Electronic Supporting Information for

Non-cyclic Formylated Dipyrromethanes as Phosphate Anion Receptors

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General

1,1'-Diacetylferrocene was obtained from Ark Pharm, Inc. All other solvents and chemicals were purchased from Aldrich, TCI, and Acros. Pyrrole was distilled at 80 °C under reduced pressure (100 mbar) prior to use. Other solvents and reagents were used without further purification. Compounds **3b** and **4b** were prepared as reported previously.¹ The NMR spectra were referenced to residual protic solvent peaks. All NMR spectroscopic solvents were purchased from Cambridge Isotope Laboratories.

Syntheses of Compounds 6a–7b

1,1'-Bis(1,1-di(1*H*-pyrrol-2-yl)ethyl)ferrocene (**6a**):

1,1'-Diacetylferrocene (500 mg, 1.85 mmol) was dissolved in pyrrole (12 mL, 185 mmol). Dry nitrogen gas was bubbled through this solution for 10 min. Trifluoroacetic acid (TFA) (0.3 mL, 3.9 mmol) was added to the mixture and the mixture was heated to 80°C for 4 hours while bubbling with N_2 . Note: Proper ventilation is required since TFA is a corrosive and low boiling substance. The reaction mixture was then cooled to room temperature and dissolved in dichloromethane (DCM). The organic solution was extracted with 0.5 M NaOH to remove the TFA. The organic layer was dried over anhydrous $MqSO₄$ and the solvent was removed. Unreacted pyrrole was recycled from this crude product mixture by distillation at 80 °C and 100 mbar. Column chromatography (silica gel) was performed using 15:1 DCM:EA (ethyl acetate) as the eluent. The yellow

fraction (Rf = 0.95) was collected and gave a yellowish green oil upon evaporation (150 mg, 16%). The oil was solidified in 1 ml of methanol. 1 H NMR $(400$ MHz, CDCl₃) δ 7.78 (bs, 4H), 6.59 (m, 4H), 6.11 (m, 4H), 5.93 (m, 4H), 4.08 (t, *J* = 1.9 Hz, 4H), 3.96 (t, *J* = 1.9 Hz, 4H), 1.95 (s, 6H) ppm. 13C NMR (100 MHz, CDCl3) δ 138.32, 116.51, 107.97, 105.48, 98.08, 68.97, 67.90, 39.48, 28.64 ppm. HRMS (CI⁺) *m*/z for C₃₀H₃₀FeN₄ [M]⁺ calcd 502.1820, found 502.1826.

1-Acetyl-1'-(1,1-di(1H-pyrrol-2-yl)ethyl)ferrocene (**6a'**):

This product was obtained as a side product from the above reaction mixture. The product is a red solid (240 mg, 34%) that elutes from the column after **6a** (for **6a'** Rf = 0.5). ¹H NMR (400 MHz, CDCl₃) δ 7.99 (bs, 2H), 6.66 (m, 2H), 6.12 (m, 2H), 5.91 (m, 2H), 4.73 (t, *J* = 2.0 Hz, 2H), 4.46 (t, *J* = 2.0 Hz, 2H), 4.22 (t, *J* = 1.9 Hz, 2H), 4.00 (t, J = 1.9 Hz, 2H), 2.31 (s, 3H), 2.00 (s, 3H) ppm. ¹³C NMR (100 MHz, CDCl₃) δ 203.05, 137.60, 117.02, 107.87, 105.76, 100.32, 79.47, 75.53, 70.62, 69.53, 68.86, 39.40,29.00, 27.62 ppm. HR-MS-CI⁺ m/z for C₂₂H₂₂FeN₂O [M]⁺ calcd 386.1082, found 386.1072.

5,5',5'',5'''-(1,1'-Ferrocenylenebis(ethane-1,1,1-triyl))tetrakis(1*H*-pyrrole-2 carbaldehyde) (**6b**):

A Vilsmeier–Haack formylation procedure identical to that reported previously¹ was used, albeit starting with 6a. The product, 6b, was obtained in 80% yield. ¹H NMR (400 MHz, DMSO-*d6*) δ 11.63 (bs, 4H), 9.41 (s, 4H), 6.83 (m, 4H), 5.67 (m, 4H), 4.07 (m, 4H), 3.87 (m, 4H), 2.02 (s, 6H) ppm. ¹³C NMR (100 MHz, DMSO*d6*) δ 178.7, 146.9, 132.3, 109.7, 95.7, 68.1, 67.9, 55.3, 25.0 ppm. 13C NMR (100 MHz, DMF-*d7*) δ 179.3, 147.7, 133.6, 110.5, 96.8, 69.1, 68.9, 41.0, 26.0 ppm. HRMS (ESI⁺) *m/z* for C₃₄H₃₀FeN₄O₄ [M+H]⁺ calcd 615.16900, found 615.16930.

1,3,5-Tris(1,1-di(1*H*-pyrrol-2-yl)ethyl)benzene (**7a**):

A modification of the published dipyrromethane-forming procedure¹ was employed starting with 1,3,5-triacetylbenene and using CH_2Cl_2 as a co-solvent. The reaction was carried out at room temperature. A co-solvent is used to reduce the formation of insoluble side products. The desired product **7a** was obtained as colourless oil in 15% yield. ¹H NMR (400 MHz, CDCl₃) δ 7.65 (bs, 6H), 6.90 (s, 3H), 6.54 (m, 6H), 6.13 (m, 6H), 5.89 (m, 6H), 1.95 (s, 9H) ppm. ¹³C NMR (100 MHz, CDCl₃) δ 146.5, 137.4, 124.8, 117.1, 108.0, 106.3, 44.7, 28.5 ppm. HRMS (ESI⁺) *m/z* for C₃₆H₃₆N₆ [M+H]⁺ calcd 553.30740, found 553.30730.

5,5',5'',5''',5'''',5'''''-(Benzene-1,3,5-triyltris(ethane-1,1,1-triyl))hexakis(1*H*-pyrrole-2-carbaldehyde) (**7b**):

The Vilsmeier–Haack formylation procedure reported previously was used,¹ albeit starting with 7a. Product 7b was obtained in 80% yield. ¹H NMR (400 MHz, DMSO-*d6*) δ 11.68 (s, 6H), 9.34 (s, 6H), 6,75 (m, 6H), 6.42 (s, 3H), 5.74 (m, 6H), 1.91 (s, 9H) ppm. 13C NMR (100 MHz, DMSO-*d6*) δ 178.87, 145.67, 145.26, 133.03, 124.63, 110.43, 109.59, 45.38, 26.95 ppm. HRMS (ESI⁺) m/z for $C_{42}H_{36}N_6O_6$ [M+Na]⁺ calcd 743.25890, found 743.25920.

Fig. SI-1 Top: Linear assembly formed by one of the atropisomers of **6b**. The N-H•••O hydrogen bonding distances range from 2.875 to 2.901 Å. Bottom: Packing of the linear ensembles shown in the top portion of the figure.

Fig. SI-2 Hydrogen bond linked dimers of **7b** and their further self-assembly into layers. Each colour indicates one dimer made up from **7b**. The N-H•••O distances for the dimer are 2.850 and 2.888 Å. The dimer in the centre is drawn in wireframe representation. The space between the layers is filled with $CHCl₃$.

Fig. SI-3 A different view of complex (TBA)₂[7b·H₂PO₄⁻]₂.

Fig. SI-4 High-resolution mass spectrum (HR-ESI⁻-MS) (electrospray ionization in negative mode) of an equimolar mixture of 3b and TBAH₂PO₄ in CHCI₃. Note that the top and bottom panels cover different mass ranges.

Fig. SI-5 HR-ESI⁻-MS reports for $[3b-H]^T$ and $[3b \cdot H_2PO_4^T]$.

Fig. SI-6 HR-ESI⁻-MS reports for two observed minor adducts, [3b·CI⁻] and [3b·CF₃CO₂⁻], that are thought to arise as the result of residual contaminants present in the MS apparatus.

1 H NMR Spectroscopy

Fig. SI-7 Top: Stacked ¹H NMR spectra corresponding to the titration of 5a (19.1 mM) with TBAH₂PO₄ (0.235 M) in CDCI₃. Bottom: Binding curve obtained by fitting the chemical shift change of the pyrrole NH signal against [TBAH₂PO₄]. K_a = 40.8 ± 0.6 M⁻¹.

Fig. SI-8 Top: Stacked ¹H NMR spectra of receptor 5b (11.5 mM) with varying quantities of H_2PO_4 recorded in CDCI₃. The doublet arising from aromatic hydrogen atoms of the benzene ring of receptor **5b** displays the largest upfield shift (∆δ = -0.36 ppm). Bottom: The chemical shift change of the pyrrole NH signal plotted against $[TBAH_2PO_4]$.

Fig. SI-9 Stacked ¹H NMR spectra corresponding to the titration of 4b with TBH₂PO₄ in CDCI₃.

Fig. SI-10 Stacked ¹H NMR spectra of receptor **7b** (15.6 mM) with varying quantities of H₂PO₄⁻ recorded in CDCl₃:DMSO- d_6 (8:1). Dashed lines show changes in the chemical shifts for the aromatic hydrogen atoms of the benzene ring of receptor **7b** (∆δ = -0.19 ppm).

UV-Vis Spectroscopy

All binding studies reported in Table 2 were carried out using commercially available Fisher Scientific CHCl $_3$ containing approximately 0.75% ethanol as a preservative and commercially available Fisher Scientific $CH₃OH$. All anions were used in the form of their commercially available tetra-n-butylammonium (TBA⁺) salts.

In the titrations carried out with intention of determining binding affinities, the concentration of the receptor in question was kept constant. This was achieved by adjusting the guest (anion) concentration within stock host (receptor) solutions. This allowed the binding studies to be carried out without having to make mathematical corrections due to change in total receptor concentration.

receptor + anion \rightarrow receptor anion

 $K_a = \frac{[receptor \cdot anion]}{[receptor] * [anion]}$

In the wavelength range of 250-400 nm:

 $\epsilon_{\lambda, \text{receptor}} \neq \epsilon_{\lambda, \text{receptor-}anion}$ ε ^λ,anion = 0

Throughout the titration

 $[receptor]_o = [receptor] + [receptor\cdot anion]$ $[anion]_o = [anion] + [receptor-anion]$

The following equation was used to determine the binding affinities:

$$
\Delta A = \frac{1 + aK + xK - \sqrt{-4axK^2 + (-1 - aK - xK)^2}}{2K} \Delta \varepsilon
$$

where,

∆A (measured change in absorbance relative to the initial solution) is the y variable;

x is concentration of guest (in the form of its TBA^+ salt) added;

 α is the initial concentration of receptor (remains constant over the course of titration);

 $\Delta \varepsilon$ is the extinction coefficient difference between the free receptor and the receptor-guest complex;

 $K(K_a)$ is the binding affinity of the receptor for the guest in question.

OriginPro 9.0 was used to fit the data in a non-linear fashion in accord with the above equation. Iterations (at a fixed α value, by changing $\Delta \varepsilon$ and K) were performed until an acceptable level of convergence was reached (chi-square tolerance value, 1 x 10⁻⁹). Fig. SI-11 through Fig. SI-19 show the UV-Vis spectra and the binding curve fittings for receptors **3b** and **7b**.

Fig. SI-11 Top: Stacked UV-Vis spectra for titration of 3b (1.3 x 10⁻⁵ M) with TBAH₂PO₄ (4.1 x 10⁻³ M) in CHCl₃ containing 3% (v/v) CH₃OH. Bottom: Binding curve and fit generated from the titration data at 305 nm. $K_a = (2.1 \pm 0.3) \times 10^3 \,\mathrm{M}^{-1}$.

Fig. SI-12 Top: Stacked UV-Vis spectra for titration of 3b (1.3 x 10⁻⁵ M) with (TBA)₃HP₂O₇ (1.3 x 10^{-3} M) in CHCl₃ containing 3% (v/v) CH₃OH. Bottom: Binding curve and fit generated from the titration data at 305 nm. $K_a = (3.8 \pm 0.6) \times 10^3 \text{ M}^{-1}$.

Fig. SI-13 Top: Stacked UV-Vis spectra for titration of 3b (1.3 x 10⁻⁵ M) with TBAHSO₄ (6.5 x 10⁻³ M) in CHCl₃ containing 3% (v/v) CH₃OH. Bottom: Stacked UV-Vis spectra of 3b (1.3 x 10⁻⁵ M) with and without TBANO₃ (4.6 x 10⁻⁴ M) in CHCl₃ containing 3% (v/v) CH₃OH.

Fig. SI-14 Stacked UV-Vis spectra of $3b$ (1.3 x 10⁻⁵ M) with and without TBACl (1.5 x 10⁻³ M) in $CHCl₃$ containing 3% (v/v) $CH₃OH$.

Fig. SI-15 Stacked UV-Vis spectra of 7b solubilized by 2.75 equivalent TBAH₂PO₄ salt in neat $CHCl₃$ (0% added CH₃OH) and increasing percentages of added CH₃OH. Spectra are normalized to eliminate the effect of dilution.

Fig. SI-16 Top: Stacked UV-Vis spectra for titration of 7b (1.1 x 10⁻⁵ M) with TBAH₂PO₄ (2.9 x 10⁻⁴ M) in CHCl₃ containing 3% (v/v) CH₃OH. Bottom: Binding curve and fit generated from the titration data at 302 nm. $K_a = (1.4 \pm 0.2) \times 10^5 \,\mathrm{M}^{-1}$.

Fig. SI-17 Top: Stacked UV-Vis spectra for titration of 7b (1.1 x 10⁻⁵ M) with (TBA)₃HP₂O₇ (2.9 x $10⁻⁴$ M) in CHCl₃ containing 3% (v/v) CH₃OH. Bottom: Binding curve and fit generated from the titration data at 302 nm. $K_a = (3.6 \pm 0.2) \times 10^4 \text{ M}^{-1}$.

Fig. SI-18 Stacked UV-Vis spectra for titration of **7b** (1.1 x 10⁻⁵ M) with TBAHSO₄ (5.7 x 10⁻⁴ M) in $CHCl₃$ containing 3% (v/v) $CH₃OH$. No saturation behaviour is observed.

Fig. SI-19 Left: Stacked UV-Vis spectra for titration of **7b** (1.1 x 10⁻⁵ M) with TBANO₃ (2.4 x 10⁻⁴) M) in CHCl3 containing 3% (v/v) CH3OH. Right: Stacked UV-Vis spectra for titration of **7b** (1.1 x 10^{-5} M) with TBACl (1.2 x 10⁻⁴ M) in CHCl₃ containing 3% (v/v) CH₃OH.

Cyclic Voltammetry

For the titration of 6b with TBAH₂PO₄ in CH₃CN containing 10% (v/v) DMF, two chemical equilibria can be written as follows.

6b (s) $\qquad \Rightarrow$ **6b** (org) K_{sp}

6b (org) + H_2PO_4 ⁻(org) \Rightarrow **6b** $\cdot H_2PO_4$ ⁻ (org) K_a

The concentration of **6b** remains constant during the titration when there is still insoluble **6b**. This approximation is especially valid for the earlier data points.

$$
[6b] = K_{\text{sp}}
$$

The peak current (*i*p) is a function of concentration as defined by the following equation:

$$
i_p = 2.69 \times 10^5 \text{ n}^{3/2} \text{v}^{1/2} \text{ADC}
$$

 $i_p = \kappa \text{ C}$

Where n is the number of electrons transferred, v is the scan rate, A is the electrode surface area, C is the concentration and D is the diffusion coefficient. In the simplified equation, κ is a derived parameter that is held constant.

$$
i_{p,0} = \kappa_{6b} \cdot [6b]
$$
\n
$$
i_{p} = \kappa_{6b} \cdot [6b] + \kappa_{complex} \cdot [6b \cdot H_{2}PO_{4}^{-}]
$$
\n
$$
\Delta i_{p} = \kappa_{complex} \cdot [6b \cdot TBAH_{2}PO_{4}^{-}]
$$
\n
$$
K_{a} = \frac{[6b \cdot H_{2}PO_{4}^{-}]}{[6b] \cdot [H_{2}PO_{4}^{-}]}
$$

$$
K_a = \frac{\Delta i_p / \kappa_{complex}}{\left(\frac{i_{p,o}}{\kappa_{6b}}\right) \cdot \left[\text{H}_2 \text{PO}_4\right]}
$$

 $[6b \cdot H_2PO_4]_{max} = 1$ mM

 $i_{p,\text{max}} = K_{complex}$ [6b $\cdot H_2PO_4$]_{max}

it is assumed that all of the initial sample of **6b** is solubilized upon formation of complex (6b·H₂PO₄⁻) and *K_{complex}* = K_{6b}

For the calculations,

$$
[\mathbf{6b}]_{\text{sat}} = i_{p,\text{max}}/[\mathbf{6b}]_{\text{max}}
$$

 $[6b \cdot H_2PO_4] = \Delta i_p (6b \cdot H_2PO_4] / i_{p,max}$

 $[H_2PO_4] = [H_2PO_4]_0 - [6b \cdot H_2PO_4]$

A plot of Δi_p against added H_2PO_4 ⁻ ([H₂PO₄⁻]_o) is shown in Fig. SI-20 and the calculated equilibrium composition is presented in Table SI-1.

Fig. SI-20 The change in anodic peak current at around 600 mV is plotted against concentration of TBAH2PO4 added. Titration voltammograms are presented in Fig. 8 of the main text

Experimental conditions		Unit		Calculated		Unit	
$[6b]_{\text{max}}$	1.0E-03	M		$[6b]_{\text{sat}}$	3.50E-04	M	
$I_{p,\text{max}}$	13.1	uA					
Experimental				Calculated			
$[H2PO4]o$	$Iil(\mu A)$	Δi	[6b·H ₂ PO ₄]	[6b]	$[6b]_t$	[H ₂ PO ₄]	K_{a}
$0.00E + 00$	4.589	$0.00E + 00$	$0.00E + 00$	3.50E-04	3.50E-04	$0.00E + 00$	n/a
3.09E-04	4.592	3.00E-03	2.29E-07	3.50E-04	3.51E-04	3.08E-04	outlier
6.10E-04	6.495	1.91E+00	1.45E-04	3.50E-04	4.96E-04	4.64E-04	8.95E+02
9.04E-04	7.615	$3.03E + 00$	2.31E-04	3.50E-04	5.81E-04	6.73E-04	9.80E+02
1.19E-03	9.057	4.47E+00	3.41E-04	3.50E-04	6.91E-04	8.49E-04	$1.15E + 03$
1.47E-03	10.07	5.48E+00	4.18E-04	3.50E-04	7.69E-04	1.05E-03	$1.14E + 03$
1.74E-03	11.1	$6.51E+00$	4.97E-04	3.50E-04	8.47E-04	1.25E-03	$1.14E + 03$
2.27E-03	12.3	7.71E+00	5.89E-04	3.50E-04	1.00E-03	1.68E-03	9.98E+02
2.78E-03	13.1	8.51E+00	6.50E-04	3.50E-04	1.00E-03	2.13E-03	8.72E+02
						$K_{a,av}$	$1.02E + 03$
						STD	$1.17E + 02$
						%std	1.15E-01
Note: $i_{p,\text{max}}$ input in the Excel sheet has an influence on calculated K_a value for 6b H ₂ PO ₄ complex formation.							

Table SI-1 Excel spreadsheet used to calculate the *K* value corresponding to the formation of $6b \cdot H_2PO_4$.

A control experiment was performed using ferrocene under the same experimental conditions as used for the study **6b**. It is important to note that there is no anodic peak current increase observed in the experiment carried with ferrocene. However, upon inspection of cyclic voltammograms corresponding to this titration, a new reduction signal at 280 mV is seen (*cf*. Fig. SI-21). This new reduction signal is ascribed to the reduction of H⁺ that originates from the H_2 PO₄⁻ anion. Consistent with this conclusion is the reduction in the intensity of the signal observed when pyridine is added to the medium (*cf*. Fig. SI-22).

Fig. SI-21 Stacked cyclic voltammogram of 1.0 mM ferrocene in CH₃CN containing 10% (v/v) DMF (black line). This solution was titrated with TBAH₂PO₄ until the TBAH₂PO₄ concentration reached 2.8 mM. TBAPF $_6$ (0.1 M) was used as the supporting electrolyte. Glassy carbon was used as the working electrode, a Pt wire as the counter electrode, and a Ag/AgCl couple as the reference electrode.

Fig. SI-22 Stacked cyclic voltammogram of TBAH₂PO₄ (15 mM) in CH₃CN containing 10% (v/v) DMF (black line). Solid ferrocene was added to achieve a 2.0 mM concentration (red line). To this solution, 0.2 mL pyridine was added (blue line). TBAPF₆ (0.1 M) was used as the supporting electrolyte. Glassy carbon was used as the working electrode, a Pt wire as the counter electrode, and a Ag/AgCl couple as the reference electrode.

X-ray Diffraction Analyses

The X-ray diffraction data collection and refinements for the crystal structures of 6b, 7b, $[3b \cdot (TBA)_3H_2P_2O_7]_2$, 4b $\cdot TBAH_2PO_4$, and $[7b \cdot TBAH_2PO_4]_2$ may be obtained from the Cambridge Crystallographic Data Centre (CCDC) by reference to CCDC numbers 1444557-1444561. Some experimental details and relevant data tables for the refinements in question are given below.

Experimental Details for X-ray Diffraction Analysis

X-ray Experimental for **6b** $(C_{17}H_{15}N_2O)_2Fe - 2 C_3H_7NO$: Crystals grew as clear, yellow prisms by slow evaporation from dimethylformamide with a small amount of dichloromethane. The data crystal had approximate dimensions; 0.27 x 0.20 x 0.09 mm. The data were collected at -140 °C on a Nonius Kappa CCD diffractometer using a Bruker AXS Apex II detector and a graphite monochromator with MoK α radiation (λ = 0.71073 Å). Reduced temperatures were maintained by use of an Oxford Cryosystems 600 low-temperature device. A total of 1110 frames of data were collected using ω and ϕ -scans with a scan range of 1.1° and a counting time of 43 seconds per frame. Details of crystal data, data collection and structure refinement are listed in Table ESI-2. Data reduction was performed using SAINT V8.27B. 2 The structure was solved by direct methods using SUPERFLIP³ and refined by full-matrix least-squares on F^2

with anisotropic displacement parameters for the non-H atoms using SHELXL- $2013⁴$ Structure analysis was aided by use of the programs PLATON98⁵ and WinGX.⁶ The hydrogen atoms bound to carbon atoms were calculated in idealized positions. The hydrogen atoms on the pyrrole nitrogen atoms were observed in a ∆F map and refined with isotropic displacement parameters.

The function, $\text{Tw}(|F_0|^2 - |F_c|^2)^2$, was minimized, where w = 1/[($\sigma(F_0)$)² + $(0.0331^*P)^2$ + (2.7996^*P)] and P = $(|F_0|^2 + 2|F_c|^2)/3$. R_w(F²) refined to 0.111, with $R(F)$ equal to 0.0471 and a goodness of fit, $S₁ = 1.01$. Definitions used for calculating $R(F), R_w(F^2)$ and the goodness of fit, S, are given below.⁷ The data were checked for secondary extinction but no correction was necessary. Neutral atom scattering factors and values used to calculate the linear absorption coefficient are from the International Tables for X-ray Crystallography (1992). 8 All figures were generated using SHELXTL/PC.⁹ Tables of positional and thermal parameters, bond lengths and angles, torsion angles and figures may be obtained from the CCDC by referencing CCDC number 1444557.

X-ray Experimental for **7b** $C_{42}H_{36}N_6O_6$ - 2 CHCl₃: Crystals grew as clusters of yellow prisms by slow evaporation from chloroform, methanol and dimethylformamide. The data crystal was cut from a larger crystal and had approximate dimensions; 0.30 x 0.23 x 0.15 mm. The data were collected on a

Rigaku SCX-Mini diffractometer with a Mercury 2+ CCD using a graphite monochromator with MoK α radiation (λ = 0.71073 Å). A total of 1080 frames of data were collected using ω -scans with a scan range of 0.5 $^{\circ}$ and a counting time of 25 seconds per frame. The data were collected at 100 K using a Rigaku XStream low temperature device. Details of crystal data, data collection and structure refinement are listed in Table ESI-3. Data reduction was performed using the Rigaku Americas Corporation's Crystal Clear version 1.40.¹⁰ The structure was solved by direct methods using $SIR2004¹¹$ and refined by fullmatrix least-squares on F^2 with anisotropic displacement parameters for the non-H atoms using SHELXL-97.⁴ Structure analysis was aided by use of the programs PLATON98⁵ and WinGX.⁶ The hydrogen atoms were calculated in ideal positions with isotropic displacement parameters set to 1.2xUeq of the attached atom (1.5xUeq for methyl hydrogen atoms).

A molecule of chloroform was disordered. The disorder resulted in two principal conformations. The disorder was modelled by assigning the variable x to the site occupancy for one component and (1-x) to the site occupancy of the alternate component. The variable x was refined while restraining the geometry of the two components to be equivalent. A common isotropic displacement parameter was refined while refining x. In this way, the major component of the disordered solvent molecule consisting of atoms, Cl4, Cl5, Cl6 and C1b refined to a site occupancy of 53(1)%. The non-H atoms of both components were ultimately refined anisotropically with their displacement parameters restrained to be approximately isotropic.

The function, $\sum w(|F_0|^2 - |F_c|^2)^2$, was minimized, where w = $1/[(\sigma(F_0))^2 +$ $(0.086^*P)^2$ + (3.5129^*P)] and P = $(|F_0|^2 + 2|F_c|^2)/3$. R_w(F²) refined to 0.2593, with R(F) equal to 0.0937 and a goodness of fit, S, = 1.16. Definitions used for calculating R(F), $R_w(F^2)$ and the goodness of fit, S, are given below.⁷ The data were checked for secondary extinction effects but no correction was necessary. Neutral atom scattering factors and values used to calculate the linear absorption coefficient are from the International Tables for X-ray Crystallography (1992). 8 All figures were generated using SHELXTL/PC.⁹ Tables of positional and thermal

parameters, bond lengths and angles, torsion angles and figures may be obtained from the CCDC by referencing CCDC number 1444558.

 X -ray Experimental for **3b**·(TBA)₂H₂P₂O₇ C₃₀H₂₆N₄O₄ - 2 C₁₆H₃₆N¹⁺ $H_2P_2O_7^2$ % CH₂Cl₂: Crystals grew as thin, colourless prisms by layering a solution of 3b· $(TBA)_{3}HP_{2}O_{7}$ in CH₂Cl₂ with *n*-pentane. The data crystal had approximate dimensions; 0.16 x 0.11 x 0.06 mm. The data were collected on an Agilent Technologies SuperNova Dual Source diffractometer using a μ -focus Cu K α radiation source (λ = 1.5418Å) with collimating mirror monochromators. A total of 850 frames of data were collected using ω-scans with a scan range of 0.5° and a counting time of 7 seconds per frame using a detector offset of +/- 41.1° and a counting time of 25 seconds per frame using a detector offset of +/- 108.3°. The data were collected at 100 K using an Oxford Cryostream low temperature device. Details of crystal data, data collection and structure refinement are listed in Table ESI-4. Data collection, unit cell refinement and data reduction were performed using Agilent Technologies CrysAlisPro V 1.171.37.31.¹² The structure was solved by direct methods using SIR97¹³ and refined by full-matrix least-squares on F2 with anisotropic displacement parameters for the non-H atoms using SHELXL-2013.⁴ Structure analysis was aided by use of the programs PLATON98 5 and WinGX. 6 The hydrogen atoms

were calculated in ideal positions with isotropic displacement parameters set to 1.2xUeq of the attached atom (1.5xUeq for methyl hydrogen atoms.

Compound **3b** and the pyrophosphate form H-bound dimers across a crystallographic inversion centre located at $\frac{1}{2}$, $\frac{1}{2}$, $\frac{1}{2}$. The pyrophosphate dianion was H-bound to itself across this centre. Reliable coordinates for the hydrogen atoms bound to the pyrophosphate could not be located in a difference electron density map. These hydrogen atoms were not included in the final refinement model.

A molecule of dichloromethane was found to be badly disordered around a crystallographic inversion centre at 0, $\frac{1}{2}$, $\frac{1}{2}$. Attempts to model the disorder were unsatisfactory. The contributions to the scattering factors due to this solvent molecule were removed by use of the utility $SQUEEZE¹⁴$ in PLATON98. PLATON98 was used as incorporated in WinGX.

The function, $\sum w(|F_0|^2 - |F_c|^2)^2$, was minimized, where w = $1/[(\sigma(F_0))^2 +$ $(0.0827^*P)^2$ + (5.3705^*P)] and P = $(|F_0|^2 + 2|F_c|^2)/3$. R_w(F²) refined to 0.171, with $R(F)$ equal to 0.0603 and a goodness of fit, $S₁ = 1.03$. Definitions used for calculating R(F), $R_w(F^2)$ and the goodness of fit, S, are given below.⁷ The data were checked for secondary extinction effects but no correction was necessary. Neutral atom scattering factors and values used to calculate the linear absorption coefficient are from the International Tables for X-ray Crystallography (1992).⁸ All figures were generated using SHELXTL/PC. 9 Tables of positional and thermal parameters, bond lengths and angles, torsion angles and figures may be obtained from the CCDC by referencing CCDC number 1444559.

X-ray Experimental for complex $4b$ ·TBAH₂PO₄ (C₃₀H₂₆N₄O₄)(C₁₆H₃₆N)¹⁺ $O_2P(OH)_2$ ¹⁻ -1/2 CHCl₃: Crystals grew as yellow plates by layering a solution of **4b**·TBAH2PO4 in CHCl3 with *n*-pentane.The data crystal had approximate dimensions; 0.18 x 0.07 x 0.05 mm. The data were collected on an Agilent Technologies SuperNova Dual Source diffractometer using a μ -focus Cu K α radiation source (λ = 1.5418Å) with collimating mirror monochromators. A total of 1659 frames of data were collected using ω-scans with a scan range of 1° and a counting time of 9 seconds per frame with a detector offset of +/- 40.8° and 20 seconds per frame with a detector offset of +/- 108.3°. The data were collected at 100 K using an Oxford Cryostream low temperature device. Details of crystal data, data collection and structure refinement are listed in Table ESI-5. Data collection, unit cell refinement and data reduction were performed using Agilent Technologies CrysAlisPro V 1.171.37.31.¹² The structure was solved by direct methods using SuperFlip¹⁵ and refined by full-matrix least-squares on F^2 with anisotropic displacement parameters for the non-H atoms using SHELXL-2013.⁴ Structure analysis was aided by use of the programs PLATON98⁵ and WinGX.⁶ The hydrogen atoms bound to carbon atoms were calculated in ideal positions with isotropic displacement parameters set to 1.2xUeq of the attached atom (1.5xUeq for methyl hydrogen atoms). The hydrogen atoms bound to the pyrrole nitrogen atoms and the hydroxyl atoms of the phosphate ion were observed in a ∆F map and refined with isotropic displacement parameters.

The function, $\sum w(|F_0|^2 - |F_c|^2)^2$, was minimized, where w = $1/[(\sigma(F_0))^2 +$ $(0.0516^*P)^2$ + (2.5503^*P)] and P = $(|F_0|^2 + 2|F_c|^2)/3$. R_w(F²) refined to 0.124, with $R(F)$ equal to 0.0500 and a goodness of fit, $S₁ = 1.05$. Definitions used for calculating R(F), $R_w(F^2)$ and the goodness of fit, S, are given below.⁷ The data were checked for secondary extinction effects but no correction was necessary. Neutral atom scattering factors and values used to calculate the linear absorption coefficient are from the International Tables for X-ray Crystallography (1992).⁸ All figures were generated using SHELXTL/PC.⁹ Tables of positional and thermal parameters, bond lengths and angles, torsion angles and figures may be obtained from the CCDC by referencing CCDC number 1444560.

 X -ray Experimental for **7b**·TBAH₂PO₄ (2 C₄₂H₃₆N₆O₆ - 2 C₁₆H₃₆N¹⁺ $H_2PO_4^{1-}$ - 3 CHCl₃): Crystals grew as thin, yellow plates by layering a solution of **7b**·TBAH₂PO₄ in CHCl₃ with *n*-pentane. The data crystal had approximate dimensions; 0.27 x 0.16 x 0.08 mm. The data were collected on an Agilent Technologies SuperNova Dual Source diffractometer using a μ -focus Cu K α radiation source (λ = 1.5418Å) with collimating mirror monochromators. A total of 1035 frames of data were collected using ω -scans with a scan range of 0.5 $^{\circ}$ and

a counting time of 14 seconds per frame using a detector offset of +/- 41.1° and a counting time of 38 seconds per frame using a detector offset of +/- 108.3°. The data were collected at 100 K using an Oxford Cryostream low temperature device. Details of crystal data, data collection and structure refinement are listed in Table ESI-6. Data collection, unit cell refinement and data reduction were performed using Agilent Technologies CrysAlisPro V 1.171.37.31.¹² The structure was solved by direct methods using $SIR97^{13}$ and refined by full-matrix leastsquares on $F²$ with anisotropic displacement parameters for the non-H atoms using SHELXL-2013.⁴ Structure analysis was aided by use of the programs PLATON98⁵ and WinGX.⁶ The hydrogen atoms were calculated in ideal positions with isotropic displacement parameters set to 1.2xUeq of the attached atom (1.5xUeq for methyl hydrogen atoms.

The two tetra-n-butyl ammonium ions had highly anisotropic displacement parameters. One of the ions was refined with a disorder model. The disorder was modelled by assigning the variable x to the site occupancy for one component of the disorder and (1-x) to the site occupancy for the alternate component. The geometry of the two components was restrained by the extensive use of SADI instructions to maintain the C-C bonds and C-C-C angles to be equivalent. A common isotropic displacement parameter was assigned to the nitrogen atoms and the methylene carbon atoms while refining the variable x. A separate isotropic displacement parameter was refined for the methyl carbon atoms.

There are several regions of unidentified disordered solvent. The solvent was badly disordered and could not be reliably identified but was probably a mixture of the solvents used for crystallization, chloroform and n-hexane. The quantity and identity of the solvent in these voids was in doubt. The squeezed out solvent was not included in the UNIT card. The contributions to the scattering factors due to this solvent molecule were removed by use of the utility SQUEEZE⁶ in PLATON98. PLATON98 was used as incorporated in WinGX.

The function, $\sum w(|F_0|^2 - |F_c|^2)^2$, was minimized, where w = $1/[(\sigma(F_0))^2 +$ $(0.1^*P)^2$] and P = $(|F_0|^2 + 2|F_c|^2)/3$. R_w(F²) refined to 0.345, with R(F) equal to 0.126 and a goodness of fit, $S₁ = 1.61$. Definitions used for calculating R(F),

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 $R_w(F^2)$ and the goodness of fit, S, are given below.⁷ The data were checked for secondary extinction effects but no correction was necessary. Neutral atom scattering factors and values used to calculate the linear absorption coefficient are from the International Tables for X-ray Crystallography (1992).⁸ All figures were generated using SHELXTL/PC.⁹ Tables of positional and thermal parameters, bond lengths and angles, torsion angles and figures may be obtained from the CCDC by referencing CCDC number 1444561.

Structure Refinement Parameters

Table ESI-2 Crystal data and structure refinement for **6b**·2DMF.

Table ESI-3 Crystal data and structure refinement for **7b**·2CHCl3.

Table ESI-4 Crystal data and structure refinement for $3b \cdot (TBA)_{2}H_{2}P_{2}O_{7}$.

Table ESI-5 Crystal data and structure refinement parameters for $4b$ ⁻TBAH₂PO₄.

Table ESI-6. Crystal data and structure refinement parameters for [**7b·**TBAH2PO4]2.

1 H and 13C NMR Spectra

Fig. SI-23 Top: ¹H NMR (400 MHz) Bottom: ¹³C NMR (100 MHz) spectra of 6a in CDCl₃.

Fig. SI-24 Top: ¹H NMR (400 MHz) Bottom: ¹³C NMR (100 MHz) spectra of 6a' in CDCl₃.

Fig. SI-25 Top: ¹H NMR (400 MHz) spectrum of **6b** in DMSO- d_6 . Bottom: ¹³C NMR (100 MHz) spectrum of **6b** in DMF-*d7*.

Fig. SI-26 Top: ¹H NMR (400 MHz) Bottom: ¹³C NMR (100 MHz) spectra of **7a** in CDCl₃.

Fig. SI-27 Top: 1 H NMR (400 MHz), bottom: 13 C NMR (100 MHz) spectra of **7b** in DMSO- d_6 .

Notes and References

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- 7. R_W(F²) = {Σw(|F_O|² |F_C|²)²/Σw(|F_O|)⁴}^{1/2} where w is the weight given each reflection.

 $R(F) = \Sigma(|F_0| - |F_C|)/\Sigma|F_0|$ for reflections with $F_0 > 4(\sigma(F_0)).$

S = $[\Sigma w(|F_0|^2 - |F_C|^2)^2/(n-p)]^{1/2}$, where n is the number of reflections and p is the number of refined parameters.

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