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Key indicators

Single-crystal X-ray study

$T = 296$ K

Mean $\sigma(\text{C}-\text{C}) = 0.013$ Å

R factor = 0.051

wR factor = 0.175

Data-to-parameter ratio = 14.6

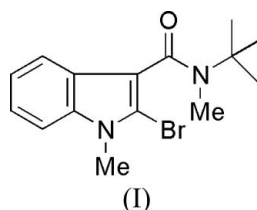
For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

2-Bromo-*N*-*tert*-butyl-*N*,1-dimethyl-1*H*-indole-3-carboxamide

The crystal structure of the title compound, $\text{C}_{15}\text{H}_{19}\text{BrN}_2\text{O}$, reveals that the amide group is twisted out of π -conjugation with the pyrrole double bond due to steric hindrance by the Br atom.

Comment

The background to this study is set out in Badenock *et al.* (2007). We now describe the X-crystal structure determination of (I).



The X-ray crystallographic analysis confirms the proposed molecular structure and atom connectivity for (I) (Fig. 1). The indole ring system is planar, with a maximum deviation of 0.025 (9) Å for atom C5. The sum of the bond angles around N1 and N2 are 360.1 and 358.4°, respectively, indicating sp^2 hybridization. However, the O1–C11–N2–C13 torsion angle of -18.9 (11)° reveals imperfect π -conjugation in the amide group due to repulsion between the *tert*-butyl group and the carbonyl oxygen. In addition, the carbonyl oxygen (O1) is severely twisted away from the bromine atom (Br1) with a O1–C11–C3–C2 torsion angle of 134.5 (9)°, indicating little or no π -conjugation between the pyrrole double bond and the carbonyl group. The C2–Br1 bond length is 1.862 (8) Å.

Experimental

To a stirred solution of *N*-*tert*-butyl-*N*,1-dimethyl-1*H*-indole-3-carboxamide (816 mg, 3.34 mmol, 1 equivalent) in tetrahydrofuran (40 ml) was added slowly *t*BuLi (3.0 ml, 5.01 mmol, 1.7 *M* in hexanes, 1.5 equivalents) at 195 K and the solution was stirred at 195 K for 1 h, then warmed to room temperature over 30 min before recooling to 195 K. At this time, the anion was treated with dried 1,2-dibromo-1,1,2,2-tetrachloroethane (1.63 g, 5.01 mmol, 1.5 equivalents) in tetrahydrofuran (20 ml). The solution was warmed to room temperature overnight, then poured on to ice–water (100 ml) and stirred for 2 h. No precipitate formed upon stirring. The aqueous layer was extracted with CH_2Cl_2 (4 × 50 ml). The organic layers were combined, washed with brine (1 × 100 ml), dried (Na_2SO_4), and concentrated *in vacuo* to give a brown oil. Purification using flash column chromatography (2:1 hexanes–ethyl acetate) gave compound

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(I) as a yellow solid (887 mg, 86%). An analytical sample of (I) was obtained by several recrystallizations from diethyl ether. Single crystals suitable for X-diffraction study were grown in diethyl ether (m.p. 378–379 K).

Crystal data

$C_{15}H_{19}BrN_2O$	$V = 1436 (2) \text{ \AA}^3$
$M_r = 323.23$	$Z = 4$
Monoclinic, $P2_1/n$	Mo $K\alpha$ radiation
$a = 7.373 (7) \text{ \AA}$	$\mu = 2.86 \text{ mm}^{-1}$
$b = 21.453 (7) \text{ \AA}$	$T = 296 (2) \text{ K}$
$c = 9.132 (9) \text{ \AA}$	$0.50 \times 0.40 \times 0.30 \text{ mm}$
$\beta = 96.06 (9)^\circ$	

Data collection

Rigaku AFC-6S diffractometer	2526 independent reflections
Absorption correction: ψ scan (North <i>et al.</i> , 1968)	992 reflections with $I > 2\sigma(I)$
$T_{\min} = 0.329$, $T_{\max} = 0.481$ (expected range = 0.291–0.425)	3 standard reflections
2526 measured reflections	every 150 reflections
	intensity decay: 1.4%

Refinement

$R[F^2 > 2\sigma(F^2)] = 0.051$	173 parameters
$wR(F^2) = 0.175$	All H-atom parameters refined
$S = 1.02$	$\Delta\rho_{\max} = 0.51 \text{ e \AA}^{-3}$
2526 reflections	$\Delta\rho_{\min} = -0.45 \text{ e \AA}^{-3}$

H atoms were included in the riding-model approximation, with C–H = 0.93–0.96 Å and $U_{\text{iso}}(\text{H}) = 1.18$ or $1.20U_{\text{eq}}(\text{C})$. Owing to the large number of weak high-angle reflections, the ratio of observed to unique reflections is low (39%), and this is a structure of low precision.

Data collection: *MSC/AFC Diffractometer Control Software* (Molecular Structure Corporation, 1994); cell refinement: *MSC/AFC Diffractometer Control Software*; data reduction: *CrystalStructure* (Rigaku/MSC, 2005); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3* (Farrugia, 1997); software used to prepare material for publication: *CrystalStructure*.

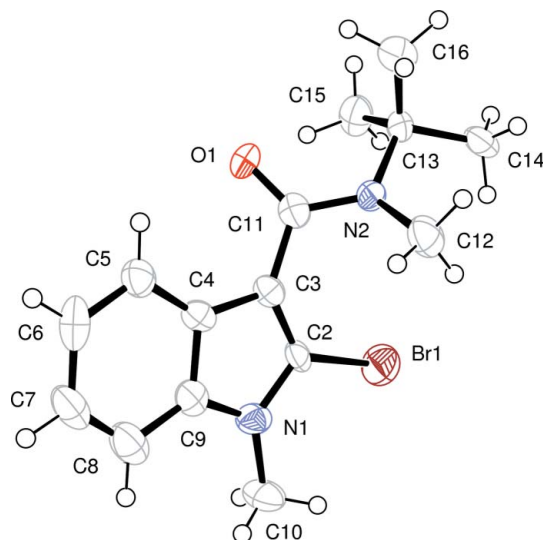


Figure 1

The molecular structure of (I), showing the atom-labelling scheme and 50% probability displacement ellipsoids.

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