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## Key indicators

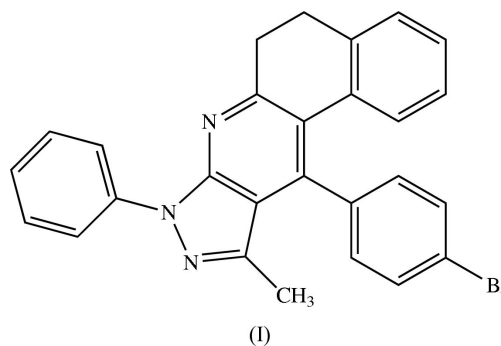
Single-crystal X-ray study  
 $T = 120$  K  
Mean  $\sigma(\text{C}-\text{C}) = 0.004$  Å  
 $R$  factor = 0.047  
 $wR$  factor = 0.102  
Data-to-parameter ratio = 17.8For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.11-(4-Bromophenyl)-10-methyl-8-phenyl-6,8-dihydro-5H-benzo[*f*]pyrazolo[3,4-*b*]-quinolineThe title compound,  $\text{C}_{27}\text{H}_{20}\text{BrN}_3$ , is isostructural with the chloro analogue: the molecules are linked by two independent  $\text{C}-\text{H} \cdots \pi(\text{arene})$  hydrogen bonds into chains of edge-fused rings.

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## Comment

The title compound, (I) (Fig. 1), is isostructural with 11-(4-chlorophenyl)-10-methyl-8-phenyl-6,8-dihydro-5H-benzo[*f*]pyrazolo[3,4-*b*]quinoline, (II) (Serrano *et al.*, 2005).The bond lengths and angles, and the molecular conformation, for (I) are all virtually identical with those for (II). Two independent  $\text{C}-\text{H} \cdots \pi(\text{arene})$  hydrogen bonds (Table 1) link the molecules of (I) into a [101] chain of centrosymmetric edge-fused rings, just as in (II). There are no direction-specific interactions between adjacent chains:  $\text{C}-\text{H} \cdots \text{N}$  and  $\text{C}-\text{H} \cdots \text{Br}$  hydrogen bonds, and aromatic  $\pi-\pi$  stacking interactions are all absent from the structure of (I).

## Experimental

Equimolar amounts of 5-amino-3-methyl-1-phenylpyrazole (173 mg, 1.0 mmol), 2-tetralone (146 mg, 1.0 mmol) and 4-bromobenzaldehyde (185.0 mg, 1.0 mmol) were placed in open Pyrex-glass vessels and irradiated in a domestic microwave oven for 4 min at 600 W. The reaction mixture was then extracted with ethanol, and, after removal of the solvent, the product was recrystallized from ethanol/dimethylformamide to give crystals suitable for single-crystal X-ray diffraction.

## Crystal data

 $\text{C}_{27}\text{H}_{20}\text{BrN}_3$   
 $M_r = 466.37$   
Triclinic,  $P\bar{1}$   
 $a = 7.0237$  (3) Å  
 $b = 12.8964$  (7) Å  
 $c = 13.3517$  (7) Å  
 $\alpha = 106.630$  (3)°  
 $\beta = 101.423$  (3)°  
 $\gamma = 102.274$  (3)°  
 $V = 1088.18$  (10) Å<sup>3</sup> $Z = 2$   
 $D_x = 1.423$  Mg m<sup>-3</sup>  
Mo  $K\alpha$  radiation  
Cell parameters from 5001 reflections  
 $\theta = 3.1-27.7^\circ$   
 $\mu = 1.91$  mm<sup>-1</sup>  
 $T = 120$  (2) K  
Plate, colourless  
 $0.36 \times 0.14 \times 0.03$  mm

## Data collection

Bruker–Nonius KappaCCD  
diffractometer  
 $\varphi$  and  $\omega$  scans  
Absorption correction: multi-scan  
(SADABS; Sheldrick, 2003)  
 $T_{\min} = 0.547$ ,  $T_{\max} = 0.945$   
223424 measured reflections

5001 independent reflections  
3175 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.085$   
 $\theta_{\text{max}} = 27.7^\circ$   
 $h = -8 \rightarrow 9$   
 $k = -16 \rightarrow 16$   
 $l = -17 \rightarrow 17$

## Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.047$   
 $wR(F^2) = 0.102$   
 $S = 1.03$   
5001 reflections  
281 parameters

H-atom parameters constrained  
 $w = 1/[\sigma^2(F_o^2) + (0.0461P)^2]$   
where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} < 0.001$   
 $\Delta\rho_{\text{max}} = 0.41 \text{ e } \text{\AA}^{-3}$   
 $\Delta\rho_{\text{min}} = -0.47 \text{ e } \text{\AA}^{-3}$

Table 1

Hydrogen-bonding geometry ( $\text{\AA}$ ,  $^\circ$ ).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$C113-H113\cdots Cg1^i$	0.95	2.71	3.588 (3)	154
$C115-H115\cdots Cg2^{ii}$	0.95	2.81	3.589 (3)	140

Symmetry codes: (i)  $-x, 1-y, -z$ ; (ii)  $1-x, 1-y, 1-z$ . Note:  $Cg1$  is the centroid of ring C81–C86, and  $Cg2$  is the centroid of ring C1, C2, C3, C4, C4A, C11B

All H atoms were located in difference maps in fully ordered sites; they were then treated as riding atoms, with C–H distances 0.95 (aromatic), 0.98 (methyl) or 0.99  $\text{\AA}$  ( $\text{CH}_2$ ), and with  $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ , or  $1.5U_{\text{eq}}(\text{C})$  for the methyl group.

Data collection: COLLECT (Hooft, 1999); cell refinement: DENZO (Otwinowski & Minor, 1997) and COLLECT; data reduction: DENZO and COLLECT; program(s) used to solve structure: OSCAIL (McArdle, 2003) and SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: OSCAIL and SHELXL97 (Sheldrick, 1997); molecular graphics: PLATON (Spek, 2003); software used to prepare material for publication: SHELXL97 and PRPKAPPA (Ferguson, 1999).

X-ray data were collected at the EPSRC X-ray Crystallographic Service, University of Southampton, England. JC

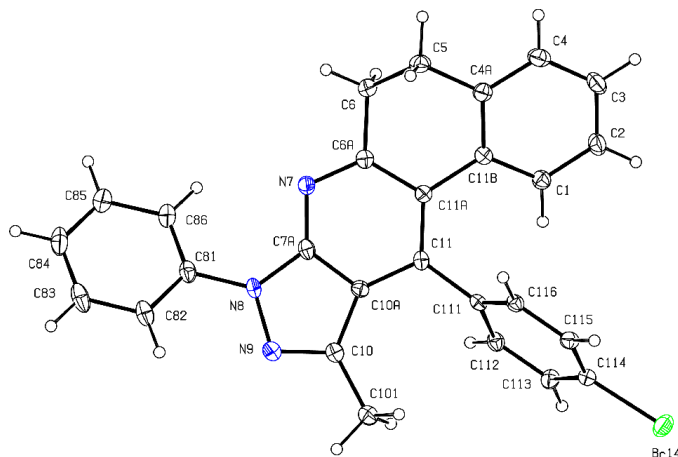


Figure 1

The molecule of compound (I), showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level.

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