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## Key indicators

Single-crystal X-ray study  
 $T = 294\text{ K}$   
Mean  $\sigma(\text{C}-\text{C}) = 0.007\text{ \AA}$   
 $R$  factor = 0.068  
 $wR$  factor = 0.155  
Data-to-parameter ratio = 19.3For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.**(S)-2,2'-Bis(dicyclohexylphosphinoamino)-1,1'-binaphthyl**The the crystal structure of the title compound,  $\text{C}_{44}\text{H}_{58}\text{N}_2\text{P}_2$ , the molecule has a non-crystallographic twofold axis. The bond lengths and angles are within the expected ranges.

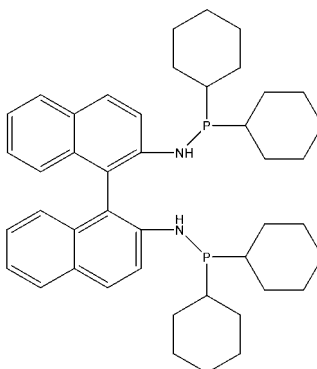
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## Comment

Aminophosphine ligands exhibit good to excellent enantioselectivity and high reactivity in the hydrogenation of prochiral olefins (Zhang *et al.*, 1998; Chan *et al.*, 1997). Recent research shows that the aminophosphine ligands derived from dialkylphosphine chloride exhibit significantly different enantioselectivity in the catalytic hydrogenation reaction due to the steric and electronic modulation of the substituent groups on the P atom (Trabesinger *et al.*, 1997; RajanBabu *et al.*, 1997). As part of our investigation of this phenomenon, we report the crystal structure of the title compound, (I).



(I)

The molecular structure of (I) (Fig. 1) shows that the torsion angles  $\text{C}9-\text{C}10-\text{C}11-\text{C}12$  and  $\text{C}1-\text{C}10-\text{C}11-\text{C}20$  are  $81.4(4)$  and  $79.9(4)^\circ$ , respectively.

## Experimental

All reactions were carried out under  $\text{N}_2$  using Schlenk techniques. (S)-2,2'-diamino-1,1'-binaphthyl (284 mg, 1.0 mmol) and 4-N,N-dimethylaminopyridine (15 mg) were mixed in a 50 ml round-bottomed Schlenk flask with a stirrer bar. The atmosphere was replaced with  $\text{N}_2$  several times. 0.8 ml dry  $\text{Et}_3\text{N}$  and 30 ml dry  $\text{CH}_2\text{Cl}_2$  were added. The mixture was cooled to 273 K with an ice bath, followed by dropwise addition of dicyclohexylphosphine chloride (0.6 ml, 2.5 mmol) over a period of 20 min. The solvent was removed under vacuum after stirring at room temperature for another 3 h. The residues were dissolved in 15 ml toluene and purified on a flash silica-gel column (30 ml toluene as eluent). Toluene was removed and 530 mg of a white solid was obtained (yield: 78%). A colorless crystal suitable for X-ray diffraction was obtained by recrystallization from a solution in EtOH and  $\text{CH}_2\text{Cl}_2$ .  $^{31}\text{P}$  NMR ( $\text{CDCl}_3$ ):  $\delta$  42.8 p.p.m.

## Crystal data

$C_{44}H_{58}N_2P_2$   
 $M_r = 676.89$   
 Monoclinic,  $P2_1$   
 $a = 10.316$  (3) Å  
 $b = 16.988$  (5) Å  
 $c = 11.635$  (3) Å  
 $\beta = 97.971$  (7)°  
 $V = 2019.4$  (10) Å<sup>3</sup>  
 $Z = 2$

$D_x = 1.113$  Mg m<sup>-3</sup>  
 Mo  $K\alpha$  radiation  
 Cell parameters from 5501 reflections  
 $\theta = 1\text{--}27.5^\circ$   
 $\mu = 0.14$  mm<sup>-1</sup>  
 $T = 294$  (2) K  
 Prism, colorless  
 $0.30 \times 0.28 \times 0.26$  mm

## Data collection

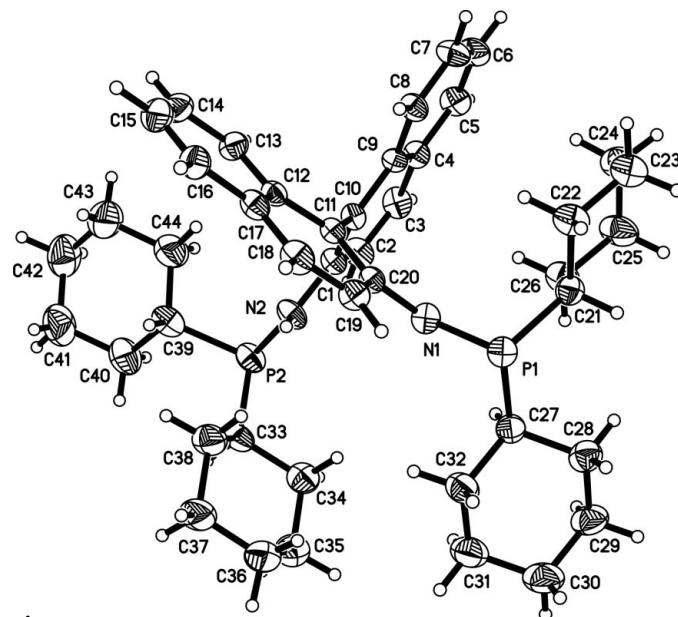
Bruker CCD area-detector diffractometer  
 $\varphi$  and  $\omega$  scans  
 Absorption correction: multi-scan (SADABS; Sheldrick, 1996)  
 $T_{\min} = 0.960$ ,  $T_{\max} = 0.965$   
 13673 measured reflections

4786 independent reflections  
 2931 reflections with  $I > 2\sigma(I)$   
 $R_{\text{int}} = 0.055$   
 $\theta_{\text{max}} = 27.6^\circ$   
 $h = -11 \rightarrow 13$   
 $k = -18 \rightarrow 22$   
 $l = -15 \rightarrow 12$

## Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.068$   
 $wR(F^2) = 0.155$   
 $S = 1.13$   
 8354 reflections  
 433 parameters  
 H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.05P)^2]$   
 where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\text{max}} < 0.001$   
 $\Delta\rho_{\text{max}} = 0.42$  e Å<sup>-3</sup>  
 $\Delta\rho_{\text{min}} = -0.30$  e Å<sup>-3</sup>  
 Absolute structure: Flack (1983)  
 Flack parameter = 0.01 (10)



**Figure 1**  
 The molecular structure of (I), with displacement ellipsoids at the 30% probability level.

Data collection: *SMART* (Bruker, 1995); cell refinement: *SMART*; data reduction: *SHELXTL-NT* (Bruker, 1995); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL-NT*; software used to prepare material for publication: *SHELXTL-NT*.

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