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Key indicators

Single-crystal X-ray study T = 298 K Mean σ (C–C) = 0.009 Å R factor = 0.067 wR factor = 0.178 Data-to-parameter ratio = 13.2

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e. Received 11 April 2006 Accepted 3 May 2006

N-[(*S*)-1-(5-Chloro-2-hydroxyphenyl)ethyl]-*N*-[(*R*)-2-hydroxy-1-phenylethyl]aminium chloride ethyl acetate solvate

The title compound, $C_{16}H_{19}CINO_2^+ \cdot Cl^- \cdot C_4H_8O_2$, was synthesised and its molecular structure determined. The absolute configuration of a new stereogenic centre is determined to be $S. N^+ - H \cdots Cl^-$ and $O - H \cdots Cl^-$ interactions connect structural components, generating a hydrogen-bonded spiral along the twofold screw axis.

Comment

The development of new chiral aminoalkylphenols has been given considerable attention owing to their application in asymmetric synthesis, which is one of the most active areas in synthetic chemistry. Most of these aminoalkylphenols are derived from easily available natural products (Cardellicchio *et al.*, 1998; Duthaler, 1994; Kelin *et al.*, 2005; Puigjaner *et al.*, 1999; Pu & Yu, 2001; Soai & Niwa, 1992; Steiner *et al.*, 2002; Wang *et al.*, 2004; Xu & Pu, 2004; Zhang *et al.*, 2003).

Chiral amino acids can be converted into the corresponding amino alcohols by reduction with sodium borohydride (McKennon *et al.*, 1993). In our previous work, R-(–)phenylglycinol was prepared by the same economical method. The precursor of known absolute configuration can be used as the internal standard for determination of the absolute configuration of a new chiral centre. The aminoalkylphenol was prepared by conventional condensation of 2-hydroxy-5chloroacetophenone with R-(–)-phenylglycinol, followed by reduction with NaBH₄. Single crystals of the title compound, (I), were obtained from an *iso*-propanol/ethyl acetate solvent mixture.



The absolute configuration of (I) is shown in Fig. 1. In the synthesis of (I) a precursor of the *R* configuration was used, thus the new chiral centre C7 of (I) is determined to be of the *S* configuration. Selected bond lengths and angles of (I) are reported in Table 1. The dihedral angle between the planes of aromatic rings C1–C6 and C11–C16 is $38.59 (17)^\circ$. The crystal packing reveals ethyl acetate as a solvent molecule with significant but unresolved disorder (Fig. 1). The intermolecular N⁺–H···Cl⁻ and O–H···Cl⁻ hydrogen bonds

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Figure 1

The asymmetric unit of (I), with displacement ellipsoids drawn at the 30% probability level.



Figure 2

A packing diagram of (I). Hydrogen bonds are shown as dashed lines.

together with an intramolecular N^+ -H···O hydrogen bond create a hydrophilic layer. Hydrogen-bond parameters are listed in Table 2 and their pattern is shown in Fig. 2.

Experimental

R-(-)-Phenylglycinol was prepared by the reduction reaction of R-(-)-phenylglycine with NaBH₄ in tetraydrofuran (THF) {80.2% yield, $[\alpha]_{D}^{24} = -25.5$ (c₆, MeOH)} (Abiko & Masamune, 1992; Demir *et* al., 1999; McKennon et al., 1993). R-(-)-Phenylglycinol (2 mmol) and 2-hydroxy-5-chloroacetophenone (2 mmol) [R-(-)-phenylglycine,NaBH₄ and 2-hydroxy-5-chloroacetophenone were purchased from J & K Chemical Ltd]. Chemicals were dissolved in methanol (15 ml) and reacted at room temperature for 12 h. After the solvent was removed, THF/ethanol (15 ml, 1:1 v/v) and NaBH₄ (8 mmol) were added at 273 K. The reaction was guenched with 5 M HCl and neutralized by NaOH solution. The aqueous solution was extracted by CHCl₃, and the organic layer was dried with anhydrous Na₂SO₄ and filtered. The solvent was removed under reduced pressure. Further purification was carried out by thin-layer sillica-gel chromatography (chloroform/methanol 30: 1). The chiral compound (I) was prepared in 80% yield, $[\alpha]_{D}^{16} = -76.5 \ (c_{0.5}, \text{CHCl}_{3})$ (Yang *et al.*,

Z = 2

 $D_x = 1.258 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation

Block, colourless

 $0.35 \times 0.21 \times 0.18 \text{ mm}$

 $\mu = 0.32 \text{ mm}^{-1}$

T = 298 (2) K

Crystal data

 $C_{16}H_{19}CINO_{2}^{+}\cdot CI^{-}\cdot C_{4}H_{8}O_{2}$ $M_{r} = 416.33$ Monoclinic, $P2_{1}$ a = 11.912 (3) Å b = 7.7221 (18) Å c = 12.312 (3) Å $\beta = 103.993$ (3)° V = 1098.9 (4) Å³

Data collection

Bruker SMART CCD area-detector diffractometer φ and ω scans Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996) $T_{\min} = 0.897, T_{\max} = 0.945$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.067$ $wR(F^2) = 0.178$ S = 1.083294 reflections 249 parameters H-atom parameters constrained

4637 measured reflections 3294 independent reflections 3077 reflections with $I > 2\sigma(I)$ $R_{int} = 0.041$ $\theta_{max} = 25.0^{\circ}$

$$\begin{split} w &= 1/[\sigma^2(F_o^2) + (0.1181P)^2 \\ &+ 0.0672P] \\ \text{where } P &= (F_o^2 + 2F_c^2)/3 \\ (\Delta/\sigma)_{\text{max}} < 0.001 \\ \Delta\rho_{\text{max}} &= 0.47 \text{ e } \text{\AA}^{-3} \\ \Delta\rho_{\text{min}} &= -0.23 \text{ e } \text{\AA}^{-3} \\ \text{Absolute structure: Flack (1983),} \\ 1195 \text{ Friedel pairs} \\ \text{Flack parameter: } -0.03 (11) \end{split}$$

Table 1Selected geometric parameters (Å, °).

C2-Cl1	1.742 (5)	C9-C11	1.494 (6)
C5-O1	1.373 (5)	C9-N1	1.498 (5)
C6-C7	1.509 (5)	C9-C10	1.518 (6)
C7-N1	1.513 (5)		
O1-C5-C6	116.4 (4)	C11-C9-C10	112.9 (3)
C6-C7-N1	110.9 (3)	N1-C9-C10	106.8 (3)
N1-C7-C8	108.1 (3)	O2-C10-C9	109.1 (4)
C11-C9-N1	112.6 (3)		

Table 2			
Hydrogen-bond	geometry	(Å,	°).

$D - H \cdots A$	<i>D</i> -H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N1 - H1B \cdot \cdot \cdot Cl2^{i}$	0.90	2.28	3.154 (3)	163
$O1 - H1 \cdot \cdot \cdot Cl2^{ii}$	0.82	2.19	2.995 (3)	169
$O2-H2\cdots Cl2$	0.82	2.35	3.156 (4)	169
N1-H1 $A\cdots O1$	0.90	2.00	2.718 (4)	135

Symmetry codes: (i) -x + 1, $y - \frac{1}{2}$, -z + 1; (ii) x, y - 1, z.

All H atoms were positioned geometrically and treated as riding, with C-H = 0.93–0.98 Å, N-H = 0.90 Å and O-H = 0.82 Å, and with $U_{iso}(H) = 1.2U_{eq}(C,N)$ or $1.5U_{eq}(C_{methyl},O)$.

Data collection: *SMART* (Bruker, 1997); cell refinement: *SMART*; data reduction: *SAINT* (Bruker, 1997); program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics:

SHELXTL (Bruker, 2001); software used to prepare material for publication: SHELXTL.

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