Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 291 KMean $\sigma(C-C) = 0.002 \text{ Å}$ R factor = 0.043 wR factor = 0.110 Data-to-parameter ratio = 20.1

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

6-Methyl-2-[2,2,6,6-tetramethyl-5-(2-pyridyl)hepta-3,4-dien-3-yl]pyridine

The title compound, $C_{21}H_{26}N_2$, a potential chiral ligand for transition metal-catalysed reactions, crystallizes with one molecule in the asymmetric unit; the molecule has a pseudo-twofold axis perpendicular to the central C=C fragment.

Received 5 January 2006 Accepted 26 January 2006



Experimental

The title compound, (I), was synthesized in racemic form by $S_{\rm N}2^\prime$ substitution of a propargyl acetate with a cyanocuprate (Krause & Hoffmann-Röder, 2004). It was dissolved in a small amount of tetrahydrofuran and hexane, and crystals were obtained by evaporation.





Figure 1

The molecular structure of the title compound, showing the labellng of all non-H atoms. Displacement ellipsoids are shown at the 30% probability level.

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organic papers

Data collection

Nonius KappaCCD diffractometer	$R_{\rm int} = 0.032$
ω scans	$\theta_{\rm max} = 27.5^{\circ}$
Absorption correction: none	$h = -12 \rightarrow 12$
16854 measured reflections	$k = -13 \rightarrow 13$
4706 independent reflections	$l = -14 \rightarrow 13$
1974 reflections with $I > 2\sigma(I)$	

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.043$	$w = 1/[\sigma^2 (F_o^2) + (0.0356P)^2]$
$wR(F^2) = 0.110$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.12	$(\Delta/\sigma)_{\rm max} = 0.001$
4706 reflections	$\Delta \rho_{\rm max} = 0.15 \text{ e} \text{ Å}^{-3}$
234 parameters	$\Delta \rho_{\rm min} = -0.15 \text{ e } \text{\AA}^{-3}$

H atoms were placed in calculated positions, with C–H = 0.93–0.96 Å, and were refined as riding, with $U_{\rm iso}({\rm H}) = 1.5U_{\rm eq}({\rm C})$ for methyl or $1.2U_{\rm eq}({\rm C})$ for others; the methyl groups were allowed to rotate but not to tip.

Data collection: *COLLECT* (Nonius, 1998); cell refinement: *DENZO* and *SCALEPACK* (Otwinowski & Minor, 1997); data reduction: *DENZO* and *SCALEPACK*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1990); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL-Plus* (Sheldrick, 1991); software used to prepare material for publication: *SHELXL, PARST95* (Nardelli, 1995) and *PLATON* (Spek, 2003).

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