## Structure Reports

Online
ISSN 1600-5368

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## Key indicators

Single-crystal X-ray study
$T=293 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.006 \AA$
Some non-H atoms missing
Disorder in solvent or counterion
$R$ factor $=0.042$
$w R$ factor $=0.115$
Data-to-parameter ratio $=19.8$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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# Binuclear trans- $\mu$-pyrazine-bis[bromotetrapyridineruthenium(II)] dihexafluorophosphate dimethylformamide disolvate 

The Ru atoms of the title compound, $\left[\mathrm{Ru}_{2} \mathrm{Br}_{2}\left(\mathrm{C}_{4} \mathrm{H}_{4} \mathrm{~N}_{2}\right)\right.$ $\left.\left(\mathrm{C}_{5} \mathrm{H}_{5} \mathrm{~N}\right)_{8}\right]\left(\mathrm{PF}_{6}\right)_{2} .2 \mathrm{C}_{3} \mathrm{H}_{7} \mathrm{NO}$, are coordinated by the four N atoms of the pyridine (py) ligands and a bromide. Two such units are bridged by a pyrazine ( pz ) unit, which is disposed about a centre of inversion, so as to form a trans pseudooctahedral geometry about Ru. The py units are in an eclipsed conformation when viewed down the internuclear axis. The $\mathrm{Ru}-\mathrm{N}(\mathrm{pz})$ distance is 2.079 (3) $\AA$, while the $\mathrm{Ru}-\mathrm{Br}$ distance is 2.5524 (4) $\AA$.

## Comment

In proceeding towards the synthesis of asymmetric binuclear complexes containing a chromophore on one terminus and a labile group on the other terminus, we have prepared several binuclear and trinuclear complexes using our synthon-based approach (Mirza \& Lever, 2003). We describe here the synthesis and a single-crystal X-ray structure of the title complex, (I), that features a centrosymmetric dication, two $\mathrm{PF}_{6}{ }^{-}$anions and two DMF solvent molecules of crystallization.

(I)

The analysis revealed that the bond distance of $\mathrm{Ru}-\mathrm{N}(\mathrm{pz})$, 2.079 (3) $\AA$, is significantly longer than the corresponding $\mathrm{Ru}-\mathrm{N}(\mathrm{pz})$ separations in the Creutz-Taube ion, $\left[\left\{\left(\mathrm{NH}_{3}\right)_{5} \mathrm{Ru}\right\}_{2}(\mu-\mathrm{pz})\right]^{4+}$ (Creutz \& Taube, 1969; Fürholz et al., 1985), which fall in the range 1.972 (4)-2.002 (2) $\AA$, and essentially the same as in the recently reported $\left[(\text { Cyclen })_{4} \mathrm{Ru}_{4}(\mu-\mathrm{pz})_{4}\right]^{9+}$ ion, at 2.020 (13) and 2.049 (12) $\AA$ (Lau et al., 2002). These distances are slightly shorter than the average $\mathrm{Ru}-\mathrm{N}(\mathrm{py})$ distance of 2.103 (3) $\AA$ calculated for (I), but similar to those in the analogous trans $-\left[\left\{\mathrm{RuCl}(\mathrm{py})_{4}\right\}_{2}(\mu-\right.$ $\mathrm{pz})]\left(\mathrm{PF}_{6}\right)_{2}$ complex (Coe et al., 1993, 1995; Serli et al., 2002). The two trans- $\left[\mathrm{Ru}(\mathrm{py})_{4}\right]$ units adopt an eclipsed conformation. The $\mathrm{Ru}-\mathrm{Br}$ bond distance of 2.5524 (4) $\AA$ is significantly longer than that in $\mathrm{Ru}(\mathrm{TPP}) \mathrm{Br}_{2}, 2.425$ (2) $\AA$ (Ke et al., 1991), owing to the strong $\sigma$-donor capacity of the pyridine ligands, although comparable distances have been observed elsewhere (Tomizawa et al., 1994). The average bond angles for $\mathrm{pz}-$ Ru - py are $91.57(10)^{\circ}$, forming a propeller conformation of the four pyridine ligands. The $\mathrm{pz}-\mathrm{Ru}-\mathrm{Br}$ bond is almost linear with an angle of 178.92 (7) ${ }^{\circ}$, while $\mathrm{py}-\mathrm{Ru}-$ py shows a slight tilt with an average angle of $176.14(10)^{\circ}$ [range 174.38 (11)-177.91 (10) ${ }^{\circ}$.

Received 25 June 2003
Accepted 24 July 2003
Online 31 July 2003


Figure 1
View of the cation with atomic numbering. Displacement ellipsoids are drawn at the $50 \%$ probability level. H atoms have been omitted for clarity.

## Experimental

$\left[\mathrm{Ru}(\mathrm{py})_{4}(\mathrm{NO}) \mathrm{Br}\right]\left(\mathrm{PF}_{6}\right)_{2} \quad(300 \mathrm{mg}, 0.37 \mathrm{mmol})$ and $\mathrm{NaN}_{3}(24 \mathrm{mg}$, 0.37 mmol ) were mixed together. Acetone ( 40 ml ) was added and the solution was degassed in the absence of light. After the mixture had been stirred for 1 h , pyrazine $(15 \mathrm{mg}, 0.18 \mathrm{mmol})$ was added. This solution was then refluxed for 2.5 h . The solvent was evaporated from the purple solution and the resulting solid was suspended in distilled water and vacuum filtered. The purple product was washed with ether 10 ml and air dried (yield 243 mg ). Crystals suitable for X-ray analysis were grown by slow diffusion of ether into a DMF solution of the product.

## Crystal data

$\left[\mathrm{Ru}_{2} \mathrm{Br}_{2}\left(\mathrm{C}_{4} \mathrm{H}_{4} \mathrm{~N}_{2}\right)\left(\mathrm{C}_{5} \mathrm{H}_{5} \mathrm{~N}\right)_{8}\right]\left(\mathrm{PF}_{6}\right)_{2} \cdot-$ $2 \mathrm{C}_{3} \mathrm{H}_{7} \mathrm{NO}$
$M_{r}=1510.98$
Monoclinic, $C 2 / c$
$a=19.0401$ (4) A
$b=14.6334$ (4) $\AA$
$c=21.2490$ (5) A
$\beta=90.5609(12)^{\circ}$
$V=5920.1$ (2) A $^{3}$
$Z=4$

## Data collection

Nonius KappaCCD diffractometer $\varphi$ scans and $\omega$ scans with $\kappa$ offsets Absorption correction: multi-scan (DENZO-SMN; Otwinowski \& Minor, 1997)
$T_{\text {min }}=0.715, T_{\text {max }}=0.961$
21516 measured reflections

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.042$
$w R\left(F^{2}\right)=0.115$
$S=1.07$
6741 reflections
341 parameters
H -atom parameters constrained
> $D_{x}=1.695 \mathrm{Mg} \mathrm{m}^{-3}$
> Mo $K \alpha$ radiation
> Cell parameters from 42564 reflections
> $\theta=2.6-27.5^{\circ}$
> $\mu=2.00 \mathrm{~mm}^{-1}$
> $T=293$ (2) K
> Prism, dark red
> $0.18 \times 0.10 \times 0.02 \mathrm{~mm}$

$$
\begin{aligned}
& 6741 \text { independent reflections } \\
& 5561 \text { reflections with } I>2 \sigma(I) \\
& R_{\text {int }}=0.046 \\
& \theta_{\max }=27.5^{\circ} \\
& h=-24 \rightarrow 24 \\
& k=-18 \rightarrow 18 \\
& l=-27 \rightarrow 27 \\
& \\
& \\
& w=1 /\left[\sigma^{2}\left(F_{o}^{2}\right)+(0.0569 P)^{2}\right. \\
& \quad+4.3116 P] \\
& \text { where } P=\left(F_{o}{ }^{2}+2 F_{c}^{2}\right) / 3 \\
& (\Delta / \sigma)_{\max }=0.001 \\
& \Delta \rho_{\max }=0.48 \text { e } \AA^{-3} \\
& \Delta \rho_{\min }=-0.90 \mathrm{e}^{-3}
\end{aligned}
$$

Table 1
Selected geometric parameters $\left(\AA^{\circ},{ }^{\circ}\right)$.

| $\mathrm{Ru} 1-\mathrm{Br} 1$ | $2.5524(4)$ | $\mathrm{Ru} 1-\mathrm{N} 3$ | $2.103(3)$ |
| :--- | ---: | :--- | ---: |
| $\mathrm{Ru} 1-\mathrm{N} 1$ | $2.095(3)$ | $\mathrm{Ru} 1-\mathrm{N} 4$ | $2.103(3)$ |
| $\mathrm{Ru} 1-\mathrm{N} 2$ | $2.112(3)$ | $\mathrm{Ru} 1-\mathrm{N} 5$ | $2.079(3)$ |
|  |  |  |  |
| $\mathrm{N} 1-\mathrm{Ru} 1-\mathrm{N} 2$ | $90.73(11)$ | $\mathrm{N} 3-\mathrm{Ru} 1-\mathrm{N} 5$ | $93.06(10)$ |
| $\mathrm{N} 1-\mathrm{Ru} 1-\mathrm{N} 3$ | $174.38(11)$ | $\mathrm{N} 4-\mathrm{Ru} 1-\mathrm{N} 5$ | $90.00(10)$ |
| $\mathrm{N} 1-\mathrm{Ru} 1-\mathrm{N} 4$ | $91.22(11)$ | $\mathrm{N} 1-\mathrm{Ru} 1-\mathrm{Br} 1$ | $86.38(8)$ |
| $\mathrm{N} 1-\mathrm{Ru} 1-\mathrm{N} 5$ | $92.55(10)$ | $\mathrm{N} 2-\mathrm{Ru} 1-\mathrm{Br} 1$ | $89.40(8)$ |
| $\mathrm{N} 2-\mathrm{Ru} 1-\mathrm{N} 3$ | $89.54(11)$ | $\mathrm{N} 3-\mathrm{Ru} 1-\mathrm{Br} 1$ | $88.02(8)$ |
| $\mathrm{N} 2-\mathrm{Ru} 1-\mathrm{N} 4$ | $177.91(10)$ | $\mathrm{N} 4-\mathrm{Ru} 1-\mathrm{Br} 1$ | $89.98(8)$ |
| $\mathrm{N} 2-\mathrm{Ru} 1-\mathrm{N} 5$ | $90.66(11)$ | $\mathrm{N} 5-\mathrm{Ru} 1-\mathrm{Br} 1$ | $178.92(7)$ |
| $\mathrm{N} 3-\mathrm{Ru} 1-\mathrm{N} 4$ | $88.44(11)$ |  |  |

During the structure refinement, the atoms of the DMF solvent molecule were observed but could not be modelled satisfactorily. The SQUEEZE routine in PLATON (Spek, 1999) was used to modify the data to account for this, and the solvent was identified as two molecules of DMF per cation. The $\mathrm{PF}_{6}{ }^{-}$anion was disordered over two positions, $A$ and $B$, with occupancies of 91 and $9 \%$, respectively. The F atoms of the $B$ position were refined isotropically with restrained geometry $[\mathrm{P}-\mathrm{F}$ bond distances $=1.60(1) \AA] . \mathrm{H}$ atoms were placed in calculated positions and treated as riding atoms $(\mathrm{C}-\mathrm{H}=0.95 \AA)$, with $U_{\text {iso }}(\mathrm{H})=1.2 U_{\text {eq }}$ (parent C).

Data collection: COLLECT (Nonius, 1997-2001); cell refinement: DENZO-SMN (Otwinowski \& Minor, 1997); data reduction: $D E N Z O-S M N$; program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Sheldrick, 1999); software used to prepare material for publication: SHELXTL.

Financial support from the Natural Science and Engineering Research Council (NSERC) of Canada is acknowledged. ABPL is indebted to the Canada Council for the Arts for a Killam Research Fellowship. We thank Dr. Eduard Rusanov for crystallographic assistance.

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