino acids with branched side chains including L-valine [D-norleucine–L-valine (1/1), $C_6H_{13}NO_2{\cdot}C_5H_{11}NO_2$, $R$ = $CH(CH_3)_2$], L-*allo*-isoleucine [D-norleucine–L-*allo*-isoleucine (1/1), $C_6H_{13}NO_2{\cdot}C_6H_{13}NO_2$, $R = CH(CH_3)CH_2CH_3$] and L-leucine [D-norleucine–L-leucine (1/1), $C_6H_{13}NO_2{\cdot}C_6H_{13}NO_2$, $R$ = $CH_2CH(CH_3)_2$]. The crystal structures are divided into distinct hydrophilic and hydrophobic layers. The polar parts of the D- and L-amino acids are related by pseudo glide-plane symmetry in all complexes except L-Leu:D-Nle, in which parts of the two amino acids are related by pseudo-inversion. Furthermore, the D-Nle molecule is disordered over two positions with nearly equal occupancy. Similarities and differences in both the crystal packing and molecular conformations of D-Nle and the partner molecules are discussed.

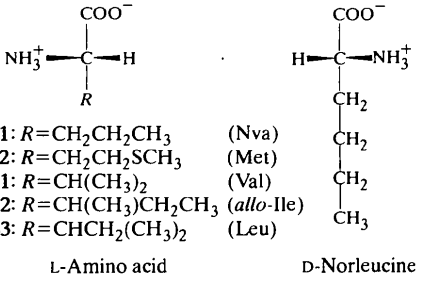
† Part I: Dalhus & Görbitz (1999).

## Comment

The crystal structures of hydrophobic amino acids fall within three categories; (i) pure enantiomers, (ii) racemates and (iii) complexes of two different hydrophobic amino acids with opposite chirality at $C^\alpha$. There are no known crystal structures incorporating two different hydrophobic amino acids with the same chirality at $C^\alpha$.

Previously, we have determined the crystal structures of seven 1:1 complexes of category (iii) involving L-isoleucine, among them L-isoleucine:D-norleucine (Dalhus & Görbitz, 1999*a*). The seven structures will be referred to as the L-Ile:D-*Xxx* complexes/series. In this paper we present the crystal structures of five additional 1:1 complexes with norleucine as the D-amino acid (D-Nle).

The investigated D-Nle complexes fall into two subcategories depending on the nature of the side chains. In the complexes L-Nva:D-Nle, (**L1**), and L-Met:D-Nle, (**L2**), both amino acids have unbranched side chains, while in L-Val:D-Nle, (**B1**), L-*allo*-Ile:D-Nle, (**B2**), and L-Leu:D-Nle, (**B3**), there is one branched and one unbranched amino-acid side chain. No crystals suitable for diffraction experiments were obtained for D-Nle complexed with L-alanine (L-Ala, $R = CH_3$) or L-$\alpha$-aminobutyric acid (L-Abu, $R = CH_2CH_3$). Among the L-Ile:D-*Xxx* complexes, alanine gave crystals of low quality compared to the other amino acids in the series.




All crystal structures are divided into distinct hydrophilic and hydrophobic layers (Figs. 1, 2 and 3). This characteristic build-up is due to the dual properties of the hydrophobic amino acids; the charged $\alpha$-amino and $\alpha$-carboxylate groups engage in hydrogen bonding with each other, while the side chains, distinctly hydrophobic in nature, are involved in van der Waals interactions only.