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Key indicators

Single-crystal X-ray study T = 120 KMean $\sigma(C-C) = 0.002 \text{ Å}$ R factor = 0.036 wR factor = 0.091 Data-to-parameter ratio = 17.6

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

Indomethacin tert-butanol solvate at 120 K

Crystals of the title compound, $C_{19}H_{16}CINO_4 \cdot C_4H_{10}O$, contain $O-H \cdot \cdot \cdot O$, $C-H \cdot \cdot \cdot O$ and $C-H \cdot \cdot \cdot \pi$ interactions.

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Comment

The crystal structure of indomethacin *tert*-butanol solvate, (I), has been previously determined at 293 K but reported only briefly (Joshi *et al.*, 1998; Stowell *et al.*, 2002). We now present details of the structure determined at 120 K.



The molecular structure is shown in Fig. 1. The dihedral angle between the mean planes passing through the C atoms of the indole ring system and the chlorophenyl ring is $69.33 (3)^{\circ}$, similar to the value of $66.51 (5)^{\circ}$ reported for unsolvated indomethacin at 120 K (Cox & Manson, 2003). The molecular geometry is also similar to that reported for the room-temperature structure of indomethacin (Kistenmacher & Marsh, 1972).

Classical O-H···O hydrogen bonding enables two tertbutanol molecules to link to two indomethacin molecules. Hydroxy atom O5 of the solvent acts as both a donor and acceptor in the formation of an $R_4^4(12)$ ring across a centre of symmetry. This is shown in Fig. 2 and details of the geometry of this hydrogen bonding, together with a weaker $C-H \cdots O$ interaction, are given in Table 2. This weaker interaction extends the hydrogen bonding to link four indomethacin molecules and four solvent molecules in an $R_6^6(30)$ ring formation (Fig. 3). There is no disorder in the methyl groups of the solvent, and five weak $C-H \cdot \cdot \pi$ interactions involving the alcohol and indomethacin are present, as listed in Table 3 and shown in Fig. 4. Two further $C-H \cdots \pi$ interactions are present. There is also a short intermolecular Cl1...Cl1^{iv} [symmetry code: (iv) 1 - x, -y, -z] contact of 3.3745 (4) Å that compares with the sum of the van der Waals radii (3.50 Å; Bondi, 1964), but there are no significant π - π interactions.

Experimental

 \odot 2003 International Union of Crystallography Printed in Great Britain – all rights reserved Indomethacin was purchased from Sigma and was recrystallized from *tert*-butanol to produce the title solvate.



Figure 1

The structure of the asymmetric unit of (I). Displacement ellipsoids are drawn at the 50% probability level.



Figure 2

Classical hydrogen bonding between carboxylic acid groups of two indomethacin molecules and hydroxy groups of two solvent molecules. Atoms marked with an ampersand (&), hash (#) and asterisk (*) are at symmetry positions (1 - x, 1 - y, 1 - z), (x, 1 + y, z) and (1 - x, 2 - y, z)1-z), respectively.

Crystal data

$C_{19}H_{16}CINO_4 \cdot C_4H_{10}O$	$D_x = 1.321 \text{ Mg m}^{-3}$
$M_r = 431.9$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 27
a = 11.9806 (1) Å	reflections
b = 12.2749(1) Å	$\theta = 2.9-27.5^{\circ}$
c = 14.7679 (2) Å	$\mu = 0.21 \text{ mm}^{-1}$
$\beta = 91.561 \ (4)^{\circ}$	T = 120 (2) K
V = 2170.97 (4) Å ³	Prism, colourless
Z = 4	$0.56 \times 0.40 \times 0.24 \mbox{ mm}$
Data collection	
Nonius KappaCCD area-detector	4405 reflections with $I >$
φ and ω scans	$R_{\rm int} = 0.047$
Absorption correction: multi-scan	$\theta_{\rm max} = 27.5^{\circ}$
(SORTAV; Blessing, 1995, 1997)	$h = -15 \rightarrow 14$
$T_{\rm min} = 0.877, T_{\rm max} = 0.957$	$k = -15 \rightarrow 15$
26 128 measured reflections	$l = -19 \rightarrow 17$
4955 independent reflections	
Refinement	
Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0405)]$

 $R[F^2 > 2\sigma(F^2)] = 0.036$ wR(F²) = 0.092 S=1.024955 reflections 282 parameters H atoms treated by a mixture of independent and constrained refinement

7 193 $> 2\sigma(I)$

$w = 1/[\sigma^2(F_o^2) + (0.0405P)^2]$
+ 0.9973P]
where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{\rm max} < 0.001$
$\Delta \rho_{\rm max} = 0.27 \text{ e} \text{ \AA}^{-3}$
$\Delta \rho_{\rm min} = -0.31 \text{ e } \text{\AA}^{-3}$



Figure 3

A partial packing diagram, showing extended hydrogen bonding linking four indomethacin molecules and four solvent molecules.

Table 1

Selected geometric parameters (Å, °).

Cl1-C14	1.7422 (12)	O4-C19	1.3183 (15)
O3-C19	1.2170 (15)	O5-C21	1.4514 (16)
C5-C4-C3	131.57 (11)	C8-C9-N1	131.44 (11)
C9-C4-C3	107.46 (10)	C4-C9-N1	107.31 (10)
C10-N1-C2-C17	-8.62(18)	C2-N1-C10-O1	-29.24(18)
C17-C2-C3-C18	1.0 (2)	O1-C10-C11-C12	138.60 (13)

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdot \cdot \cdot A$
D4−H4···O5 ⁱ	0.89 (2)	1.71 (2)	2.586 (1)	170 (2)
D5−H51···O3 ⁱⁱ	0.88 (2)	1.94 (2)	2.814 (1)	170 (2)
C15−H15···O3 ⁱⁱⁱ	0.95	2.54	3.368 (1)	145

Symmetry codes: (i) x, 1 + y, z; (ii) 1 - x, 1 - y, 1 - z; (iii) x, y - 1, z.

Table 3

С-Н	CgI	Symmetry code	$H \cdot \cdot \cdot CgI$	$C-H\cdots CgI$	$C \cdots CgI$
C13-H13 C17-H17C C22-H22A C23-H23B C24-H24A C24-H24B	2 3 1 1 1 2	$\begin{array}{c} 1-x,1-y,-z\\ \frac{1}{2}-x,\frac{1}{2}+y,\frac{1}{2}-z\\ \frac{1}{2}-x,-\frac{1}{2}+y,\frac{1}{2}-z\\ 1-x,1-y,1-z\\ 1-x,1-y,1-z\\ 1-x,1-y,1-z\end{array}$	2.63 2.82 3.20 3.21 3.13 3.03	164 134 119 135 130 124	3.556 (1) 3.576 (1) 3.776 (2) 3.960 (2) 3.828 (2) 3.663 (2)
C24-H24C	3	$-\frac{1}{2} + x, \frac{1}{2} - , \frac{1}{2} + z$	2.93	149	3.805 (2)

† CgI represent the centre of gravity of a ring, with I = 1 for the five-membered ring, I = 2for the six-membered ring (indole system) and I = 3 for the chlorophenyl ring. The symmetry applies to the CgI position.

The coordinates of the hydroxy H atoms were freely refined; the other H atoms were placed in calculated positions and allowed to ride



Figure 4

Five $C-H\cdots\pi$ interactions (shown as double-dashed lines) involving methyl H atoms of the solvent. Ring centres are marked with a dot.

on their parent atoms. For all H atoms, $U_{\rm iso}$ is 1.2 (non-methyl) or 1.3 (methyl) times $U_{\rm eq}$ of the parent atom.

Data collection: *DENZO* (Otwinowski & Minor, 1997) and *COLLECT* (Hooft, 1998); cell refinement: *DENZO* and *COLLECT*;

data reduction: *DENZO* and *COLLECT*; program(s) used to solve structure: *SIR*97 (Altomare *et al.*, 1999); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2002); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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