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A stacked pyrazolo[3,4-*d*]pyrimidine-based flexible molecule: the effect on stacking of an ethyl group in comparison with a methyl group[1]

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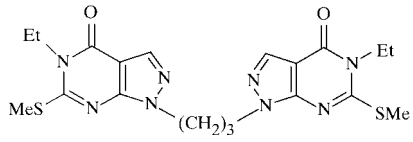
In the crystal structure of 1,1′-(1,3-propanediyl)bis(5-ethyl-6-methylthio-4,5-dihydro-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-one), $C_{19}H_{24}N_8O_2S_2$, the pairs of pyrazolo[3,4-*d*]pyrimidine rings of the molecule stack between the heterocyclic rings, due to intramolecular π–π interactions. The substituted ethyl and methyl groups are comparable as far as intramolecular stacking is concerned.

Comment

Interactions between aromatic units play a significant role in chemistry (Hunter, 1994), biology and crystal engineering (Desiraju, 1995). While π–π stacking is, by consensus, an important non-covalent interaction in DNA and proteins, the nature of this interaction remains under debate (Guckian *et al.*, 2000). The use of a 'propylene linker' was first documented by Brown *et al.* (1968) for the promotion of intramolecular stacking. Recently, we have reported convenient syntheses (Avasthi *et al.*, 1995, 1998) and X-ray studies (Biswas *et al.*, 1995; Maulik *et al.*, 1998, 2000) of four novel 'propylene-linker' compounds based on pyrazolo[3,4-*d*]pyrimidines as new flexible models for studying aromatic π–π interactions (APPI). One of these four compounds, 1,1′-(1,3-propanediyl)bis(5-methyl-6-methylthio-4,5-dihydro-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-one), (I), showed beautiful inter- and intramolecular stacking due to APPI (Maulik *et al.*, 1998). Since the X-ray structure of (I) was unique (a U-motif) for the demonstration of inter- and intramolecular stacking, it was thought worthwhile to replace the *N*-methyl group of (I) with an *N*-ethyl group, to determine the robustness of the U-motif and its consequence on intermolecular stacking. In this communication, we report the X-ray structure of the newly synthesized compound, 1,1′-(1,3-propanediyl)bis(5-ethyl-6-methylthio-4,5-dihydro-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-one), (II) (Avasthi & Aswal, 2001).



(II)

The conformation of (II) is shown in Fig. 1. The molecule is folded at the centre of the bridge [C10—C11—C12 = 114.9 (2)°], due to intramolecular APPI between the pyrazolo[3,4-*d*]pyrimidine rings. For comparison, the corresponding angle in (I) is 115.2 (2)°. In compound (II), as in (I), the two pyrazolo[3,4-*d*]pyrimidine rings are positioned in such a way that only a part of the pyrimidinyl rings overlap (Fig. 1). The overlapping six-membered rings are separated by an average distance of 3.415 (3) Å [3.37 (1) Å in (I)], thus confirming the presence of intramolecular APPI.

The pyrazolo[3,4-*d*]pyrimidine rings of (II) are nearly planar [maximum deviation = −0.062 (2) Å] and the angle between the least-squares planes is 12.5 (1)° [12.4 (5)° in (I)]. The packing diagram (Fig. 2) shows that the molecules are stacked in the *a* direction in such a way that similar sides of the U-motif are adjacent to each other. The approximate inter-

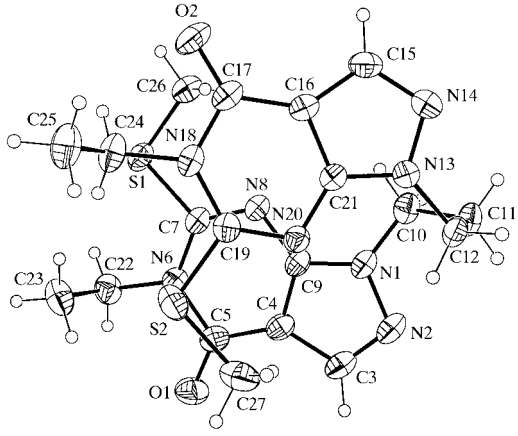


Figure 1
The molecular view of (II), showing the intramolecular stacking and displacement ellipsoids at the 30% probability level. H atoms are shown as small spheres of arbitrary radii.

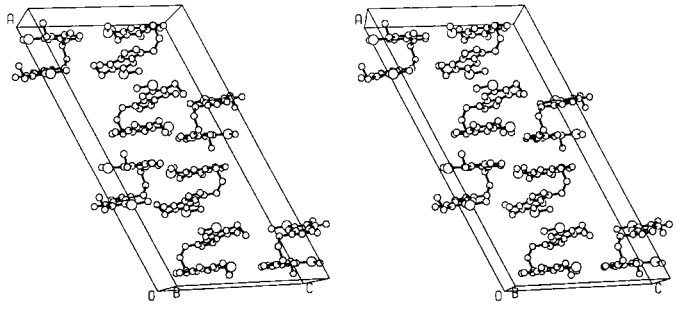


Figure 2
A stereoview crystal-packing diagram for (II).

[1] CDRI communication No. 6184.

molecular spacings between adjacent rings are 3.7 and 4.0 Å in (I) and (II), respectively.

In conclusion, replacement of the *N*-methyl group in (I) with an *N*-ethyl group in (II) has not produced any significant change in the U-motif produced by intramolecular stacking due to APPI. However, the intermolecular packing pattern has changed, due to the presence of the bulky ethyl group.

Experimental

Compound (II) was synthesized using a method similar to that described earlier by Avasthi *et al.* (1998) for the synthesis of (I), except that ethyl iodide was used in place of methyl iodide. Diffraction-quality crystals of (II) were obtained by slow evaporation of an ethyl acetate solution at room temperature.

Crystal data

$C_{19}H_{24}N_8O_2S_2$
M_r = 460.58
Monoclinic, *C*2/*c*
a = 31.385 (2) Å
b = 9.129 (1) Å
c = 16.840 (1) Å
β = 115.520 (3)°
V = 4354.1 (6) Å^3
Z = 8
D_x = 1.405 Mg m^{-3}
Mo *K*α radiation
Cell parameters from 58 reflections
θ = 4.7–12.5°
μ = 0.28 mm^{-1}
T = 293 (2) K
Block, colourless
0.43 × 0.36 × 0.33 mm

Data collection

Bruker *P*4 diffractometer
$\theta/2\theta$ scans
4602 measured reflections
3826 independent reflections
3276 reflections with $I > 2\sigma(I)$
R_{int} = 0.013
θ_{max} = 25°
$h = -1 \rightarrow 37$
$k = -1 \rightarrow 10$
$l = -20 \rightarrow 18$
3 standard reflections
every 97 reflections
intensity decay: none

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.036
$wR(F^2)$ = 0.097
S = 1.05
3826 reflections
285 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0401P)^2 + 3.2946P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max}$ = 0.001
$\Delta\rho_{max}$ = 0.20 e Å^{-3}
$\Delta\rho_{min}$ = −0.30 e Å^{-3}
Extinction correction: *SHELXL*97 (Sheldrick, 1997)
Extinction coefficient: 0.00100 (11)

All H atoms were placed in geometrically idealized positions and allowed to ride on their parent atoms (C—H = 0.96–0.97 Å), to which each was bonded for the final cycles of refinement.

Data collection: *XSCANS* (Siemens, 1996); cell refinement: *XSCANS*; data reduction: *XSCANS*; program(s) used to solve structure: *SHELXTL* (Bruker, 1997); program(s) used to refine structure: *SHELXTL*; molecular graphics: *NRCVAX* (Gabe *et al.*, 1989), *ORTEP* (Johnson, 1965) and *PLUTO* (Motherwell & Clegg, 1978); software used to prepare material for publication: *SHELXTL*.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: VJ1145). Services for accessing these data are described at the back of the journal.

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