Sharing the salt bowl: Counterion identity drives *N*-alkyl resorcinarene affinity and selectivity for pyrophosphate in water

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1. GENERAL INFORMATION

The *N*-alkyl ammonium resorcinarene salts (NARYs) were synthesized according to reported procedures.^{1–4} The reagents for synthesis and the phosphates (K_3PO_4 , Na_4PPi , Na_2AMP , Na_2ADP , and Na_2ATP) were purchased from commercial sources and used without purification. The synthesis of C3OHNARCI, CyNARCI, and BnNARCI are reported elsewhere.¹ ¹H, ¹³C and ³¹P NMR spectra were recorded on a Bruker Avance DRX 400 (400 MHz for ¹H, 100 MHz for ¹³C and 161.89 MHz for ³¹P) spectrometer. All signals are given as δ values in ppm using residual solvent signals as the internal standard. Coupling constants are given in Hz. Melting points were determined with a Stuart capillary melting point apparatus. Experimental details for the synthesis and characterization data of C3OHNARBr, C3OHNAROTf, CyNARBr, BnNARBr, NpNARCI, NpNARBr and NpNAROTf are below.

2. SYNTHESIS

The resorcinarene **1** and the hydroxyl tetrabenzoxazine **2** were synthesized by reported procedure.¹

a. General procedure for the synthesis of tetrabenzoxazines from the resorcinarenes. To a solution of the resorcinarene (5.5 mmol) and excess formaldehyde (6 mL) in ethanol (40 mL) was added the amine (23.3 mmol) in ethanol (15 mL) slowly and stirred at room temperature for 24 h. The precipitate that separated was filtered, recrystallized in a methanol/n-hexane mixture and used in the next step without any further purification.

b. General procedure for the synthesis of the *N*-alkyl ammonium resorcinarene chlorides from the tetrabenzoxazines. A solution of the tetrabenzoxazine (0.92 mmol), 3 mL of concentrated acid and 4 mL of H_2O in 40 mL of isopropanol is heated under reflux. Water and formaldehyde were removed by azeotropic distillation with chloroform. The remaining isopropanol was evaporated, and the crude product triturated with diethyl ether. The product was recrystallized accordingly to yield the pure product.



Figure S1. General representation of N-alkyl ammonium resorcinarene salts, R-NARX4.

2.1 Synthetic details of N-propanol ammonium resorcinarene bromide, C3OHNARBr₄



Figure S2. Synthesis of N-propanol ammonium resorcinarene bromide, C3OHNARBr₄.

The tetrabenzoxazine **2** (1.0 g, 0.92 mmol), isopropanol (40 ml), hydrobromic acid (3 ml), and H₂O (4 ml). The crude product mixture was recrystallized in a 1:1 (v/v) mixture of tetrahydrofuran and diethyl ether. The resulting precipitate was washed with acetonitrile, THF, Diethyl ether, and dried (393.7 mg, 30.2% yield). Melting point > 300°C. ESI-TOF-HRMS (Positive ion mode, sprayed from MeOH): m/z found 361.86320 [M-4Br-1H]⁺³; calc. 361.8752, m/z found 582.25461[M-3Br-1H]⁺²; calc. 582.2723. ¹H NMR (400 MHz in D₂O/[D₆]DMSO 9/1 v/v, 298 K) δ (ppm): 1.50 (m, 8H,CH₂), 2.33 (m, 8H,CH₂), 3.13 (t, J = 5.27 Hz, 8H, CH₂), 3.30 (m, 8H, CH₂), 3.65(t, J = 6.52 Hz, 8H, CH₂), 3.81 (q, J = 5.70 Hz, 8H, CH₂), 4.28 (t, J = 7.64 Hz, 8H,CH₂), 4.45 (t, J = 7.97 Hz, 4H, CH), 7.49 (s, 4H, CH); ¹³C NMR: (100 MHz, 298 K in CD₃OD) δ (ppm) = 29.9, 34.3, 41.2, 48.4, 56.3, 61.4, 81.7, 126.9, 150.4.



Figure S3. ¹H NMR of *N*-propanol ammonium resorcinarene bromide, C3OHNARBr₄, in $D_2O/[D_6]DMSO 9/1$, v/v at 298 K.



Figure S4. ¹³C NMR of *N*-propanol ammonium resorcinarene bromide, C3OHNARBr₄, in [D₆]DMSO at 298 K.



2.2 Synthetic details of N-propanol ammonium resorcinarene triflate, C3OHNAROTf₄

Figure S5. Synthesis of N-propanol ammonium resorcinarene triflate, C3OHNAROTf₄.

The tetrabenzoxazine **2** (1.0 g 0.92 mmol), isopropanol (40 ml), concentrated triflic acid (3 ml), and H₂O (4 ml). The precipitate was washed with ethyl acetate and then with diethyl ether (371.8 mg, 23.8 %). Melting points = 155-157°C. ESI-TOF-HRMS (Positive ion mode, sprayed from MeOH): m/z found 271.64498 [M-4CF₃SO₃]⁺⁴; calc. 271.6583, m/z found 617.27153 [M-3CF₃SO₃-1H]⁺², calc. 617.2891. ¹H NMR (400 MHz in D₂O) δ (ppm):1.43 (t, J = 5.99 Hz, 8H, CH₂), 1.74 (t, J = 5.99 Hz, 8H, CH₂) 2.19 (s, 8H, CH₂), 2.97, (t, J = 6.99 Hz, 8H, CH₂), 3.50 (t J = 5.99 Hz, 8H, CH₂), 3.57 (t, J = 6.24 Hz, 8H, CH₂), 4.19(s, 8H, CH₂), 4.36 (t, J = 7.23 Hz, 4H, CH), 7.29 (s, 4H, CH); ¹³C NMR: (100 MHz, 298 K in [D₆]DMSO) δ (ppm) = 21.1, 29.5, 31.3, 34.5, 41.4, 49.4, 56.6, 60.7, 108.6, 117.3, 119.8, 122.4, 125.0, 126.4, 150.87, 171.0.



Figure S6. ¹H NMR of *N*-propanol ammonium resorcinarene triflate, C3OHNAROTf₄, in D₂O at 298 K.



Figure S7. ¹³C NMR of *N*-propanol ammonium resorcinarene triflate, C3OHNAROTf₄, in [D₆]DMSO at 298 K.

2.3 Synthetic details of N-cyclohexyl ammonium resorcinarene bromide, CyNARBr₄



Figure S8. Synthesis of N-cyclohexyl ammonium resorcinarene bromide, CyNARBr₄.

Resorcinarene, **1** (5.0 g, 6.9 mmol) and excess formaldehyde solution 36 % (28 mL), ethanol (60 ml), cyclohexylamine (2.87 mL, 25.18 mmol) in ethanol (15 mL). The *N*-cyclohexyltetrabenzoxazine precipitate was filtered and dried and used in the next step without further purification. The *N*-cyclohexyltetrabenzoxazine **3** (1.0 g, 0.92 mmol), isopropanol (40 ml), concentrated hydrobromic acid (3 ml), and H₂O (4 ml). The precipitate was washed with ethyl acetate and then with diethyl ether to give the CyNARBr₄ product (371.8 mg, 23.8 % yield). Melting point > 300°C. ESI-TOF-HRMS (Positive ion mode, sprayed from MeOH): m/z found 583.37324 [M-4Br-2H]⁺²; calc. 583.3742, m/z found 623.33316 [M-3Br-H]⁺², calc. 623.3373. ¹H NMR (400 MHz in D₂O) δ (ppm): 0.9 (m, 12H, CH₂), 1.19 (m, 12H, CH₂), 1.53 (m, 12H, CH₂), 1.56 (d, J = 12.42 Hz, 8H, CH₂), 1.79 (d, J = 11.61 Hz, 8H, CH₂), 2.26 (q, J = 7.55 Hz, 8H, CH₂), 2.68 (m, 4H, CH), 3.60 (t, J = 6.47 Hz, 8H, CH₂), 4.19 (s, 8H, CH₂), 4.38 (t, J = 7.84 Hz, 4H, CH), 7.37 (s, 4H, ArH); ¹³C NMR: (100 MHz, 298 K in D₂O) δ (ppm) = 14.0, 23.8, 24.2, 28.7, 29.5, 29.7, 34.2, 38.6, 56.5, 61.5, 65.9, 109.0, 125.3, 126.9, 150.1.

Figure S9:. ¹H NMR of N-cyclohexyl ammonium resorcinarene bromide, CyNARBr₄ in D₂O at 298 K.

Figure S10. ¹³C NMR of *N*-cyclohexyl ammonium resorcinarene bromide, CyNARBr₄ in D₂O at 298 K.

Figure S11. Synthesis of N-benzyl ammonium resorcinarene bromide, BnNARBr₄.

Resorcinarene, **1** (5.0 g, 6.9 mmol) and excess formaldehyde solution 36 % (28 mL), ethanol (60 ml), benzylamine (3.18 mL, 29.11 mmol) in ethanol (15 mL). The *N*-benzyl tetrabenzoxazine precipitate was filtered and dried and used in the next step without further purification. The *N*-benzyltetrabenzoxazine **4** (1.0 g 0.92 mmol), isopropanol (40 ml), concentrated hydrobromic acid (3 ml), and H₂O (4 ml). The precipitate was washed with ethyl acetate and then with diethyl ether to give the BnNARBr₄ product (371.8 mg, 23.8 %). Melting point > 250°C, ESI-TOF-HRMS (Positive ion mode, sprayed from MeOH): m/z found 399.87685 [M-4Br-1H]⁺³; calc. 399.8768, m/z found 1197.61758 [M-4Br-3H]⁺; calc. 1197.6159. ¹H NMR (400 MHz in D₂O/[D₆]DMSO 9/1, δ (ppm): 1.51(m, 8H, CH₂), 2.36(q, J = 7.06 Hz, 8H, CH₂), 3.67 (t, J = 6.98 Hz, 8H, CH₂), 3.81 (s, 8H, CH₂), 4.28 (s, 8H,

CH₂), 4.30 (t, J = 4.42 Hz, 4H, CH), 6.75 (m, 20H, Ar), 7.58 (s, 4H, CH); 13 C NMR: (100 MHz, 298 K in CD₃OD) δ (ppm) = 30.4, 34.6, 42.7, 50.7, 56.5, 60.9, 108.9, 126.5, 129.1, 129.3, 129.5, 130.6, 132.0, 150.7,

Figure S12. ¹H NMR of *N*-benzyl ammonium resorcinarene bromide, BnNARBr₄, in $D_2O/[D_6]DMSO$ 9/1, v/v at 298 K.

Figure S13. ¹³C NMR of *N*-benzyl ammonium resorcinarene bromide, BnNARBr₄, in [D₆]DMSO at 298 K.

2.5 Synthetic details of N-naphthyl ammonium resorcinarene chloride, NpNARCl₄

Figure S14. Synthesis of N-naphthyl ammonium resorcinarene chloride, NpNARCl₄.

Resorcinarene, **1** (5.0 g, 6.9 mmol) and excess formaldehyde solution 36 % (28 mL), ethanol (60 ml), 1napthylmethylamine (4.25 mL, 29 mmol) in ethanol (15 mL). The precipitate was filtered and dried and used in the next step without further purification. The naphthyltetrabenzoxazine, **5** (0.5 g, 0.36 mmol), isopropanol (25 mL), 1.5 mL concentrated HCl (37 %), 2 mL H₂O.The crude product was then recrystallized with methanol and then triturated in diethyl ether to give the NpNARCl₄ product (0.23 g, 42 % yield). Melting points > 300°C. ESI-TOF-HRMS (Positive ion mode, sprayed from MeOH): m/z Found 699.34303 [M-4Cl-2H]⁺²; calc. 699.3429, m/z found 1433.66197 [M-3Cl-2H]⁺; calc. 1433.6551. ¹H NMR (400 MHz in D₂O/[D₆]DMSO 9/1) δ (ppm): 1.56 (m, 8H, CH₂), 2.43 (q, J = 7.66 Hz, 8H, CH₂), 3.72 (t, J = 6.4 Hz, 8H, CH₂), 3.85 (s, 8H, CH₂), 3.96 (s, 8H, CH₂), 4.41 (t, J = 8.21 Hz, 4H, CH) 6.60-7.7 (m, Ar, 32H): ¹³C NMR: (400 MHz, 298 K in D₂O/[D₆]DMSO 9/1) δ (ppm) = 30.9, 31.6, 35.9, 42.3, 47.2, 63.1, 110.4, 122.5, 126.6, 127.0, 127.3, 128.2, 129.1, 130.8, 131.7, 134.5, 151.6.

Figure S15. ¹H NMR of *N*-naphthyl ammonium resorcinarene chloride, NpNARCl₄, in $D_2O/[D_6]DMSO$ 9/1 v/v at 298 K.

Figure S16. ¹³C NMR of *N*-naphthyl ammonium resorcinarene chloride, NpNARCl₄, in $D_2O/[D_6]DMSO$ 9/1 v/v at 298 K.

2.6 Synthetic details of N-naphthyl ammonium resorcinarene bromide, NpNARBr₄

Figure S17. Synthesis of N-naphthyl ammonium resorcinarene bromide, NPNARBr

Naphthyl-tetrabenzoxazine (0.5 g .36 mmol), isopropanol (25 mL), 1.5 mL concentrated hydrobromic acid, 2 mL H₂O. The crude product was then recrystallized with methanol and then triturated in diethyl ether to give the NpNARBr product (0.14g, 28% yield). Melting point > 300 °C. ESI-TOF-HRMS (Positive ion mode, sprayed from MeOH): *m/z* Found 699.34361 [M-4Br-2H]⁺²; calc. 699.3429, m/z found 466.56612 [M-4Br-1H]⁺³; calc. 466.5643. ¹H NMR (400 MHz in D₂O/[D₆]DMSO 9/1, v/v), δ (ppm): 1.65 (m, H8, CH₂), 2.44 (q, J = 7.51 Hz, H8, CH₂), 7.72 (t, J = 6.41 Hz, 8H, CH₂), 3.87 (d, J = 6.33 Hz, 8H, CH₂), 6.96 (s, 8H, CH₂), 4.41 (m, 4H, CH), 6.63-7.74 (m, 32H, ArH); ¹³C NMR: (100 MHz, 298 K in CD₃OD) δ (ppm) = 26.0, 31.5, 34.7, 41.6, 47.2, 61.0, 123.8, 125.8, 126.6, 126.7, 127.3, 128.1, 129.2, 129.7, 130.2, 131.7, 133.7, 150.7.

Figure S18. ¹H NMR of *N*-naphthyl ammonium resorcinarene bromide, NpNARBr₄, in $D_2O/[D_6]DMSO$ 9/1, v/v at 298 K.

Figure S19. ¹³C NMR of *N*-naphthyl ammonium resorcinarene bromide, NpNARBr₄, in [D₆]DMSO at 298 K.

2.7 Synthetic details of N-naphthyl ammonium resorcinarene triflate, NpNAROTf₄

Figure S20. Synthesis of N-naphthyl ammonium resorcinarene triflate, NpNAROTf₄.

Naphthyl-tetrabenzoxazine (0.5 g .36 mmol), isopropanol (25 mL), 1.0 mL of triflic acid (99%) in 6 mL H₂O.The crude product was then recrystallized with methanol and then triturated in diethyl ether to give the NpNAROTf product (0.97g, 70 %). Melting point > 300 °C; ESI-TOF-HRMS (Positive ion mode, sprayed from MeOH): m/z found 699.34245 [M-4CF₃SO₃-2H]⁺²; calc. 699.3429, m/z found 774.32331 [M-3CF₃SO₃-H]⁺², calc. 774.3228. ¹H NMR (400 MHz in D₂O) δ (ppm): 1.55 (m, 8H, CH₂), 2.41 (q, J = 7.63 Hz, 8H, CH₂), 3.71 (t, J = 6.43Hz, 8H, CH₂), 3.83 (s, 8H, CH₂), 3.96 (s, 8H, CH₂), 4.39 (t, J = 7.65 Hz, 4H, CH₁) 6.55-8.17 (m, 32H, Ar): ¹³C NMR: (100 MHz, 298 K in CD₃OD) δ (ppm) = 22.5, 31.3, 35.4, 41.8, 46.8, 62.3, 109.8, 119.3, 122.2, 122.5, 126.1, 126.6, 131.3, 134.0, 151.1.

Figure S21. ¹H NMR of *N*-naphthyl ammonium resorcinarene triflate, NpNAROTf₄, in D₂O at 298 K.

Figure S22. ¹³C NMR of *N*-naphthyl ammonium resorcinarene triflate, NpNAROTf₄, in [D₆]DMSO at 298 K.

3. ISOTHERMAL TITRATION CALORIMETRY (ITC) EXPERIMENTS

VP-ITC instrument by MicroCal was used to determine the molar enthalpy (Δ H) of complexation. Subsequent fitting of the data to a 1:1 and 1:2 binding model using origin proprietary software provides association constants (K), change in enthalpy (Δ H) and change in entropy (Δ S). The ITC experiment was carried out by filling the sample cell with the receptor (0.25 mM) and filling the syringe with the phosphate titrants (5 mM), and titrating via computer-automated injector at 298 K. Blank titrations into plain solvent were also performed and subtracted from the corresponding titration to remove any effect from the heats of dilution from the titrant.

Figure S23. ITC traces of the titration of receptors with PPi at 298 K. The data was fitted to a two-sites binding model for (a) PPi@C3OHNAR(Br)₄, (b) PPi@CyNAR(Br)₄, (c) PPi@BnNAR(OTf)₄ and (d) PPi@NpNAR(Br)₄ in H₂O (90%) / DMSO (10%). (e) PPi@C3OHNAR(Br)₄ (f) PPi@CyNAR(Br)₄, (g) PPi@BnNAR(Br)₄ and (h) PPi@NpNAR(Br)₄ in Tris buffer pH 7.4 (90%) /DMSO (10%). The displaced anions are represented in parentheses.

Figure S24. ITC traces of the titration of receptors with PPi at 298 K. The data was fitted to a two set of sites binding model for (a) PPi@NpNAR(Cl)₄, (b) PPi@NpNAR(Br)₄ and (c) PPi@NpNAR(OTf)₄ in 90% H₂O/10% DMSO. (d) PPi@NpNAR(Cl)₄, (e) PPi@NpNAR(Br)₄ and (f) PPi@NpNAR(OTf)₄ were fitted to two binding sites model in 90% Tris buffer pH 7.4/10% DMSO. The displaced anions are represented in parentheses.

Figure S25. ITC traces of the titration of receptors with PPi at 298 K. The data was fitted to a two set of sites binding model for (a) PPi@C3OHNAR(Cl)₄, (b) PPi@C3OHNAR(Br)₄, (c) PPi@C3OHNAR(OTf)₄ in 90% H₂O/10% DMSO. (d) PPi@C3OHNAR(Cl)₄ (e) PPi@C3OHNAR(Br)₄ (f) PPi@C3OHNAR(OTf)₄ in 90% Tris buffer pH 7.4/10% DMSO. The displaced anions are represented in parentheses.

Figure S26. ITC traces of the titration of receptors with PO_4^- at 298 K. ITC data could not be fitted to any binding model for (a) $PO_4^-@C3OHNAR(Br)_4$, (b) $PO_4^-@C3OHNAR(OTf)_4$ in 90% $H_2O/10\%$ DMSO. (c) $PO_4^-@C3OHNAR(Br)_4$ (d) $PO_4^-@C3OHNAR(OTf)_4$ in 90% Tris buffer pH 7.4/10% DMSO. The displaced anions are represented in parentheses.

Figure S27. ITC traces of the titration of receptors with AMP at 298 K. ITC data was fitted to two set of sites binding model for (a) AMP@C3OHNAR(Br)₄ and (b) AMP@C3OHNAR(OTf)₄ in 90% H₂O/10% DMSO. (c) AMP@C3OHNAR(Br)₄ was fitted to one set of sites and (d) AMP@C3OHNAR(OTf)₄ to two set of sites in 90% Tris buffer pH 7.4/10% DMSO. The displaced anions are represented in parentheses.

Figure S28. ITC traces of the titration of receptors with ADP at 298 K. ITC data was fitted to one set of sites binding model for (a) ADP@C3OHNAR(Br)₄ and (b) ADP@C3OHNAR(OTf)₄ in 90% H₂O/10% DMSO. (c) ADP@C3OHNAR(Br)₄ could not be fitted to any binding model and (d) ADP@C3OHNAR(OTf)₄ to one set of sites in 90% Tris buffer pH 7.4/10% DMSO. The displaced anions are represented in parentheses.

Figure S29. ITC traces of the titration of receptors with ATP at 298 K. ITC data could not be fitted to any binding model for (a) ATP@C3OHNAR(Br)₄. Data was fitted to one set of sites for (b) ATP@C3OHNAR(OTf)₄ in 90% H₂O/10% DMSO. (c) ATP@C3OHNAR(Br)₄ and (d) ATP@C3OHNAR(OTf)₄ were fitted to one set of sites in 90% Tris buffer pH 7.4/10% DMSO. The displaced anions are represented in parentheses.

Figure S30. ITC traces of the titration of receptors with AMP at 298 K. ITC data was fitted to two set of sites binding model for (a) AMP@NpNAR(Br)₄ and (b) AMP@NpNAR(OTf)₄ in 90% $H_2O/10\%$ DMSO. (c) AMP@NpNAR(Br)₄ was fitted to one set of sites and (d) AMP@NpNAR(OTf)₄ could not be fitted to any binding model in 90% Tris buffer pH 7.4/10% DMSO. The displaced anions are represented in parentheses.

Figure S31. ITC traces of the titration of receptors with ADP at 298 K. ITC data was fitted to one set of sites binding model for (a) ADP@NpNAR(Br)₄ and (b) ADP@NpNAR(OTf)₄ in 90% H₂O/10% DMSO. (c) ADP@NpNAR(Br)₄ was fitted to one set of sites and (d) ADP@NpNAR(OTf)₄ could not be fitted to any binding model in 90% Tris buffer pH 7.4/10% DMSO. The displaced anions are represented in parentheses.

Figure S32. ITC traces of the titration of receptors with ATP at 298 K. ITC data could not be fitted for (a) ATP@NpNAR(Br)₄, data was fitted to one set of sites binding model for (b) ATP@NpNAR(OTf)₄ in 90% H₂O/10% DMSO. (c) ATP@NpNAR(Br)₄ and (d) ATP@NpNAR(OTf)₄ were fitted to one set of sites binding model in 90% Tris buffer pH 7.4/10% DMSO. The displaced anions are represented in parentheses.

Figure S33. ITC traces of the titration of receptors with PO_4^- at 298 K. ITC data could not be fitted for (a) PO_4^- @NpNAR(Br)₄ and (b) PO_4^- @NpNAR(OTf)₄ in 90% H₂O/10% DMSO. (c) PO_4^- @NpNAR(Br)₄ and (d) PO_4^- @NpNAR(OTf)₄ were fitted to one set of sites binding model in 90% Tris buffer pH 7.4/10% DMSO. The displaced anions are represented in parentheses.

Complex	<i>K</i> ₁ (× 10⁵) M ⁻¹	<i>ΔH</i> ₁ kcal/mol	7ΔS₁ kcal/m ol	∆G₁ kcal/mol	Complex	<i>K</i> ₂ (× 10 ⁵) Μ ⁻ 1	∆H₂ kcal/mol	<i>TΔS₂</i> kcal/mol	ΔG₂ kcal/mol
PPi@ <mark>Cy</mark> NAR(Br) ₄	1.3±0.1	-6.5±1.4	-0.9	-5.6	PPi@ <mark>Cy</mark> NAR(Br) ₄	0.9±0.2	13±1.1	17	-4.0
PPi@ <mark>Bn</mark> NAR(Br) ₄	3.6±0.6	-1.0±0.4	5.2	-6.2	PPi@ <mark>Bn</mark> NAR(Br) ₄	1.4±0.1	9.8±0.4	14	-4.2

Table S1. Thermodynamic binding parameters of formed complexes between $PPi@Cy-NAR(Br)_4$ and $PPi@Bn-NAR(Br)_4$ in mixed buffer systems

Table S2. Thermodynamic binding parameters of formed complexes between PPi@C3OH-NAR(X) in mixed water and buffer systems

Complex	K ₁	ΔH_1	T∆S₁	ΔG1	Complex	K ₁	ΔH_1	T∆S₁	∆G₁
	(× 10 ⁵) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(× 10 ⁴) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
PPi@C3OH- NAR(<mark>Cl)₄</mark>	3.6±0.3	-1.7±0.2	5.9	-7.6	PPi@C3OH- NAR(<mark>Cl)₄</mark>	2.0±0.2	-4.5±0.6	1.4	-5.9
					PPi@C3OH- NAR(<mark>Br)₄</mark>	6.1±0.8	3.6±0.2	10	-6.5
PPi@C3OH- NAR(<mark>OTf)₄</mark>	6.2±0.8	5.7±0.3	14	-7.9	PPi@C3OH- NAR(<mark>OTf)₄</mark>	7.4±0.8	-1.5±0.4	5.1	-6.6
Complex	K ₂	∆H₂	T∆S₂	∆G₂	Complex	K ₂	∆H₂	T∆S₂	∆G₂
	(× 10⁵) M⁻¹	kcal/mol	kcal/mol	kcal/mol		(×10³) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
PPi@C3OH- NAR(<mark>Cl)₄</mark>	0.6±0.1	6.7±0.1	13	-6.1	PPi@C3OH- NAR(<mark>Cl)₄</mark>	0.8±0.01	1.8±0.1	22	-21
					PPi@C3OH- NAR(<mark>Br)₄</mark>	2.2±0.8	2.1±0.1	7.2	-5.1
PPi@C3OH- NAR(<mark>OTf)₄</mark>	4.6±2.1	-4.1±0.2	2.2	-6.2	PPi@C3OH- NAR(<mark>OTf)₄</mark>	0.7±0.2	4.5±1.1	8.4	-3.9
	00% 420/					00% BUIEEED /1			

Table S3. Thermodynamic binding parameters of formed complexes between PPi@Np-NAR(X) in mixed water and buffer systems

Complex	K ₁	ΔH_1	TΔS1	ΔG1	Complex	K ₁	ΔH_1	TΔS1	ΔG1
	(× 10 ⁵) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(× 10⁵) M⁻¹	kcal/mol	kcal/mol	kcal/mol
					PPi@Np- NAR <mark>(Cl)₄</mark>	2.0±0.2	-4.5±0.6	1.3	-5.8
					PPi@Np- NAR <mark>(Br)</mark> ₄	6.3±1.6	0.4±0.3	6.7	-6.2
					PPi@Np- NAR <mark>(OTf)</mark> ₄	7.4±0.8	-1.5±0.4	4.8	-6.3
Complex	K2	∆H₂	T∆S₂	∆G₂	Complex	K ₂	ΔH₂	T∆S₂	∆G₂
	(× 10 ⁵) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(×10³) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
					PPi@Np- NAR(<mark>Cl)₄</mark>	0.8±0.1	0.8±0.1	22	-22
					PPi@Np- NAR(<mark>Br)₄</mark>	5.2±0.8	2.10±0.1	7.2	-5.1
					PPi@Np- NAR <mark>(OTf)</mark> ₄	0.8±0.3	4.5±1.1	8.4	-3.9

90% H20/10% DMSO

90% BUFFER/10% DMSO

Table S4. Thermodynamic binding parameters of formed complexes between $PO_4@C3OH-NAR(X)$ in mixed water and buffer systems

Complex	K ₁	ΔH_1	TΔS1	ΔG1	Complex	K ₁	ΔH1	T∆S₁	ΔG1
	(× 10 ⁵) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(× 10 ⁵) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
PO ₄ @C3OH- NAR <mark>(Br)</mark> 4	Does not fit				PO ₄ @C3OH- NAR <mark>(Br)</mark> 4	Does not fit			
PO₄@COH- NAR <mark>(OTf)</mark> ₄	Does not fit				PO₄@COH- NAR <mark>(OTf)</mark> ₄	Does not fit			
Complex	K ₂	ΔH₂	T∆S₂	∆G₂	Complex	K ₂	∆H₂	T∆S₂	∆G₂
	(× 10 ⁵) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(×10 ⁵) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
PO ₄ @C3OH- NAR <mark>(Br)</mark> 4	Does not fit				PO ₄ @C3OH- NAR <mark>(Br)</mark> 4	Does not fit			
PO₄@COH- NAR <mark>(OTf)</mark> ₄	Does not fit				PO₄@COH- NAR <mark>(OTf)</mark> ₄	Does not fit			
	90% H20/	'10% DMSO				90% BUFFER/1	.0% DMSO		

Table S5. Thermodynamic binding parameters of formed complexes between AMP@C3OH-NAR(X) in mixed water and buffer systems

Complex	K ₁	ΔH_1	T∆S₁	∆G₁	Complex	K ₁	ΔH_1	T∆S₁	∆G₁
	(× 10 ⁴) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(× 104) M-1	kcal/mol	kcal/	kcal/mol
								mol	
AMP@C3OH- NAR <mark>(Br)</mark> 4	3.5±0.7	9.6±1.5	16	-6.2	AMP@C3OH- NAR <mark>(Br)</mark> 4	0.7±0.1	6.2±0.7	11	-5.2
AMP@C3OH- NAR <mark>(OTf)</mark> 4	5.7±0.4	-5.2±0.3	1.3	-6.5	AMP@C3OH- NAR <mark>(OTf)</mark> ₄	5.5±0.5	-5.9±1.2	0.6	-6.5
Complex	K2	∆H₂	T∆S₂	∆G₂	Complex	K ₂	ΔH₂	T∆S₂	∆G₂
	(× 10 ⁵) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(×10⁴) M⁻¹	kcal/mol	kcal/	kcal/mol
								moi	
AMP@C3OH-	1.4±4.0	-2.5±1.0	4.5	-7	AMP@C3OH-	-	-	-	-
NAR <mark>(Br)</mark> 4					NAR <mark>(Br)</mark> ₄				
AMP@COH-	0.2±0.03	1.4±0.2	20	-18	AMP@C3OH-	2.2±0.1	15±1.4	21	-5.9
NAR <mark>(OTf)</mark> 4					NAR <mark>(OTf)</mark> 4				
	90% H20/1	0% DMSO			9	0% BUFFER/109	6 DMSO		

Table S6. Thermodynamic binding parameters of formed complexes between ADP@C3OH-NAR(X) in mixed water and buffer systems

Complex	K ₁	ΔH_1	T∆S₁	ΔG1	Complex	K ₁	ΔH_1	T∆S₁	∆G₁
	(× 10²) M ⁻	kcal/mol	kcal/mol	kcal/mol		(× 10²) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
	1								
ADP@C3OH-	1.7±0.2	-105±13	-102	-3.1	ADP@C3OH-	Does not fit	-	-	-
NAR(Br) ₄					NAR(Br) ₄				
ADP@C3OH-	7±0.2	-3.2±0.5	0.6	-3.9	AMP@COH-	3.0±0.2	-434±26	-429	-4.9
NAR <mark>(OTf)</mark> 4					NAR <mark>(OTf)</mark> 4				
Complex	K ₂	∆H₂	T∆S₂	∆G₂	Complex	K ₂	∆H₂	T∆S₂	∆G₂
	(× 10 ⁵) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(×10 ⁴) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
ADP@C3OH-	-	-	-	-	ADP@C3OH-	-	-	-	-
NAR(Br) ₄					NAR(Br) ₄				
ADP@C3OH-	-	-	-	-	ADP@C3OH-	-	-	-	-
NAR <mark>(OTf)</mark> 4					NAR <mark>(OTf)</mark> 4				
	90% H20/	10% DMSO				90% BUFFER/	10% DMSO		

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Table S7. Thermodynamic binding parameters of formed complexes between ATP@C3OH-NAR(X) in mixed water and buffer systems

Complex	K1	ΔH_1	TΔS1	ΔG1	Complex	K ₁	ΔH_1	TΔS1	ΔG1
	(× 10 ³) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(× 10 ¹) M ⁻¹	kcal/mol	kcal/m	kcal/mol
								ol	
ATP@C3OH	Does not fit	-	-	-	ATP@C3OH	9.4±1	-1151±115	-1147	-3.7
-NAR <mark>(Br)</mark> 4					-NAR <mark>(Br)</mark> 4				
ATP@C3OH	3.4±0.2	-30±0.7	-25	-4.8	ATP@C3OH	10.7±1.3	-898±100	-894	-64
-NAR <mark>(OTf)</mark> 4					-NAR <mark>(OTf)</mark> 4				
Complex	K ₂	ΔH₂	T∆S₂	∆G₂	Complex	K ₂	∆H₂	T∆S₂	∆G₂
	(× 10⁵) M⁻¹	kcal/mol	kcal/mol	kcal/mol		(×10⁴) sM⁻¹	kcal/mol	kcal/m	kcal/mol
						v - y -		ol	
ATP@C3OH	-	-	-	-	ATP@C3OH	-	-	-	-
-NAR <mark>(Br)</mark> 4					-NAR(Br) ₄				
ATP@C3OH	-	-	-	-	ATP@C3OH	-	-	-	-
-NAR <mark>(OTf)</mark> 4					-NAR <mark>(OTf)</mark> 4				

90% H20/10% DMSO

90% BUFFER/10% DMSO

Table S8. Thermodynamic binding parameters of formed complexes between PO₄@Np-NAR(X) in mixed water and buffer systems

Complex	K1	∆H₁	TΔS1	ΔG1	Complex	K ₁	ΔH_1	TΔS1	ΔG1
	(× 10 ⁵) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(× 10 ⁴) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
PO4@Np- NAR <mark>(Br)₄</mark>	Does not fit				PO4@Np- NAR <mark>(Br)</mark> 4	0.1±0.004	13±5.1	17	-4.3
PO4@Np- NAR <mark>(OTf)₄</mark>	Does not fit				PO4@Np- NAR <mark>(OTf)₄</mark>	2.7±0.2	-25±0.5	-19	-6.0
Complex	K ₂	∆H₂	T∆S₂	∆G₂	Complex	K2	∆H₂	T∆S₂	∆G₂
	(× 10⁵) M⁻¹	kcal/mol	kcal/mol	kcal/mol		(×10⁵) M⁻¹	kcal/mol	kcal/mol	kcal/mol
PO4@Np-	Does not fit				PO4@Np-	-	-	-	-
NAR <mark>(Br)</mark> 4					NAR <mark>(Br)</mark> 4				
DOLONI	Deservet fit				PO4@Np-	-	_	_	_
PO4@Np-	Does not fit							-	
PO4@Np- NAR <mark>(OTf)</mark> ₄	Does not fit				NAR(OTf)₄		_	-	

90% H20/10% DMSO

90% BUFFER/10% DMSO

Table S9. Thermodynamic binding parameters of formed complexes between AMP@Np-NAR(X) in mixed wa	iter
and buffer systems	

K ₁	ΔH_1	T∆S₁	∆G₁	Complex	K ₁	ΔH_1	T∆S₁	∆G₁
(× 10 ⁴) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(× 10³) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
1.2±0.6	-5.9±0.9	2.4	-8.3	AMP@Np- NAR <mark>(Br)</mark> 4	1.4±0.2	7.3±0.6	12	-4.3
2±0.5	-3.3±0.2	5.3	-8.6	AMP@Np- NAR <mark>(OTf)</mark> ₄	Does not fit	-	-	-
К2	ΔH₂	T∆S₂	∆G₂	Complex	<i>K</i> ₂	∆H₂	TΔS₂	∆G₂
(× 10 ³) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(×10⁴) M⁻¹	kcal/mol	kcal/mol	kcal/mol
3.8±1.34	3.7±0.4	11	-7.6	AMP@Np- NAR <mark>(Br)</mark> ₄	-	-	-	-
2.6±0.4	4.0±0.1	11	-7.4	AMP@Np- NAR(OTf)	-	-	-	-
	K1 (× 10 ⁴) M ⁻¹ 1.2±0.6 2±0.5 K2 (× 10 ³) M ⁻¹ 3.8±1.34 2.6±0.4	K_I ΔH_I (× 10 ⁴) M ⁻¹ kcal/mol 1.2±0.6 -5.9±0.9 2±0.5 -3.3±0.2 K_2 ΔH_2 (× 10 ³) M ⁻¹ kcal/mol 3.8±1.34 3.7±0.4 2.6±0.4 4.0±0.1	K_I ΔH_I $T\Delta S_I$ (× 10 ⁴) M ⁻¹ kcal/mol kcal/mol 1.2±0.6 -5.9±0.9 2.4 2±0.5 -3.3±0.2 5.3 K_2 ΔH_2 $T\Delta S_2$ (× 10 ³) M ⁻¹ kcal/mol kcal/mol 3.8±1.34 3.7±0.4 11 2.6±0.4 4.0±0.1 11	K_I ΔH_I $T\Delta S_I$ ΔG_I $(\times 10^4)$ M ⁻¹ kcal/mol kcal/mol kcal/mol 1.2 ± 0.6 -5.9 ± 0.9 2.4 -8.3 2 ± 0.5 -3.3 ± 0.2 5.3 -8.6 K_2 ΔH_2 $T\Delta S_2$ ΔG_2 $(\times 10^3)$ M ⁻¹ kcal/mol kcal/mol kcal/mol 3.8 ± 1.34 3.7 ± 0.4 11 -7.6 2.6 ± 0.4 4.0 ± 0.1 11 -7.4	K_I ΔH_I $T\Delta S_I$ ΔG_I Complex (× 10 ⁴) M ⁻¹ kcal/mol kcal/mol kcal/mol kcal/mol cal/mol 1.2±0.6 -5.9±0.9 2.4 -8.3 AMP@Np-NAR(Br)_4 2±0.5 -3.3±0.2 5.3 -8.6 AMP@Np-NAR(OTf)_4 K_2 ΔH_2 $T\Delta S_2$ ΔG_2 Complex (× 10 ³) M ⁻¹ kcal/mol kcal/mol kcal/mol AMP@Np-NAR(OTf)_4 3.8±1.34 3.7±0.4 11 -7.6 AMP@Np-NAR(Br)_4 2.6±0.4 4.0±0.1 11 -7.4 AMP@Np-NAR(OTf)_4	K_I ΔH_I $T\Delta S_I$ ΔG_I Complex K_I $(\times 10^4)$ M ⁻¹ kcal/mol kcal/mol kcal/mol kcal/mol kcal/mol ($\times 10^3$) M ⁻¹ 1.2 ± 0.6 -5.9 ± 0.9 2.4 -8.3 AMP@Np- NAR(Br)_4 1.4 ± 0.2 2 ± 0.5 -3.3 ± 0.2 5.3 -8.6 AMP@Np- NAR(OTf)_4 Does not fit K_2 ΔH_2 $T\Delta S_2$ ΔG_2 Complex K_2 $(\times 10^3)$ M ⁻¹ kcal/mol kcal/mol kcal/mol complex K_2 3.8 ± 1.34 3.7 ± 0.4 11 -7.6 AMP@Np- NAR(Br)_4 $ 2.6\pm 0.4$ 4.0 ± 0.1 11 -7.4 AMP@Np- NAR(OTf)_4 $-$	K_I ΔH_1 $T\Delta S_I$ ΔG_1 Complex K_I ΔH_I $(\times 10^4)$ M ⁻¹ kcal/mol kcal/mol kcal/mol kcal/mol kcal/mol kcal/mol 1.2 ± 0.6 -5.9 ± 0.9 2.4 -8.3 AMP@Np- NAR(Br)_4 1.4 ± 0.2 7.3 ± 0.6 2 ± 0.5 -3.3 ± 0.2 5.3 -8.6 AMP@Np- NAR(OTf)_4 Does not fit $ K_2$ ΔH_2 $T\Delta S_2$ ΔG_2 Complex K_2 ΔH_2 $(\times 10^3)$ M ⁻¹ kcal/mol kcal/mol kcal/mol $ (\times 10^4)$ M ⁻¹ kcal/mol 3.8 ± 1.34 3.7 ± 0.4 11 -7.6 AMP@Np- NAR(OTh)_4 $ 2.6\pm 0.4$ 4.0 ± 0.1 111 -7.4 AMP@Np- NAR(OTh)_4 $ -$	K_1 ΔH_1 $T\Delta S_1$ ΔG_1 Complex K_1 ΔH_1 $T\Delta S_1$ $(\times 10^4)$ M ⁻¹ kcal/molkcal/molkcal/molkcal/molkcal/molkcal/mol 1.2 ± 0.6 -5.9 ± 0.9 2.4 -8.3 $AMP@Np-$ NAR(Br)_4 1.4 ± 0.2 7.3 ± 0.6 12 2 ± 0.5 -3.3 ± 0.2 5.3 -8.6 $AMP@Np-$ NAR(OTf)_4 $Does not fit$ $ K_2$ ΔH_2 $T\Delta S_2$ ΔG_2 Complex K_2 ΔH_2 $T\Delta S_2$ $(\times 10^3)$ M ⁻¹ kcal/molkcal/molkcal/mol cal/mol K_2 ΔH_2 $T\Delta S_2$ $(\times 10^3)$ M ⁻¹ $AMP@Np-$ kcal/mol K_2 ΔH_2 $T\Delta S_2$ cal/mol cal/mol cal/mol 3.8 ± 1.34 3.7 ± 0.4 11 -7.6 $AMP@Np-$ NAR(DTf)_4 $ 2.6\pm0.4$ 4.0 ± 0.1 11 -7.4 $AMP@Np-$ NAR(OTf)_4 $ -$

90% H20/10% DMSO

90% BUFFER/10% DMSO

Complex	<i>K</i> ₁	ΔH_1	TΔS1	ΔG1	Complex	K ₁	ΔH_1	TΔS1	ΔG1
	(× 10²) M ⁻¹	kcal/mol	kcal/mol	kcal/mol		(× 10 ⁴) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
ADP@Np- NAR <mark>(Br)</mark> ₄	5.1±0.3	-19±4.4	-15	-3.7	ADP@Np- NAR(Br) ₄	0.2±0.1	-31±5.7	-24	-6.3
ADP@Np- NAR <mark>(OTf)</mark> ₄	1.4±0.4	-82±2.1	-79	-2.8	ADP@Np- NAR <mark>(OTf)₄</mark>	2.4±2	1.2±2.7	7.2	-6
Complex	K ₂	ΔH ₂	T∆S₂	∆G₂	Complex	K ₂	∆H₂	T∆S₂	∆G₂
	(× 104) M-1	kcal/mol	kcal/mol	kcal/mol		(×10²) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
ADP@Np-	4.2±0.7	-23±3	-17	-6.3	ADP@Np-	-	-	-	-
NAR <mark>(Br)</mark> 4					NAR(Br) ₄				
ADP@Np-	-	-	-	-	ADP@Np-	8.2±4.2	-18±5.1	-14	-4
NAR <mark>(OTf)</mark> 4					NAR(OTf) ₄				

Table S10. Thermodynamic binding parameters of formed complexes between ADP@Np-NAR(X) in mixed water and buffer systems

90% H20/10% DMSO

90% BUFFER/10% DMSO

Table S11. Thermodynamic binding parameters of formed complexes between ATP@Np-NAR(X) in mixed water and buffer systems

Complex	K ₁	ΔH1	TΔS1	ΔG1	Complex	K ₁	ΔH_1	TΔS1	ΔG1
	(× 10²) M ⁻ 1	kcal/mol	kcal/mol	kcal/mol		(× 10³) M ⁻¹	kcal/mol	kcal/mol	kcal/mol
ATP@Np- NAR <mark>(Br)</mark> 4	Does not fit	-	-	-	ATP@Np- NAR(Br) ₄	1.1±0.1	-34±1.5	-30	-4.1
ATP@Np- NAR <mark>(OTf)₄</mark>	Does not fit	-	-	-	ATP@Np- NAR <mark>(OTf)</mark> 4	Does not fit	-	-	-
Complex	<i>K</i> ₂ (× 10 ⁴) Μ ⁻¹	∆H₂ kcal/m	<i>T∆S</i> ₂ kcal/mol	∆G₂ kcal/mol	Complex	<i>K</i> ₂ (×10²) Μ ⁻¹	∆H₂ kcal/mol	TΔS₂ kcal/mol	∆G₂ kcal/mol
ATP@Np-	_	-	_	_	ATP@Np-	_	-		_
NAR <mark>(Br)</mark> ₄ ATP@Np- NAR <mark>(OTf)</mark> ₄	-	-	-	-	NAR(Br)₄ ATP@Np- NAR(OTf)₄	-	-	-	-

90% H20/10% DMSO

90% BUFFER/10% DMSO

4. NMR SPECTROSCOPY

For the pure samples' preparation, 2 mM stock solutions of either the receptors or the phosphates were prepared in 90 % D_2O , 10 % [D_6]DMSO. For pure receptors, 250 µl of the stock solution was pipetted into NMR tube and diluted with 250µl of 90 % D_2O , 10 % [D_6]DMSO pure solvent to give 1 mM sample concentration.

For 1:1 host-guest (receptor-phosphate) mixtures, 250 μ l of the host and 250 μ l of the guests were pipetted into an NMR tube to give a 1 mM concentration ratio of hosts and guests. The ¹H NMR were collected were calibrated using D₂O signal as internal standard. For ³¹P NMR, concentrated H₃PO₄ in a 2 mm NMR tube was inserted into the sample as an external calibrant, calibrated at 0 ppm.

For NMR titration experiment, stock solutions of 10mM C3OH-NAR(Br)₄, C3OH-NAR(Otf)₄ and 100mM of PPi were prepared in 100% D_2O . 100ul of the PPi solution was titrated into an NMR tube containing 500ul of stock receptor solution to give equivalence of 0.20, 0.38, 0.57, 0.74, 0.91, 1.07, 1.23, 1.38, 1.53, 1.74, 1.94, 2.13 and 2.96.

For Job's plot measurement, 10 mM concentration of the host and guest were prepared.⁵ 12 NMR samples were prepared with host-guest ratio of 0.00:0.50, 0.05:0.45, 0.10:0.40, 0.15:0.35, 0.20:0.30, 0.25:0.25, 0.30:0.20, 0.35:0.15, 0.40:0.10, 0.45:0.05, 0.50:0.00. The y-axis is the chemical shift change of the host. The X-axis is the mole fraction.

a) Job Plot Spectra

JOB PLOT EXPERIMENTS

Figure S34. Job Plot of the binding pocket's aromatic (left) and methylene (right) H-NMR signal changes per equivalence of PPi added.

b) ¹H-NMR Spectra

Figure S35. ¹H NMR titration spectra (D_2O , 298 K) of C_3OH -NAR(Br)₄ showing signal changes per equivalence of pyrophosphate added.

Figure S36. ¹H NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of the pure host: (a) NpNARCl₄, (c) NpNARBr₄, (e) NpNAROTf₄, and equimolar mixtures of (b) PPi@NpNAR(Cl)₄, (b) PPi@NpNAR(Br)₄, (b) PPi@NpNAR(OTf)₄. The displaced anions are represented in parentheses. Star represents the residual D_2O solvent. The dash lines give an indication of the signal changes in ppm.

Figure S37. ¹H NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of the pure host: (a) C3OHNARCI₄, (c) C3OHNARBr₄, (e) C3OHNAROTf₄, and equimolar mixtures of (b) AMP@C3OHNAR(CI)₄, (b) AMP@C3OHNAR(Br)₄, (b) AMP@C3OHNAR(OTf)₄. The displaced anions are represented in parentheses. Star represents the residual D_2O solvent. The dash lines give an indication of the signal changes in ppm.

Figure S38. ¹H NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of the pure host: (a) C3OHNARCl₄, (c) C3OHNARBr₄, (e) C3OHNAROTf₄, and equimolar mixtures of (b) ADP@C3OHNAR(Cl)₄, (b) ADP@C3OHNAR(Br)₄, (b) ADP@C3OHNAR(OTf)₄. The displaced anions are represented in parentheses. Star represents the residual D_2O solvent. The dash lines give an indication of the signal changes in ppm.

Figure S39. ¹H NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of the pure host: (a) C3OHNARCI₄, (c) C3OHNARBr₄, (e) C3OHNAROTf₄, and equimolar mixtures of (b) ATP@C3OHNAR(CI)₄, (b) ATP@C3OHNAR(Br)₄, (b) ATP@C3OHNAR(OTf)₄. The displaced anions are represented in parentheses. Star represents the residual D_2O solvent. The dash lines give an indication of the signal changes in ppm.

Figure S40. ¹H NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of the pure host: (a) NpNARCl₄, (c) NpNARBr₄, (e) NpNAROTf₄, and equimolar mixtures of (b) AMP@NpNAR(Cl)₄, (b) AMP@NpNAR(Br)₄, (b) AMP@NpNAR(OTf)₄. The displaced anions are represented in parentheses. Star represents the residual D_2O solvent. The dash lines give an indication of the signal changes in ppm.

Figure S41. ¹H NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of the pure host: (a) NpNARCl₄, (c) NpNARBr₄, (e) NpNAROTf₄, and equimolar mixtures of (b) ADP@NpNAR(Cl)₄, (b) ADP@NpNAR(Br)₄, (b) ADP@NpNAR(OTf)₄. The displaced anions are represented in parentheses. Star represents the residual D_2O solvent. The dash lines give an indication of the signal changes in ppm.

Figure S42. ¹H NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of the pure host: (a) NpNARCl₄, (c) NpNARBr₄, (e) NpNAROTf₄, and equimolar mixtures of (b) ATP@NpNAR(Cl)₄, (b) ATP@NpNAR(Br)₄, (b) ATP@NpNAR(OTf)₄. The displaced anions are represented in parentheses. Star represents the residual D_2O solvent. The dash lines give an indication of the signal changes in ppm.

Figure S43. ¹H NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of the pure host: (a) NpNARCl₄, (c) NpNARBr₄, (e) NpNAROTf₄, and equimolar mixtures of (b) PO₄³⁻@NpNAR(Cl)₄, (b) PO₄³⁻@NpNAR(Br)₄, (b) PO₄³⁻@NpNAR(OTf)₄. The displaced anions are represented in parentheses. Star represents the residual D_2O solvent. The dash lines give an indication of the signal changes in ppm.

a) ³¹P-NMR Spectra

Figure S44. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) PPi, and equimolar mixtures of (b) PPi@NpNAR(Cl)₄, (c) PPi@NpNAR(Br)₄ and (d) PPi@NpNAR(OTf)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S45. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) PO_4^{3-} , and equimolar mixtures of (b) PO_4^{3-} @C3OHNAR(CI)₄, (c) PO_4^{3-} @C3OHNAR(Br)₄ and (d) PO_4^{3-} @C3OHNAR(OTf)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S46. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) PO_4^{3-} , and equimolar mixtures of (b) PO_4^{3-} @NpNAR(Cl)₄, (c) PO_4^{3-} @NpNAR(Br)₄ and (d) PO_4^{3-} @NpNAR(OTf)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S47. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) PO_4^{3-} , and equimolar mixtures of (b) PO_4^{3-} @C3OHNAR(Br)₄, (c) PO_4^{3-} @CyNAR(Br)₄, (d) PO_4^{3-} @BnNAR(Br)₄ and (e) PO_4^{3-} @NpNAR(Br)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S48. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) AMP, and equimolar mixtures of AMP@C3OHNAR(CI)₄, (c) AMP@C3OHNAR(Br)₄ and (d) AMP@C3OHNAR(OTf)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S49. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) AMP, and equimolar mixtures of (b) AMP@NpNAR(CI)₄, (c) AMP@NpNAR(Br)₄ and (d) AMP@NpNAR(OTf)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S50. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) AMP, and equimolar mixtures of (b) AMP@C3OHNAR(Br)₄, (c) AMP@CyNAR(Br)₄, (d) AMP@BnNAR(Br)₄ and (e) AMP@NpNAR(Br)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S51. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) ADP, and equimolar mixtures of ADP@C3OHNAR(CI)₄, (c) ADP@C3OHNAR(Br)₄ and (d) ADP@C3OHNAR(OTf)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S52. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) ADP, and equimolar mixtures of (b) ADP@NpNAR(Cl)₄, (c) ADP@NpNAR(Br)₄ and (d) ADP@NpNAR(OTf)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S53. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) AMP, and equimolar mixtures of (b) ADP@C3OHNAR(Br)₄, (c) ADP@CyNAR(Br)₄, (d) ADP@BnNAR(Br)₄ and (e) ADP@NpNAR(Br)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S54. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) ATP, and equimolar mixtures of ATP@C3OHNAR(Cl)₄, (c) ATP@C3OHNAR(Br)₄ and (d) ATP@C3OHNAR(OTf)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S55. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) ATP, and equimolar mixtures of (b) ATP@NpNAR(CI)₄, (c) ATP@NpNAR(Br)₄ and (d) ATP@NpNAR(OTf)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

Figure S56. ³¹P NMR spectra ($D_2O/[D_6]DMSO 9/1 v/v$, 298 K) of (a) ATP, and equimolar mixtures of (b) ATP@C3OHNAR(Br)₄, (c) ATP@CyNAR(Br)₄, (d) ATP@BnNAR(Br)₄ and (e) ATP@NpNAR(Br)₄. The displaced anions are represented in parentheses. The dash lines give an indication of the signal changes in ppm.

5. COMPUTATIONAL MODELLING

All structures were calculated using the Gaussian 09 suite of programs⁶ applying at the ω B97X-D⁶/6-311-G(d,p) level of theory and SCRF=SMD solvation model using generic keyword to consider a solvation cluster of 1DMSO:9H₂O (according to experimental concentration) for solvent effects. To further validated both long-ranged and short-ranged interactions within the systems, the single point calculations were done using the dispersion-corrected functional (B39W91) which is appropriate for modelling the H-bonding and dispersive non-covalent host–guest interactions. Structure visualization was performed using GaussView v5.0.8.4 and Maestro 11.⁷

We evaluated the change in Gibbs free energy (ΔG) for binding event, as

$\Delta G = BE + \Delta E_{zpe} + T\Delta S + \Delta PV$

The BE can be determined directly by analyzing the DFT total energies:

$\Delta G = BE + \Delta E_{zpe} + T\Delta S + \Delta PV = [E_{complex} - (E_H + E_G)] + [Ezpe_{complex} - (E_H + E_G)] + T[S_{complex} - (S_H + S_G)]$

where Ecomplex, EH, and EG are the DFT total energies of the complex, free host, and guest, respectively. Δ Ezpe and Δ S are the zero-point energy difference and the entropy difference between the complex and reactants, respectively.

To obtain insights into the dynamical behavior of the counteranion at the molecular level, a molecular dynamics (MD) study was performed for the complexation of the Np-host with the OTf anions using the OPLS-2005 force field using the disordered system approach of Desmond⁸ to build a solvation cluster of 1DMSO:9H₂O (according to experimental concentration) enveloping the host-guest complex (the solute) consisting of 2NpNAR4+ system plus 8OTf- counterions in the box of co-mixture of 400DMSO:1200H₂O molecules. The energy of the system was further minimized with 1000 steps of steepest descent followed by 3500 steps of conjugate gradient minimization. The molecular dynamics simulations started with a 1 fs integration time step; the complex structure was then relaxed for 10 ps. The temperature of the relaxed system was equilibrated at 300K via 5 and 0 ns of MD by 2 fs time steps using the Langevin dynamics applying a collision frequency of 10 ps⁻¹ with a velocity limit of 5 temperature units. The generated coordinates after were then applied to do 5 ns followed by 10 ns and 20 ns molecular dynamics using 2 fs time steps, with temperature being fixed at 300 K applying the Langevin dynamics a collision frequency of 1 ps⁻¹ and a velocity limit of 20 temperature units. The pressure of the solvated system was then equilibrated at 1 bar at a specified density in a constant pressure periodic boundary applying an isotropic pressure scaling method using a pressure relaxation time of 2 ps with the time step of the 2 fs with a cut-off of 9 Å for the non-bonded interaction.

Figure S57. The calculated Natural charge density (obtained by NBO analysis) on each atom in the **2PPi@C3OHNARCY** complex. The higher electron density on the phosphorous atoms in the cavity would be reflected in a greater upfield shift in their resonances. The near symmetry of the system leads to each pair of phosphorous atoms having almost the same charge density.

Thermodynamic Data

C3OHNAR(CI)₄

```
# opt=calcfc freq=noraman wb97xd/6-311g(d,p) scrf=(solvent=generic,rea
d,smd) nosymm 5d temperature=298
Zero-point correction= 1.465575
(Hartree/Particle)
Thermal correction to Energy= 1.552187
Thermal correction to Enthalpy= 1.553131
Thermal correction to Gibbs Free Energy= 1.339647
Sum of electronic and zero-point Energies= -5449.315358
Sum of electronic and thermal Energies= -5449.228746
Sum of electronic and thermal Enthalpies= -5449.227802
Sum of electronic and thermal Free Energies= -5449.441286
```

C3OHNAR(OTf)₄

NpNAR(CI)₄

```
# opt=calcfc freq=noraman wb97xd/6-311g(d,p) scrf=(solvent=generic,rea
d,smd) 5d temperature=298
Zero-point correction= 1.737478
(Hartree/Particle)
Thermal correction to Energy= 1.835067
Thermal correction to Enthalpy= 1.836011
Thermal correction to Gibbs Free Energy= 1.602751
Sum of electronic and zero-point Energies= -6371.991672
Sum of electronic and thermal Energies= -6371.894083
Sum of electronic and thermal Enthalpies= -6371.893140
Sum of electronic and thermal Free Energies= -6372.126400
```

PPi@C3OHNAR

opt=calcfc freq=noraman wb97xd/6-311g(d,p) scrf=(solvent=generic,rea
d,smd) nosymm 5d temperature=298

Zero-point correction=	1.496575
(Hartree/Particle)	
Thermal correction to Energy=	1.582116
Thermal correction to Enthalpy=	1.583059
Thermal correction to Gibbs Free Energy=	1.379358
Sum of electronic and zero-point Energies=	-4817.926247
Sum of electronic and thermal Energies=	-4817.840706
Sum of electronic and thermal Enthalpies=	-4817.839762
Sum of electronic and thermal Free Energies=	-4818.043463

PPi@NpNAR

```
# opt=calcfc freq=noraman wb97xd/6-311q(d,p) scrf=(solvent=generic,rea
d, smd) nosymm 5d temperature=298
Zero-point correction=
                                               1.763045
(Hartree/Particle)
Thermal correction to Energy=
                                                1.861000
Thermal correction to Enthalpy=
                                                1.861944
Thermal correction to Gibbs Free Energy=
                                               1.634207
Sum of electronic and zero-point Energies=
                                                  -5740.604973
Sum of electronic and thermal Energies=
                                                  -5740.507018
Sum of electronic and thermal Enthalpies=
                                                   -5740.506074
 Sum of electronic and thermal Free Energies=
                                                   -5740.733812
```

2PPi@C3OHNAR

```
# opt=calcfc freq=noraman wb97xd/6-311g(d,p)
scrf=(solvent=generic,read,smd) geom=connectivity 5d temperature=298
Zero-point correction=
                                                1.531757
(Hartree/Particle)
Thermal correction to Energy=
                                               1.634988
Thermal correction to Enthalpy=
                                                1.635932
Thermal correction to Gibbs Free Energy=
                                               1.390701
Sum of electronic and zero-point Energies=
                                                  -6676.997482
Sum of electronic and thermal Energies=
                                                  -6676.894252
Sum of electronic and thermal Enthalpies=
                                                  -6676.893308
Sum of electronic and thermal Free Energies=
                                                  -6677.138539
```

2PPi@NpNAR

opt=calcfc freq=noraman wb97xd/6-311g(d,p) scrf=(solvent=generic,read,smd) nosymm 5d temperature=298 Zero-point correction= 1.799290 (Hartree/Particle) Thermal correction to Energy= 1.913218 Thermal correction to Enthalpy= 1.914162 Thermal correction to Gibbs Free Energy= 1.650245 Sum of electronic and zero-point Energies= -7599.688795 Sum of electronic and thermal Energies= -7599.574867 Sum of electronic and thermal Enthalpies= -7599.573923

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