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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=183 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.004 \AA$
$R$ factor $=0.078$
$w R$ factor $=0.142$
Data-to-parameter ratio $=14.1$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## 2,6-Bis(3,5-dimethylpyrazol-1-ylmethyl)-4-methylphenol

The crystal structure of the title compound, $\mathrm{C}_{19} \mathrm{H}_{24} \mathrm{~N}_{4} \mathrm{O}$, has been determined in the monoclinic space group $P 2_{1} / c$. The two pyrazole substituents are arranged trans to each other; the dihedral angle between them is $83.9(1)^{\circ}$. There is an intramolecular hydrogen bond, with an $\mathrm{O} \cdots \mathrm{N}$ distance of 2.769 (4) $\AA$, and an intermolecular hydrogen bond, with an $\mathrm{O} \cdots \mathrm{N}$ distance of 3.197 (4) $\AA$.

## Comment

Like other tripod multidentate ligands, the pentadentate 2,6-bis(3,5-dimethylpyrazol-1-ylmethyl)-4-methylphenol, (I), has a good capacity for coordination with transition metals ions, giving rise to chelate complexes with intense colors.

(I)

Suzuki et al. (1981) linked two bis(2-pyridylmethyl)amine groups to two arms of 2,6-bis(chloromethyl)-4-methylphenol, resulting in a tripod multidentate ligand, 2,6-bis[bis(2-pyridylmethyl)-amino methyl]-4-methylphenol, $\mathrm{C}_{33} \mathrm{H}_{34} \mathrm{~N}_{6} \mathrm{O}$. In the current work, we have joined two 3,5-dimethylpyrazole groups to two arms of 2,6-bis(chloromethyl)-4-methylphenol and produced a new pentadentate ligand, (I). As the most stable configuration, the two pyrazole groups of the molecule are arranged trans to each other, with a dihedral angle of $83.9(1)^{\circ}$. The compound acts as a versatile ligand for metal ions (such as $\mathrm{Zn}^{2+}$ ) by coordinating through pyrazole N and hydroxy O atoms after deprotonation and intramolecular rotation.

The geometric parameters of (I) are listed in Table 1, and the molecular conformation and crystal packing are illustrated in Figs. 1 and 2. .

## Experimental

Compound (I) was synthesized via a modification of the method of Kamaras et al. (1994). The smaller ligand, 3,5-dimethylpyrazole, which acts as the chelating arm in the target compound, was prepared according to the method of Wiley \& Hexner (1963). To a solution of 3,5-dimethylpyrazole in dimethylformamide, containing NaH , was added dropwise 2,6-bis(chloromethyl)-4-methylphenol, with vigorous stirring at room temperature (yield $80 \%$; m.p. 398 K ). 2,6-Bis[1-(3,5-

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Figure 1
A view of the molecular structure of (I), with the atom-numbering scheme. Displacement ellipsoids are drawn at the $50 \%$ probability level and H atoms are shown as small spheres of arbitrary radii.
dimethyl)pyrazolemethyl]-4-methylphenol ( 100 mg ) was dissolved in $\mathrm{CHCl}_{3}(2 \mathrm{ml})$, and the solution was allowed to evaporate slowly over several days. Brown crystals suitable for X-ray diffraction were collected once all of the solution had evaporated.

## Crystal data

$\mathrm{C}_{19} \mathrm{H}_{24} \mathrm{~N}_{4} \mathrm{O}$
$M_{r}=324.42$
Monoclinic, $P 2_{1} / c$
$a=9.508(3) \AA \AA$
$b=18.747(6) \AA$
$c=10.116(3) \AA$
$\beta=105.085(5)^{\circ}$
$V=1741.0(9) \AA^{3}$
$Z=4$

## Data collection

Bruker SMART CCD area-detector diffractometer
$\omega$ scans
Absorption correction: multi-scan
(SADABS; Sheldrick, 1996)
$T_{\text {min }}=0.984, T_{\text {max }}=0.992$
7045 measured reflections
$D_{x}=1.238 \mathrm{Mg} \mathrm{m}^{-3}$
Mo $K \alpha$ radiation
Cell parameters from 8255
$\quad$ reflections
$\theta=2.4-19.6^{\circ}$
$\mu=0.08 \mathrm{~mm}^{-1}$
$T=183(2) \mathrm{K}$
Slab, colorless
$0.2 \times 0.2 \times 0.1 \mathrm{~mm}$

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.078$
$w R\left(F^{2}\right)=0.142$
$S=0.98$
3053 reflections
217 parameters


Figure 2
The crystal packing of (I), viewed down the $b$ axis.

Table 1
Hydrogen-bonding geometry $\left(\AA^{\circ},^{\circ}\right)$.

| $D-\mathrm{H} \cdots A$ | $D-\mathrm{H}$ | $\mathrm{H} \cdots A$ | $D \cdots A$ | $D-\mathrm{H} \cdots A$ |
| :--- | :--- | :--- | :--- | :--- |
| O1-H1 $\cdots \mathrm{N} 1$ | 0.84 | 1.95 | $2.769(4)$ | 163 |
| O1-H1 2 N 2 | 0.84 | 2.56 | $3.197(4)$ | 133 |

All H atoms were initially located in a difference Fourier map. They were then constrained to as riding, with $\mathrm{C}-\mathrm{H}=0.98-1.00 \AA$ and $U_{\text {iso }}(\mathrm{H})=1.2$ or $1.5 U_{\text {eq }}(\mathrm{C})$ of the parent atom. .

Data collection: SMART (Bruker, 2000); cell refinement: SMART; data reduction: SAINT (Bruker, 2000) and SHELXTL/PC (Sheldrick, 1999); program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL/PC; software used to prepare material for publication: $S H E L X T L / P C$.

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