Acta Crystallographica Section E
Structure Reports Online
ISSN 1600-5368

2-Cyano-3-dimethylamino-*N*-(2,5-dimethylphenyl)acrylamide

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Key indicators

Single-crystal X-ray study
T = 293 K
Mean σ(C–C) = 0.003 Å
R factor = 0.058
wR factor = 0.168
Data-to-parameter ratio = 19.7

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

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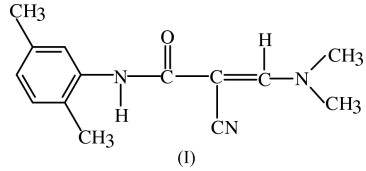
Received 23 January 2003
Accepted 3 February 2003
Online 21 February 2003

In the title compound, $C_{14}H_{17}N_3O$, the dihedral angle between the benzene ring and amido group is 4.1 (1)°. The molecular structure is stabilized by intramolecular C—H···O and N—H···N hydrogen bonds, and the packing of the molecules in the solid state is stabilized by weak intermolecular C—H···O hydrogen bonds.

Comment

As part of our studies on the conformation of *N*-aromatic amide derivatives, the crystal structure determination of the title compound, (I), was undertaken. These compounds are analogues of the active metabolites of the immunosuppressive drug leflunomide, which are known to act, in part, by inhibiting the tyrosine kinase epidermal growth factor receptor (EGFR) (Mattar *et al.*, 1993). EGFR is a membrane-associated tyrosine kinase, which serves as an endogenous negative regulator of apoptosis in breast cancer cells (Uckun *et al.*, 1998). The present study reports the structure of (I) (Fig. 1), and examines the effects of substituents on the hydrogen-bonding system and on the crystal packing.



(I)

The dihedral angle between the benzene ring and amido group is 4.1 (1)° and the geometry of the amido group is comparable to those in similar acetanilides (Haisa *et al.*, 1977). The C10—C11 bond length [1.417 (3) Å] agrees with the expected Csp^2—Csp bond length of 1.416 Å (Ghosh *et al.*, 1999) and also agrees well with values for similar types of bonds reported in the Cambridge Structural Database (Allen & Kennard, 1993). The C11—N12 [1.148 (2) Å] length is shorter than the expected cyano bond length of 1.165 Å (Ghosh *et al.*, 1999). Similar observations have been noted in the crystal structures of other leflunomide metabolite analogues (Ghosh & Uckun, 1999; Ghosh *et al.*, 1999) and acrylamide derivatives (Yogavel *et al.*, 2003). The distortion and enlargement of the angles C6—C1—N7, C1—N7—C8 and N7—C8—O9 from the trigonal value (120°) is due to the intramolecular C6—H6···O9 hydrogen bond (Table 2). The cyano-acrylamide side chain is planar and π-conjugation along it causes variations in the bond distances with respect to localized double and single bonds. The intramolecular N7—H7···N12 hydrogen bond causes a twist around C1—N7 [C6—C1—N7—C8 = 4.0 (3)°]. A *C*(7) graph-set motif (Bernstein *et*

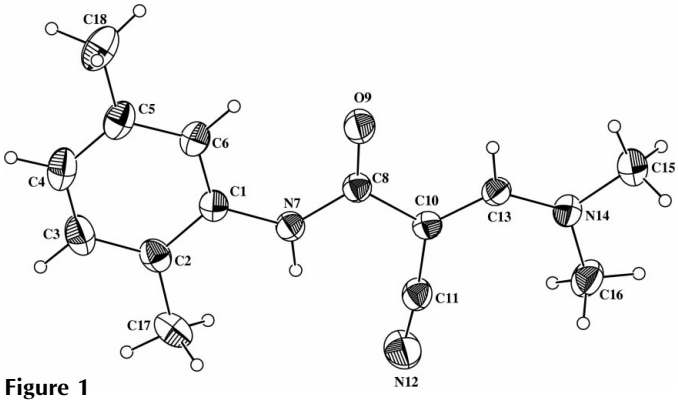


Figure 1
The molecular structure of (I), showing the atom-numbering scheme and 35% probability displacement ellipsoids.

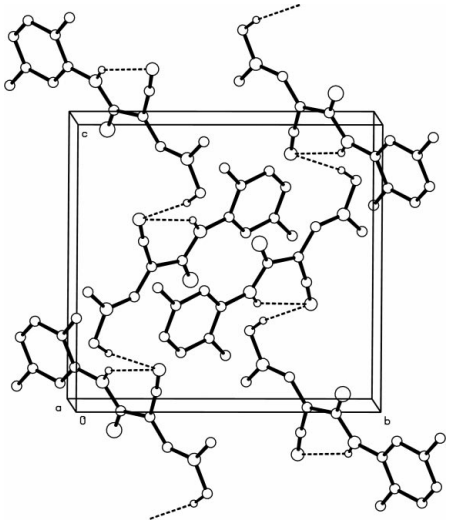


Figure 2
The crystal structure of (I), viewed down the *a* axis.

al., 1995) is formed *via* C15—H15*A*···N12($-\frac{1}{2}+x$, $\frac{1}{2}-y$, $\frac{1}{2}+z$), creating a chain that runs parallel to the *c* axis. Two such anti-parallel chains are shown in Fig. 2.

Experimental

N-(2,5-Dimethylphenyl)cyanoacetamide (0.005 mol) was dissolved in 6 ml DMF and cooled in an ice-bath. To this solution, 1.4 ml of $POCl_3$ (0.015 mol) was slowly added with constant stirring. The reaction mixture was allowed to warm to room temperature and further stirred for 3–4 h. The residue was then poured on to crushed ice and neutralized with 10% NaOH. The crude product was collected *in vacuo*, washed with water and dried. The product was further purified by recrystallization from an ethyl acetate–petroleum mixture.

Crystal data

$C_{14}H_{17}N_3O$
M_r = 243.31
Monoclinic, $P2_1/n$
a = 9.9315 (2) Å
b = 11.8940 (4) Å
c = 11.3979 (4) Å
β = 97.079 (14)°
V = 1336.12 (8) Å^3
Z = 4
D_x = 1.210 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 3509 reflections
θ = 2.5–28.3°
μ = 0.08 mm^{-1}
T = 293 (2) K
Plate, colourless
0.46 × 0.32 × 0.24 mm

Data collection

Siemens SMART CCD area-detector diffractometer
ω scans
Absorption correction: none
9076 measured reflections
3291 independent reflections
2001 reflections with $I > 2\sigma(I)$
R_{int} = 0.040
θ_{max} = 28.3°
$h = -12 \rightarrow 13$
$k = -13 \rightarrow 15$
$l = -10 \rightarrow 15$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.058
$wR(F^2)$ = 0.168
S = 1.02
3291 reflections
167 parameters
H-atom parameters constrained
$w = 1/[\sigma^2(F_o^2) + (0.0822P)^2 + 0.114P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.21 e Å^{-3}
$\Delta\rho_{min}$ = −0.16 e Å^{-3}

Table 1
Selected geometric parameters (Å, °).

C1—N7	1.410 (2)	C10—C11	1.417 (3)
N7—C8	1.365 (2)	C11—N12	1.148 (2)
C8—O9	1.216 (2)	C13—N14	1.323 (2)
C8—C10	1.485 (2)	N14—C15	1.453 (2)
C10—C13	1.374 (2)	N14—C16	1.453 (2)
C6—C1—N7	122.57 (16)	C13—C10—C8	116.89 (15)
C8—N7—C1	129.93 (14)	N14—C13—C10	130.86 (16)
O9—C8—N7	123.11 (16)	C13—N14—C15	120.53 (16)
N7—C8—C10	114.79 (14)	C13—N14—C16	124.21 (16)
C13—C10—C11	125.91 (16)	C15—N14—C16	115.07 (16)
C6—C1—N7—C8	−4.0 (3)	N7—C8—C10—C13	−175.17 (15)
C1—N7—C8—C10	−176.25 (15)	C8—C10—C13—N14	−179.30 (17)

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

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N7—H7···N12	0.86	2.62	3.313 (2)	139
C6—H6···O9	0.93	2.26	2.876 (2)	124
C13—H13···O9	0.93	2.37	2.762 (2)	105
C15—H15*A*···N12^{i}	0.96	2.63	3.566 (3)	166

Symmetry code: (i) $x-\frac{1}{2}, \frac{1}{2}-y, z-\frac{1}{2}$.

All H atoms were fixed geometrically and allowed to ride on the parent non-H atoms.

Data collection: *SMART* (Siemens, 1996); cell refinement: *SAINT* (Siemens, 1996); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *ZORTEP* (Zsolnai, 1997) and *PLATON* (Spek, 1990); software used to prepare material for publication: *SHELXL*97 and *PARST* (Nardelli, 1995).

Financial support from the Department of Biotechnology (DBT), India is gratefully acknowledged.

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