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1-Benzyl-2-(1*H*-indol-3-yl)-5-oxopyrrolidine-2-carbonitrile

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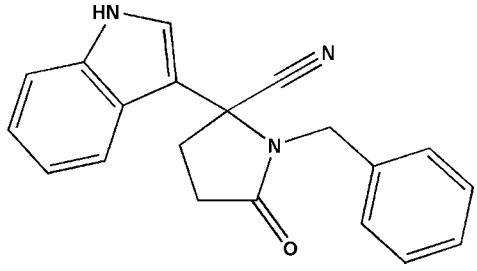
Key indicators: single-crystal X-ray study; T = 293 K; mean σ(C–C) = 0.002 Å; R factor = 0.047; wR factor = 0.130; data-to-parameter ratio = 16.6.

In the title compound, $C_{20}H_{17}N_3O$, a potential anti-human immunodeficiency virus type 1 (HIV-1) non-nucleoside reverse-transcriptase inhibitor, the pyrrolidine ring has an envelope conformation. In the crystal structure, adjacent molecules are connected into infinite chains *via* an N—H···O hydrogen bond.

Related literature

For details of the synthesis, see: Martirosyan *et al.* (2000, 2004). For details of the pharmacological properties of compounds of this family, see: De Clercq (1996). For the crystal structures of some analogs of the title compound, see: Karapetyan *et al.* (2002); Tamazyan *et al.* (2002).



Experimental

Crystal data

$C_{20}H_{17}N_3O$
M_r = 315.37
Triclinic, $P\overline{1}$
a = 7.5781 (15) Å
b = 9.4521 (19) Å
c = 12.409 (3) Å
α = 78.02 (3)°
β = 83.05 (3)°
γ = 69.68 (3)°
V = 814.2 (3) Å^3
Z = 2
Mo $K\alpha$ radiation
μ = 0.08 mm^{-1}
T = 293 (2) K
0.4 × 0.3 × 0.2 mm

Data collection

Enraf–Nonius CAD-4 diffractometer
Absorption correction: none
9470 measured reflections
4735 independent reflections
3450 reflections with $I > 2\sigma(I)$
R_{int} = 0.020
3 standard reflections
frequency: 180 min
intensity decay: none

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.047
$wR(F^2)$ = 0.130
S = 1.02
4735 reflections
285 parameters
H atoms treated by a mixture of independent and constrained refinement
$\Delta\rho_{max}$ = 0.18 e Å^{-3}
$\Delta\rho_{min}$ = −0.20 e Å^{-3}

Table 1
Hydrogen-bond geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
N11—H11···O6^{i}	0.90 (2)	2.01 (2)	2.866 (2)	158 (2)

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

Data collection: *CAD-4 Manual* (Enraf–Nonius, 1988); cell refinement: *CAD-4 Manual*; data reduction: *HELENA* (Spek, 1997); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker 2000) and *ORTEPII* (Johnson, 1976); software used to prepare material for publication: *SHELXTL*.

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Supplementary data and figures for this paper are available from the IUCr electronic archives (Reference: SU2039).

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supporting information

Acta Cryst. (2008). E**64**, o368 [doi:10.1107/S1600536807067670]

1-Benzyl-2-(1*H*-indol-3-yl)-5-oxopyrrolidine-2-carbonitrile

Rafael Tamazyan, Ayvazyan Armen, Martirosyan Ashot, Gasparyan Sahak and Raymond Schinazi

S1. Comment

Our interest in the X-ray structural investigation of the title compound was stimulated by its potential HIV-1 RT inhibition properties. Compounds of this type belong to family of non-nucleoside reverse transcriptase inhibitors (NNRTIs).

A view of the molecular structure of the title compound is given in Fig. 1. A l l the bond distances in the molecule are in good agreement with their mean statistical values, except bond C2—C7 which is relatively short, 1.493 (2) Å. We believe that this shortening is caused by the inductive effect of the carbonitryl group C7 ≡N11.

In the crystal structure infinite chains along [010] direction are formed *via* an intermolecular N—H···O hydrogen bond (see Fig. 2 and Table 1).

S2. Experimental

The title compound was synthesized by the cycloalkylation of N1-benzyl-N1-cyano(1*H*-3-indolyl)methyl-3-chloro-propanamide in the phase-transfer catalysis condition (Martirosyan *et al.*, 2000, 2004). The compound as synthesized is a racemic mixture. Colorless crystals, suitable for X-ray analysis, were grown from a methanol solution of the compound.

S3. Refinement

The H-atoms were located from difference Fourier syntheses and freely refined: N—H = 0.90 (2) Å; C—H = 0.94 (2) - 1.02 (2) Å.

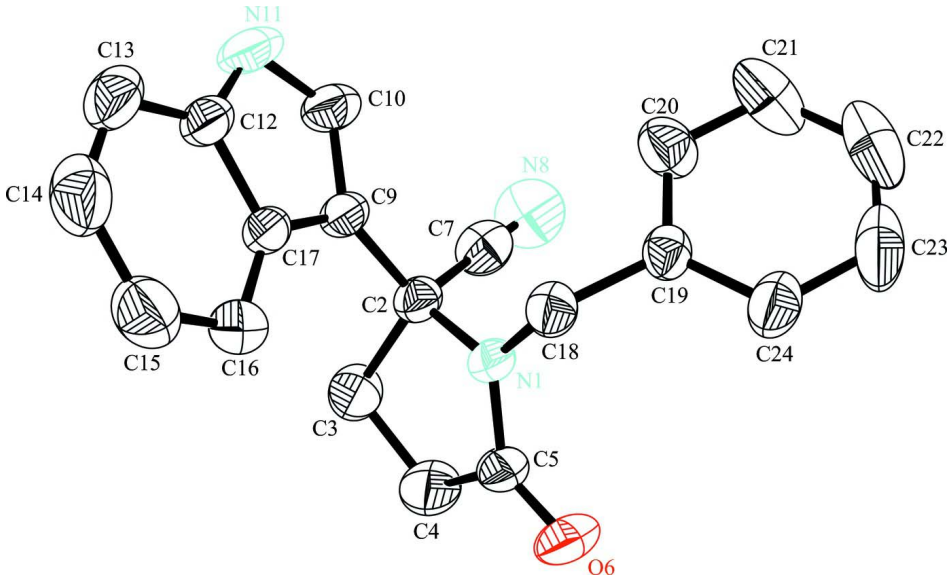

Figure 1

A view of molecular structure of the title compound, showing the atomic numbering scheme and displacement ellipsoids drawn at the 50% probability level. H atoms are omitted for clarity.

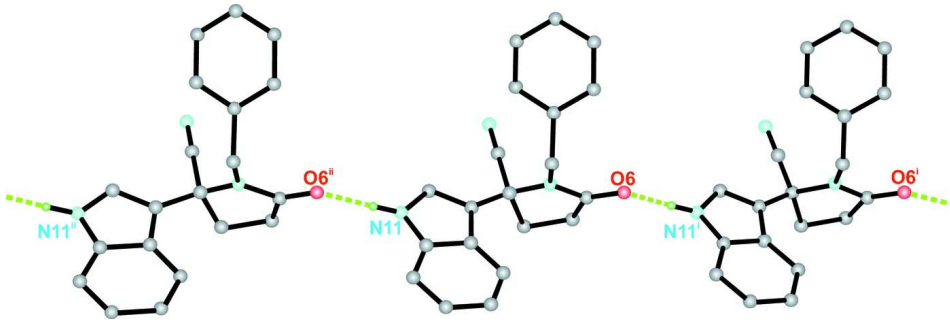

Figure 2

partial view of the crystal packing showing the formation of the infinite chain of molecules formed *via* hydrogen bonding [for clarifity only H atoms participating in bonding are depicted]. Symmetry codes: (i) *x*, 1 + *y*, *z*; (ii) *x*, -1 + *y*, *z*.

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Crystal data

$C_{20}H_{17}N_3O$
$M_r = 315.37$
Triclinic, $P\overline{1}$
Hall symbol: -P 1
$a = 7.5781\ (15)$ Å
$b = 9.4521\ (19)$ Å
$c = 12.409\ (3)$ Å
$\alpha = 78.02\ (3)°$
$\beta = 83.05\ (3)°$
$\gamma = 69.68\ (3)°$
$V = 814.2\ (3)$ Å^3
$Z = 2$
$F(000) = 332$
$D_x = 1.286$ Mg m^{-3}
Mo $K\alpha$ radiation, $\lambda = 0.71073$ Å
Cell parameters from 22 reflections
$\theta = 14.2–17.5°$
$\mu = 0.08$ mm^{-1}
$T = 293$ K
Prism, colourless
0.4 × 0.3 × 0.2 mm

Data collection

Enraf–Nonius CAD-4 diffractometer
Radiation source: fine-focus sealed tube
Graphite monochromator
$\theta/2\theta$ scans
9470 measured reflections
4735 independent reflections
3450 reflections with $I > 2\sigma(I)$
$R_{int} = 0.020$
$\theta_{max} = 30.0°$, $\theta_{min} = 1.7°$
$h = -10 \rightarrow 10$
$k = -13 \rightarrow 13$
$l = -17 \rightarrow 17$
3 standard reflections every 180 min
intensity decay: none

Refinement

Refinement on F^2
Least-squares matrix: full
$R[F^2 > 2\sigma(F^2)] = 0.047$
$wR(F^2) = 0.130$
$S = 1.02$
4735 reflections
285 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 atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.0649P)^2 + 0.0907P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max} = 0.18$ e Å^{-3}
$\Delta\rho_{min} = -0.20$ e Å^{-3}

Special details

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_{iso}*/U_{eq}
N1	0.22574 (14)	0.71961 (10)	0.23198 (8)	0.0367 (2)
C2	0.20774 (17)	0.64700 (12)	0.14116 (9)	0.0385 (2)
C3	0.3119 (3)	0.72278 (16)	0.04282 (12)	0.0552 (4)
H3A	0.448 (3)	0.655 (2)	0.0402 (14)	0.066 (5)*
H3B	0.258 (2)	0.728 (2)	−0.0253 (16)	0.069 (5)*
C4	0.2913 (3)	0.87637 (17)	0.07212 (14)	0.0642 (4)
H4A	0.182 (3)	0.955 (3)	0.0430 (19)	0.096 (7)*
H4B	0.408 (3)	0.908 (3)	0.049 (2)	0.102 (7)*
C5	0.26566 (17)	0.85107 (13)	0.19576 (12)	0.0453 (3)
O6	0.27772 (15)	0.93414 (11)	0.25649 (10)	0.0628 (3)
C7	0.0051 (2)	0.69595 (15)	0.11645 (11)	0.0503 (3)
N8	−0.1486 (2)	0.73626 (18)	0.09409 (14)	0.0761 (4)
C9	0.28897 (17)	0.47561 (12)	0.16540 (9)	0.0379 (2)
C10	0.2034 (2)	0.37431 (15)	0.15315 (11)	0.0480 (3)
H10	0.076 (2)	0.3968 (19)	0.1273 (14)	0.063 (5)*

H11	0.298 (3)	0.140 (2)	0.1869 (15)	0.073 (5)*
N11	0.32401 (19)	0.22756 (13)	0.18058 (10)	0.0543 (3)
C12	0.48874 (19)	0.23143 (13)	0.21285 (10)	0.0435 (3)
C13	0.6498 (2)	0.11135 (15)	0.24876 (12)	0.0574 (4)
H13	0.655 (2)	0.009 (2)	0.2546 (15)	0.068 (5)*
C14	0.7955 (2)	0.14884 (19)	0.27645 (14)	0.0656 (4)
H14	0.911 (3)	0.066 (2)	0.3034 (16)	0.079 (5)*
C15	0.7826 (2)	0.30164 (19)	0.26931 (15)	0.0641 (4)
H15	0.887 (3)	0.324 (2)	0.2894 (16)	0.078 (5)*
C16	0.62465 (19)	0.42094 (15)	0.23300 (12)	0.0498 (3)
H16	0.620 (2)	0.5269 (19)	0.2264 (14)	0.059 (4)*
C17	0.47300 (17)	0.38670 (12)	0.20376 (9)	0.0379 (2)
C18	0.20486 (17)	0.65739 (14)	0.34923 (10)	0.0395 (2)
H18A	0.258 (2)	0.5459 (17)	0.3571 (12)	0.047 (4)*
H18B	0.280 (2)	0.6986 (17)	0.3851 (13)	0.054 (4)*
C19	0.00691 (16)	0.70242 (13)	0.40041 (9)	0.0376 (2)
C20	−0.1177 (2)	0.63319 (19)	0.38244 (12)	0.0545 (3)
H20	−0.077 (2)	0.557 (2)	0.3324 (15)	0.070 (5)*
C21	−0.2973 (2)	0.6704 (3)	0.43232 (14)	0.0744 (5)
H21	−0.385 (3)	0.624 (2)	0.4196 (19)	0.098 (7)*
C22	−0.3538 (3)	0.7749 (2)	0.50150 (15)	0.0782 (6)
H22	−0.484 (3)	0.800 (2)	0.5378 (19)	0.099 (7)*
C23	−0.2317 (3)	0.8426 (2)	0.52187 (14)	0.0750 (5)
H23	−0.264 (3)	0.914 (3)	0.5704 (19)	0.095 (7)*
C24	−0.0502 (2)	0.80719 (16)	0.47138 (11)	0.0542 (3)
H24	0.038 (2)	0.858 (2)	0.4834 (14)	0.065 (5)*

Atomic displacement parameters (Å²)

	U^{11}	U^{22}	U^{33}	U^{12}	U^{13}	U^{23}
N1	0.0439 (5)	0.0279 (4)	0.0399 (5)	−0.0152 (4)	0.0056 (4)	−0.0083 (3)
C2	0.0494 (6)	0.0315 (5)	0.0350 (5)	−0.0157 (5)	0.0037 (5)	−0.0062 (4)
C3	0.0742 (10)	0.0429 (7)	0.0425 (7)	−0.0210 (7)	0.0150 (7)	−0.0026 (5)
C4	0.0842 (11)	0.0384 (7)	0.0649 (9)	−0.0266 (7)	0.0159 (8)	0.0017 (6)
C5	0.0426 (6)	0.0272 (5)	0.0655 (8)	−0.0132 (4)	0.0051 (5)	−0.0089 (5)
O6	0.0691 (7)	0.0387 (5)	0.0905 (8)	−0.0253 (5)	0.0011 (6)	−0.0228 (5)
C7	0.0609 (8)	0.0433 (6)	0.0447 (7)	−0.0147 (6)	−0.0096 (6)	−0.0040 (5)
N8	0.0693 (9)	0.0762 (10)	0.0782 (10)	−0.0154 (7)	−0.0267 (8)	−0.0059 (8)
C9	0.0500 (6)	0.0304 (5)	0.0358 (5)	−0.0170 (5)	0.0045 (5)	−0.0089 (4)
C10	0.0624 (8)	0.0415 (6)	0.0490 (7)	−0.0263 (6)	−0.0024 (6)	−0.0121 (5)
N11	0.0788 (8)	0.0341 (5)	0.0594 (7)	−0.0295 (5)	0.0002 (6)	−0.0122 (5)
C12	0.0605 (7)	0.0309 (5)	0.0390 (6)	−0.0180 (5)	0.0111 (5)	−0.0089 (4)
C13	0.0738 (10)	0.0326 (6)	0.0532 (8)	−0.0100 (6)	0.0146 (7)	−0.0041 (5)
C14	0.0545 (9)	0.0536 (8)	0.0666 (10)	−0.0005 (7)	0.0081 (7)	0.0005 (7)
C15	0.0467 (8)	0.0635 (9)	0.0771 (11)	−0.0168 (7)	0.0016 (7)	−0.0070 (8)
C16	0.0471 (7)	0.0418 (6)	0.0622 (8)	−0.0188 (5)	0.0056 (6)	−0.0105 (6)
C17	0.0475 (6)	0.0299 (5)	0.0369 (5)	−0.0156 (4)	0.0097 (5)	−0.0095 (4)
C18	0.0411 (6)	0.0387 (6)	0.0377 (6)	−0.0114 (5)	−0.0004 (5)	−0.0090 (4)

C19	0.0429 (6)	0.0351 (5)	0.0307 (5)	−0.0093 (4)	0.0006 (4)	−0.0049 (4)
C20	0.0553 (8)	0.0719 (9)	0.0436 (7)	−0.0304 (7)	0.0050 (6)	−0.0144 (6)
C21	0.0521 (9)	0.1182 (16)	0.0534 (9)	−0.0380 (10)	0.0035 (7)	−0.0031 (9)
C22	0.0529 (9)	0.0940 (13)	0.0560 (9)	−0.0023 (9)	0.0154 (7)	0.0060 (9)
C23	0.0899 (13)	0.0588 (9)	0.0509 (8)	0.0010 (9)	0.0230 (8)	−0.0149 (7)
C24	0.0726 (9)	0.0435 (7)	0.0429 (7)	−0.0147 (6)	0.0073 (6)	−0.0138 (5)

Geometric parameters (Å, º)

N1—C5	1.3542 (15)	C13—C14	1.370 (3)
N1—C18	1.4634 (16)	C13—H13	0.944 (18)
N1—C2	1.4775 (15)	C14—C15	1.398 (2)
C2—C7	1.493 (2)	C14—H14	0.99 (2)
C2—C9	1.4979 (16)	C15—C16	1.375 (2)
C2—C3	1.5562 (18)	C15—H15	0.96 (2)
C3—C4	1.521 (2)	C16—C17	1.4018 (18)
C3—H3A	1.009 (18)	C16—H16	0.976 (16)
C3—H3B	0.969 (18)	C18—C19	1.5076 (17)
C4—C5	1.502 (2)	C18—H18A	0.977 (15)
C4—H4A	0.95 (2)	C18—H18B	0.983 (16)
C4—H4B	1.02 (2)	C19—C20	1.3824 (19)
C5—O6	1.2269 (16)	C19—C24	1.3842 (17)
C7—N8	1.142 (2)	C20—C21	1.383 (2)
C9—C10	1.3695 (17)	C20—H20	0.989 (18)
C9—C17	1.4348 (18)	C21—C22	1.366 (3)
C10—N11	1.3689 (19)	C21—H21	0.95 (2)
C10—H10	0.994 (17)	C22—C23	1.365 (3)
N11—C12	1.3707 (19)	C22—H22	1.00 (2)
N11—H11	0.90 (2)	C23—C24	1.399 (2)
C12—C13	1.391 (2)	C23—H23	0.94 (2)
C12—C17	1.4120 (15)	C24—H24	0.986 (17)
C5—N1—C18	122.70 (10)	C14—C13—H13	122.7 (10)
C5—N1—C2	112.91 (10)	C12—C13—H13	120.0 (10)
C18—N1—C2	124.39 (9)	C13—C14—C15	121.35 (15)
N1—C2—C7	109.37 (10)	C13—C14—H14	119.6 (11)
N1—C2—C9	113.04 (10)	C15—C14—H14	119.1 (11)
C7—C2—C9	110.17 (11)	C16—C15—C14	121.65 (16)
N1—C2—C3	101.87 (10)	C16—C15—H15	118.9 (11)
C7—C2—C3	108.24 (12)	C14—C15—H15	119.4 (11)
C9—C2—C3	113.77 (10)	C15—C16—C17	118.50 (13)
C4—C3—C2	104.09 (11)	C15—C16—H16	120.4 (9)
C4—C3—H3A	111.4 (10)	C17—C16—H16	121.1 (9)
C2—C3—H3A	107.7 (10)	C16—C17—C12	118.72 (12)
C4—C3—H3B	115.6 (11)	C16—C17—C9	134.95 (11)
C2—C3—H3B	109.1 (11)	C12—C17—C9	106.31 (11)
H3A—C3—H3B	108.5 (14)	N1—C18—C19	116.05 (10)
C5—C4—C3	104.26 (11)	N1—C18—H18A	106.8 (9)

C5—C4—H4A	108.1 (14)	C19—C18—H18A	109.9 (8)
C3—C4—H4A	112.0 (13)	N1—C18—H18B	103.9 (9)
C5—C4—H4B	109.1 (14)	C19—C18—H18B	108.7 (9)
C3—C4—H4B	112.6 (13)	H18A—C18—H18B	111.5 (12)
H4A—C4—H4B	110.6 (19)	C20—C19—C24	118.62 (13)
O6—C5—N1	124.06 (13)	C20—C19—C18	120.58 (11)
O6—C5—C4	126.73 (12)	C24—C19—C18	120.70 (12)
N1—C5—C4	109.21 (11)	C19—C20—C21	120.72 (15)
N8—C7—C2	177.60 (16)	C19—C20—H20	118.9 (10)
C10—C9—C17	107.09 (11)	C21—C20—H20	120.3 (10)
C10—C9—C2	126.59 (12)	C22—C21—C20	120.49 (18)
C17—C9—C2	126.31 (10)	C22—C21—H21	118.2 (14)
N11—C10—C9	109.47 (13)	C20—C21—H21	121.3 (14)
N11—C10—H10	122.1 (10)	C23—C22—C21	119.72 (16)
C9—C10—H10	128.4 (10)	C23—C22—H22	120.8 (12)
C10—N11—C12	109.29 (11)	C21—C22—H22	119.5 (12)
C10—N11—H11	127.3 (11)	C22—C23—C24	120.51 (16)
C12—N11—H11	122.9 (11)	C22—C23—H23	122.7 (14)
N11—C12—C13	129.75 (12)	C24—C23—H23	116.8 (14)
N11—C12—C17	107.83 (12)	C19—C24—C23	119.93 (17)
C13—C12—C17	122.42 (14)	C19—C24—H24	118.7 (10)
C14—C13—C12	117.34 (13)	C23—C24—H24	121.3 (10)

Hydrogen-bond geometry (Å, º)

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N11—H11···O6^{i}	0.90 (2)	2.01 (2)	2.866 (2)	158 (2)

Symmetry code: (i) *x*, *y*−1, *z*.