# metal-organic papers

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#### Key indicators

Single-crystal X-ray study T = 203 KMean  $\sigma(C-C) = 0.005 \text{ Å}$  R factor = 0.027 wR factor = 0.071 Data-to-parameter ratio = 15.8

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

# Solvated CrBr<sub>2</sub>(thf)<sub>2</sub>, a linear chain in the solid state

In the title compound, dibromobis(tetrahydrofuran-O)chromium(II), [CrBr<sub>2</sub>(C<sub>4</sub>H<sub>8</sub>O)<sub>2</sub>], CrBr<sub>2</sub> is solvated by two tetrahydrofuran (thf) molecules, with a Cr-O distance of 2.072 (3) Å and a Cr-Br distance of 2.5825 (5) Å. The Cr atom lies on the center of inversion. The Cr atom is octahedrally coordinated, with the thf Cr-O bond orthogonal to the Cr-Br bond, and the vacant sites are occupied with a Cr $\cdots$ Br intermolecular interaction of 2.9874 (5) Å. The latter interaction is almost orthogonal to the Cr-O vector. This extends the system into a linear chain along the [100] direction.

## Comment

 $CrBr_2(thf)_2$ , (I), bears a close resemblance to the parent compound CrBr<sub>2</sub> (Tracy et al., 1962). Both show slightly distorted octahedral coordination and both have similar inplane Cr-Br bond distances, 2.5825 (5) Å in (I) and 2.545 (1) Å in CrBr<sub>2</sub>. The solvent molecule, thf in this case, occupies an in-plane coordination site with a Cr-O distance of 2.072 (3) Å. The solvent molecule is coordinated orthogonally to the Cr–Br vector with an angle of 90.009  $(8)^{\circ}$ . The thf molecule is in a half-chair conformation with a total puckering amplitude of  $Q_{\rm T} = 0.363$  Å (Cremer & Pople, 1975). The orientation of the thf molecule is influenced by the intramolecular interactions C4-H4A...Br1 and C1- $H1A \cdots Br1^{i}$  (see Table 1) which tilt the ring towards each Br atom. The out-of-plane coordination site is occupied by an intermolecular Cr1···Br1<sup>ii</sup> interaction of 2.9874 (5) Å [symmetry code: (ii) 1 + x, y, z]. The corresponding interaction in  $CrBr_2$  has a  $Cr \cdots Br$  distance of 2.998 (1) Å. The distortion



from ideal octahedral geometry is also reflected in the Br1– Cr1–Br1<sup>ii</sup> angle of 94.65 (2)°. With the thf molecules occupying the other coordination sites, (I) can only form a staggered chain instead of the planar sheets found in CrBr<sub>2</sub>. In this case, the direction of propagation is along [100] (Fig. 1). Other solvent coordinated Cr<sup>II</sup>Br<sub>2</sub> species that are octahedrally coordinated show a wide range of Cr–Br distances. The complex CrBr<sub>2</sub>(CH<sub>3</sub>CN)<sub>2</sub> (Halepoto *et al.*, 1990), which also forms linear chains, has an in-plane Cr–Br distance of 2.545 Å and an out-of-plane distance of 2.976 (1) Å. However,

© 2001 International Union of Crystallography Printed in Great Britain – all rights reserved d, dibromobis(tetrahydrofuran-O)-  $_4H_8O)_2$ ], CrBr<sub>2</sub> is solvated by two olecules, with a Cr-O distance of 3r distance of 2.5825 (5) Å. The Cr er of inversion. The Cr atom is

# **Experimental**

CrBr<sub>2</sub>(thf)<sub>2</sub> was synthesized as a side product during the attempted synthesis of a chromocene bromide. Tetramethylethylenediyl( $\eta^5$ -biscyclopentadienyl)chromocene<sup>II</sup> carbonyl (331 mg, 1.1 mmol) was reacted with 1-bromo-2-methylpropane (155 mg, 1.1 mmol) in tetrahydrofuran for 20 h at 378 K, with no color change. Dibromomethane (excess) was then added to increase the bromide concentration. Excess solvent and reagents were removed under reduced pressure and the green residue redissolved in tetrahydrofuran (20 ml) and filtered. The resulting solution was concentrated to promote crystallization and cooled in a 278 K refrigerator overnight. The supernatant was decanted yielding a green crystalline product. The supernatant was concentrated under reduced pressure to yield a fine pale green powder. Combined yield 68 mg, 19.1%, m.p. > 573 K.

Z = 1

 $D_x = 2.126 \text{ Mg m}^{-2}$ 

Cell parameters from 839

 $0.25 \times 0.20 \times 0.15 \ \mathrm{mm}$ 

50 frames remeasured standard

intensity decay: none

every beginning and end reflec-

Mo  $K\alpha$  radiation

reflections

 $\theta = 2.2-27.4^{\circ}$  $\mu = 8.18 \text{ mm}^{-1}$ 

T = 203 (2) KPlate, pale yellow

 $\theta_{\rm max} = 25.0^\circ$ 

 $h = -4 \rightarrow 4$ 

 $k=-8\rightarrow 8$ 

 $l = -11 \rightarrow 11$ 

reflections

tions

#### Crystal data

 $\begin{bmatrix} CrBr_2(C_4H_8O)_2 \end{bmatrix} \\ M_r = 356.03 \\ Triclinic, P\overline{1} \\ a = 4.1043 (7) \text{ Å} \\ b = 7.4530 (13) \text{ Å} \\ c = 9.2875 (16) \text{ Å} \\ \alpha = 87.777 (3)^{\circ} \\ \beta = 78.619 (3)^{\circ} \\ \gamma = 87.281 (3)^{\circ} \\ V = 278.07 (8) \text{ Å}^3 \end{bmatrix}$ 

## Data collection

Siemens SMART 1000 diffractometer  $\omega$  scans Absorption correction: empirical (SADABS; Sheldrick, 1999)  $T_{min} = 0.184, T_{max} = 0.293$ 2917 measured reflections 962 independent reflections 897 reflections with  $I > 2\sigma(I)$  $R_{int} = 0.029$ 

## Refinement

Refinement on $F^2$	$w = 1/[\sigma^2(F_o^2) + (0.0436P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.027$	+ 0.1523P]
$wR(F^2) = 0.071$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.08	$(\Delta/\sigma)_{\rm max} = 0.001$
962 reflections	$\Delta \rho_{\rm max} = 0.58 \ {\rm e} \ {\rm \AA}^{-3}$
61 parameters	$\Delta \rho_{\rm min} = -0.70 \text{ e} \text{ \AA}^{-3}$
H-atom parameters constrained	

## Table 1

Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdot \cdot \cdot A$
$\begin{array}{c} C4-H4A\cdots Br1\\ C1-H1A\cdots Br1^{i} \end{array}$	0.98 0.98	2.99 2.99	3.599 (4) 3.607 (4)	122 122
Summatry and (i) 1	x 1 y 1 y	-		

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

Data collection: *SMART* (Bruker, 1997); cell refinement: *SMART*; data reduction: *SAINT-Plus* (Bruker, 1999); program(s) used to solve



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#### Figure 1

Packing diagram of (I) showing the staggered propagation along the [100] direction. H atoms have been omitted for clarity.

structure: *SHELXTL* (Sheldrick, 1998); program(s) used to refine structure: *SHELXTL*; molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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