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Key indicators

Single-crystal X-ray study T = 173 K Mean σ (C–C) = 0.002 Å R factor = 0.030 wR factor = 0.075 Data-to-parameter ratio = 15.9

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

N-Benzoyl-N'-(1,1-dimethyl-3-oxobutyl)-

hydrazine hydrochloride

The crystal structure of the title compound, $C_{13}H_{19}N_2O_2^+ \cdot Cl^-$, is stabilized by intra- and intermolecular hydrogen bonds, forming centrosymmetric dimers.

Comment

The aim of our investigations (Ton, 2004) was to synthesize 1benzoyl-2-(2-propylidene)hydrazone by reacting acetone and benzoic acid hydrazide in the presence of HCl, in order to examine the intra- and intermolecular hydrogen-bond interactions in the solid state. Unfortunately, we obtained crystals of (I) instead.



The bond lengths and angles in (I) do not show unusual values. One of the H atoms bonded to N2 forms two intramolecular hydrogen bonds to both carbonyl O atoms. The other one and the H atom bonded to N1 form a hydrogen bond to the Cl^- ion. This results in the formation of centrosymmetric dimers (Fig. 2).

Experimental

In a 100 ml flask, ten drops of concentrated HCl were added dropwise to 20 ml acetone. 2 g of anhydrous sodium sulfate and 0.97 g (0.0071 mol) benzhydrazide were then added to the solution, which was stirred for 20 h and subsequently filtered. The excess acetone was removed. Afterwards, the residue was crystallized from acetone.



Figure 1

Perspective view of the title compound, with the atom numbering. Displacement ellipsoids are drawn at the 50% probability level. The dashed line indicates a hydrogen bond.

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Crystal data

 $\begin{array}{l} C_{13}H_{19}N_2O_2^+ \cdot Cl^-\\ M_r = 270.75\\ Monoclinic, P2_1/c\\ a = 7.087 (1) Å\\ b = 21.023 (2) Å\\ c = 10.019 (1) Å\\ \beta = 99.042 (9)^\circ\\ V = 1474.2 (3) Å^3\\ Z = 4 \end{array}$

Data collection

Stoe IPDS-II two-circle diffractometer ω scans Absorption correction: multi-scan (*MULABS*; Spek, 1990; Blessing, 1995) $T_{\min} = 0.927, T_{\max} = 0.957$ 16453 measured reflections

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.030$ $wR(F^2) = 0.075$ S = 0.952832 reflections 178 parameters

Table 1

Selected geometric parameters (Å, °).

N1-C1	1.3564 (19)	N2-C2	1.5192 (18)
N1-N2	1.4185 (16)		
C1-N1-N2	114.56 (12)	N2-N1-H1	115.3 (13)
C1-N1-H1	123.8 (13)	N1 - N2 - C2	114.32 (11)

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$N2 - H2B \cdots Cl1^{i}$ $N1 - H1 \cdots Cl1$ $N2 - H2A = O1$	0.97 (2) 0.839 (19) 0.855 (18)	2.05(2) 2.29(2) 2.056(18)	3.0184 (13) 3.1291 (13) 2.5818 (16)	171.7 (16) 174.4 (17) 110.1 (14)
$N2-H2A\cdots O1$ $N2-H2A\cdots O2$	0.855(18) 0.855(18)	2.050 (18) 2.071 (18)	2.7323 (16)	133.6 (15)

Symmetry code: (i) -x, -y, 1 - z.

 $D_x = 1.220 \text{ Mg m}^{-3}$ Mo K\alpha radiation Cell parameters from 11582 reflections $\theta = 3.5-25.8^{\circ}$ $\mu = 0.26 \text{ mm}^{-1}$ T = 173 (2) K Block, colourless $0.30 \times 0.23 \times 0.21 \text{ mm}$

2832 independent reflections 2190 reflections with $I > 2\sigma(I)$ $R_{int} = 0.050$ $\theta_{max} = 25.9^{\circ}$ $h = -8 \rightarrow 8$ $k = -25 \rightarrow 25$ $l = -12 \rightarrow 12$

H atoms treated by a mixture of independent and constrained refinement $w = 1/[\sigma^2(F_o^2) + (0.0461P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} < 0.001$ $\Delta\rho_{max} = 0.20 \text{ e } \text{\AA}^{-3}$ $\Delta\rho_{min} = -0.18 \text{ e } \text{\AA}^{-3}$



Figure 2

Packing diagram of the title compound, viewed along the a axis. Hydrogen bonds are shown as dashed lines.

H atoms bonded to C atoms were refined with fixed individual displacement parameters $[U_{iso}(H) = 1.2U_{eq}(C) \text{ or } 1.5U_{eq}(C_{methyl})]$ using a riding model, with aromatic C-H = 0.95 Å, methyl C-H = 0.98 Å and methylene C-H = 0.99 Å. The methyl groups were allowed to rotate but not to tip. H atoms bonded to N atoms were refined isotropically.

Data collection: X-AREA (Stoe & Cie, 2001); cell refinement: X-AREA; data reduction: X-AREA; program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: PLATON (Spek, 1990); software used to prepare material for publication: SHELX97 and PLATON.

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