Acta Crystallographica Section E
Structure Reports Online
ISSN 1600-5368

2-(Cyclopentylsulfanyl)-6-(1-naphthoyl)-pyrimidin-4(3*H*)-one

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Key indicators

Single-crystal X-ray study
T = 295 K
Mean σ(C–C) = 0.004 Å
R factor = 0.039
wR factor = 0.117
Data-to-parameter ratio = 13.5

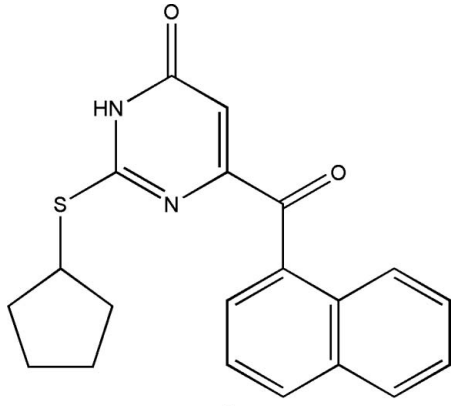
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

Received 20 January 2006
Accepted 13 March 2006

In the structure of the title compound, $C_{20}H_{18}N_2O_2S$, the carbonyl group, the naphthyl ring system and the cyclopentyl ring are not in the plane of the pyrimidinyl ring. In the crystal structure, pairs of molecules are connected into dimers *via* N—H···O hydrogen bonding

Comment

Reverse transcriptase is a key target for inhibition of the human immunodeficiency virus type 1 (HIV-1) replication (De Clercq, 1990; Mitsuya *et al.*, 1990). In recent years, great effort has been made in the design and synthesis of potent HIV-1 non-nucleoside RT inhibitors (NNRTIs) (Pedersen & Pedersen, 1999). Dihydroalkoxybenzyloxopyrimidines (DABOs) are one of the most respresentative classes of non-nucleoside RT inhibitors developed in the last decade. Since the original synthesis of dihydroalkoxybenzyloxopyrimidines by Artico *et al.* (1993), a large number of similar compounds have been synthesized (Mai *et al.*, 1997, 2001; Vig *et al.*, 1998) in order to find novel potent drugs for AIDS therapy. Based on our previous research in this field, we postulated that the introduction of a hydrogen-bond acceptor at the C-6 position of DABOs may be beneficial in enhancing the interaction between the inhibitor and reverse transcriptase. We have therefore synthesized a number of new 6-(1-naphthoyl)-substituted dihydroalkoxybenzyloxopyrimidines. As the structures of these compounds are unknown, we have structurally characterized the title compound, (I).



(I)

In the structure of (I), the carbonyl group, the naphthyl ring system and the cyclopentyl ring are not in the plane of the pyrimidinyl ring. The cyclopentyl ring is in an envelope conformation. The dihedral angle between the pyrimidinyl and carbonyl planes is 25.78 (10)° and that between the carbonyl and naphthyl planes is 29.04 (7)°.

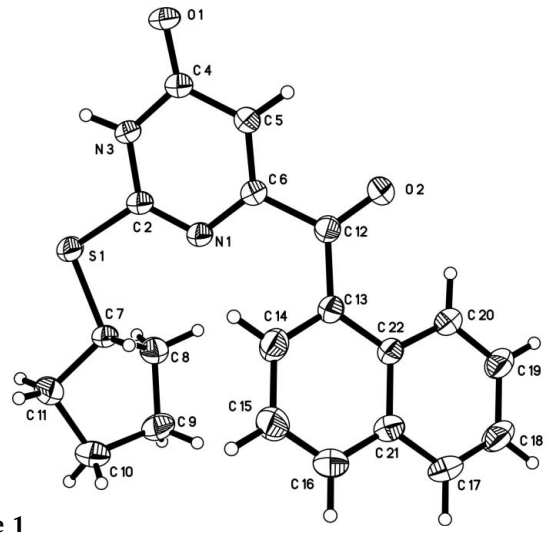


Figure 1
View of the molecular structure of (I), showing the atom-labeling scheme. Displacement ellipsoids are drawn at the 30% probability level. H atoms are shown as small spheres of arbitrary radii.

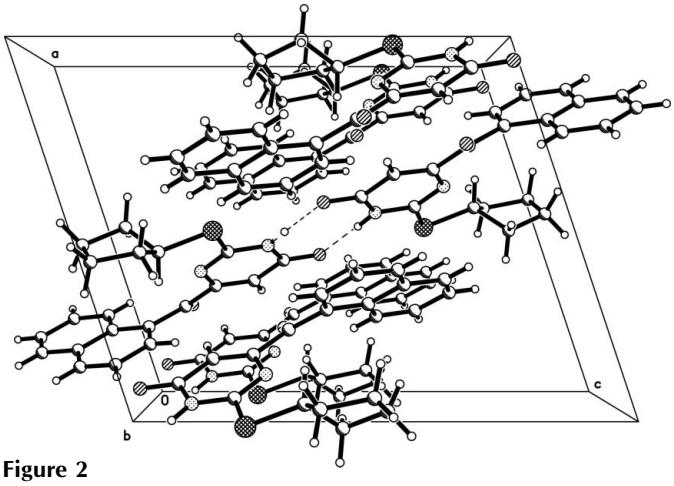


Figure 2
The crystal structure of (I), viewed along the *b* axis. Intermolecular N—H···O hydrogen bonds are shown as dashed lines.

In the crystal structure, pairs of molecules are connected into dimers *via* intermolecular N—H···O hydrogen bonding between amine atom N3 and carbonyl atom O1. These dimers are located on centres of inversion (Table 2 and Fig. 2). The distance between neighbouring naphthyl planes (3.219 Å) indicates π–π stacking interactions. No π–π stacking is found between the pyrimidinyl planes.

Experimental

6-(1-Cyano-1-naphthylmethyl)-2-(cyclopentylsulfanyl)pyrimidin-4(3*H*)-one (2.00 g, 5.5 mmol) was dissolved in 8 ml anhydrous DMF under a nitrogen atmosphere. The solution was cooled to 264 K and NaH (0.16 g; 6.6 mmol 60% in paraffin) was added dropwise. The resulting mixture was allowed to warm to room temperature and stirred for about 48 h by passing air into the reaction mixture. The light-yellow solution was neutralized with acetic acid and concentrated under reduced pressure to give a white residue. Afterwards, 100 ml of water were added. The precipitate was filtered off and recrystallized from ethyl acetate to give the title compound as colorless block-like crystals suitable for X-ray diffraction (yield: 1.67 g, 4.8 mmol, 86.1%; m.p. 459.4–460.4 K). Analysis calculated for $C_{20}H_{18}N_2O_2S$: C 68.55, H 5.18, N 7.99, S 9.15%; found: C 68.37, H 5.19, N 8.02, S 9.12%.

Crystal data

$C_{20}H_{18}N_2O_2S$	D_x = 1.344 Mg m^{-3}
M_r = 350.42	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 25 reflections
a = 11.920 (2) Å	θ = 11.7–12.5°
b = 10.312 (3) Å	μ = 0.20 mm^{-1}
c = 14.855 (4) Å	T = 295 (2) K
β = 108.43 (2)°	Prism, colorless
V = 1732.3 (7) Å^3	0.40 × 0.30 × 0.20 mm
Z = 4	

Data collection

Enraf–Nonius CAD-4 diffractometer	R_{int} = 0.024
$\omega/2\theta$ scans	θ_{max} = 25.2°
Absorption correction: ψ scan (North *et al.*, 1968)	$h = -14 \rightarrow 13$
T_{min} = 0.923, T_{max} = 0.961	$k = 0 \rightarrow 12$
3499 measured reflections	$l = -1 \rightarrow 17$
3109 independent reflections	3 standard reflections
1579 reflections with $I > 2\sigma(I)$	frequency: 60 min
	intensity decay: none

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0519P)^2 + 0.0074P]$ where $P = (F_o^2 + 2F_c^2)/3$
$R[F^2 > 2\sigma(F^2)]$ = 0.039	$(\Delta/\sigma)_{max} < 0.001$
$wR(F^2)$ = 0.117	$\Delta\rho_{max}$ = 0.24 e Å^{-3}
S = 1.01	$\Delta\rho_{min}$ = −0.20 e Å^{-3}
3109 reflections	Extinction correction: *SHELXL97*
231 parameters	Extinction coefficient: 0.0037 (10)
H atoms treated by a mixture of independent and constrained refinement	

Table 1
Selected geometric parameters (Å, °).

S1—C2	1.750 (3)	C4—C5	1.431 (4)
S1—C7	1.813 (2)	C6—C12	1.527 (4)
C2—N3	1.359 (3)	C12—C13	1.486 (3)
N3—C4	1.375 (3)		
N3—C2—S1	115.48 (19)	C5—C6—C12	119.1 (2)
C2—N3—C4	122.9 (2)	C13—C12—C6	119.1 (2)
N3—C4—C5	113.8 (2)		
S1—C2—N3—C4	178.5 (2)	C4—C5—C6—C12	178.6 (2)
C2—N3—C4—C5	1.7 (4)	C5—C6—C12—C13	156.0 (2)
N3—C4—C5—C6	−1.9 (4)		

Table 2
Hydrogen-bond geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
N3—H3X···O1^{i}	0.879 (17)	1.898 (17)	2.776 (3)	177 (3)

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

H atoms were found in a difference Fourier map. The N-bound H atom was refined freely. C-bound H atoms were refined as riding, with C—H = 0.93–0.98 Å and U_{iso}(H) = 1.2U_{eq}(C).

Data collection: *CAD-4 Software* (Enraf–Nonius, 1994); cell refinement: CAD-4; data reduction: *XCAD4* (Harms & Wocadlo,

1994); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Version 1.05; Farrugia, 1997); software used to prepare material for publication: *SHELXL97*.

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