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Key indicators

Single-crystal X-ray study T = 120 KMean $\sigma(\text{C-C}) = 0.002 \text{ Å}$ R factor = 0.037 wR factor = 0.115Data-to-parameter ratio = 26.7

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

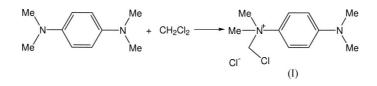
N-Chloromethyl-4-(dimethylamino)-*N*,*N*-dimethylanilinium chloride

In the cation of the title compound $C_{11}H_{18}ClN_2^+ \cdot Cl^-$, the quaternary N atom has a distorted tetrahedral geometry, and the other N a nearly planar-trigonal (owing to conjugation with the benzene ring) bonding geometry.

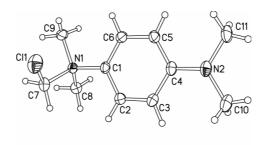
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Comment

The title compound, (I), was obtained as an accidental byproduct while co-crystallizing N,N,N',N'-tetramethyl-1,4phenylenediamine (TMPD) and octafluoronaphthalene (OFN) from CH₂Cl₂ (Collings et al., 2004). The asymmetric unit comprises one chloride anion and one Me₂(ClCH₂)N⁺-C₆H₄-NMe₂ cation. This cation has been structurally studied earlier as its tetraphenylborate salt dichloromethane solvate (II) by Winter (2001), and the non-chlorinated analogue trimethyl{4-(dimethylamino)phenyl}ammonium cation as its ozonide salt (III) by Assenmacher & Jansen (1995). Unfortunately, the precision of both structure determinations was limited (R = 0.09), in (III) owing to disorder of the ozonide anion and to chemical instability (the compound explodes at 303 K), and in (II) probably because of some unrecognized disorder, as indicated by the discrepant N⁺-CH₃ bond lengths of 1.50 (1) and 1.62 (1) Å.



The atom N2 has nearly planar geometry, the sum of the bond angles being 358.1°. The C10/N2/C11 plane forms an angle of 11.9 (1)° with the benzene ring plane, so that the $p\pi$ orbitals of N2 and C4 are nearly coplanar. This and the N2–C4 bond distance of 1.371 (2) Å are indicative of strong



🕑 Cl2

ellipsoids are drawn at the 50% probability level.

Figure 1 The cation and anion in the structure of (I). Atomic displacement

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 π -conjugation. The quaternary atom N1 has a distorted tetrahedral environment. The chloride anion is surrounded by eight H atoms of four different cations at Cl···H distances of 2.46 (2) to 2.60 (2) Å (calculated for the idealized C-H bond lengths of 1.08 Å).

Experimental

Slow evaporation at room temperature of a dichloromethane solution of equimolar amounts of TMPD and OFN yielded mainly co-crystals of TMPD and OFN (1:1) and a few smaller crystals of different habit, which were identified by the present study as (I).

Crystal data

 $C_{11}H_{18}ClN_2^+ \cdot Cl^ M_r = 249.17$ Monoclinic, P21/c a = 15.121 (3) Å b = 7.234(1) Å c = 12.773(2) Å $\beta = 114.95 \ (1)^{\circ}$ V = 1266.8 (4) Å³ Z = 4Data collection Bruker SMART 6000 CCD areadetector diffractometer ω scans Absorption correction: by integration (XPREP in SHELXTL; Bruker, 2001b) $T_{\rm min}=0.923,\ T_{\rm max}=0.962$

17336 measured reflections

Mo $K\alpha$ radiation Cell parameters from 977 reflections $\theta = 10.2 - 26.9^{\circ}$ $\mu = 0.48 \text{ mm}^{-1}$ T = 120 (2) KParallelepiped, colourless $0.22 \times 0.15 \times 0.10 \text{ mm}$

 $D_x = 1.306 \text{ Mg m}^{-3}$

3689 independent reflections 2994 reflections with $I > 2\sigma(I)$ $R_{\rm int} = 0.047$ $\theta_{\rm max} = 30.0^{\circ}$ $h = -21 \rightarrow 21$ $k = -10 \rightarrow 10$ $l = -17 \rightarrow 17$

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Refinement
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Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0621P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.037$	+ 0.4607P]
$wR(F^2) = 0.115$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.05	$(\Delta/\sigma)_{\rm max} = 0.001$
3689 reflections	$\Delta \rho_{\rm max} = 0.48 \text{ e } \text{\AA}^{-3}$
138 parameters	$\Delta \rho_{\rm min} = -0.51 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

Methyl groups bonded to N2 were refined as rigid bodies rotating around the N2-C bonds, and other H atoms were treated as riding on the corresponding C atoms in idealized positions. The C-H distances were fixed at 0.98 Å for methyl, 0.99 Å for methylene, 0.95 Å for benzene H atoms, with $U_{iso}(H) = 1.5U_{eq}(C)$ for methyl H atoms and $1.2U_{eq}(C)$ for the rest.

Data collection: SMART (Bruker, 2001a); cell refinement: SMART; data reduction: SAINT (Bruker, 2001a); program(s) used to solve structure: SHELXTL (Bruker, 2001b); program(s) used to refine structure: SHELXTL; molecular graphics: SHELXTL; software used to prepare material for publication: SHELXTL.

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