Supporting Information

Quantitative evaluation of anion-π interactions in solution

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Materials and Methods. All chemicals were purchased from commercial sources and used without further purification. 1H NMR and 13C NMR spectra were carried out in deuterated solvents on Bruker Avance 400 and 500 Ultrashield spectrometers. Mass analyses were performed on Waters LCT Premier (ESI mode). ITC analyses were performed using a MicroCal VP-ITC Microcalorimeter.

X-ray Structure Determination. Crystals of the solvates of 2a, 2c and 2h were obtained by crystallization from a saturated solution of acetonitrile at room temperature. The crystals of the solvates of 2b and 2g were grown from dichloromethane and dimethylformamide saturated solutions respectively. The obtained crystals were extremely sensitive to loosing solvent and were prepared in short time under inert conditions immersed in perfluoropolyether as protecting oil for manipulation. After several trials a dataset of enough quality could be obtained. Single crystals suitable for X-ray diffraction analysis of the complexes TEA·Cl@2d, TBA·Cl 2e, TMA·Cl@2f and TBA·Cl@2d were obtained after slow evaporation of concentrated solutions (acetonitrile or dichloromethane) containing the receptor and the tetraalkylammonium salt in a 1:1 ratio.

Data Collection. Measurements were made on a Bruker-Nonius diffractometer equipped with a APPEX 2 4K CCD area detector, a FR591 rotating anode with Mo Kα radiation, Montel mirrors as monochromator and a Kryoflex low temperature device (T = -173 °C). Full-sphere data collection was used with ω and φ scans.[1]

Structure Solution and Refinement. SHELXTL Version 6.10 (Sheldrick, 2000) was used.[2]

(1) Crystal data for 2a+acetonitrile at 100 K: C52H48N6 (C48H42N4 + 2 x ACN), 756.96 gmol⁻¹, monoclinic, P21/m, a = 8.9275(12) Å, b = 13.7864(19) Å, c = 16.686(3) Å, β = 90.126(4)°, V = 2053.7(5) Å³, Z = 2, ρcalcd = 1.224 Mg/m³, R₁ = 0.0484 (0.0852), wR2 = 0.1080 (0.1243), for 3164 reflections with I>2σ(I) (for 4510 reflections [Rint: 0.0633] with a total measured of 20096 reflections), goodness-of-fit on F² = 1.011, largest diff. peak (hole) = 0.439 (-0.289) e Å⁻³. This structure refines as a twin with a monoclinic cell with a beta angle of approximately 90° which
emulates an orthorhombic cell (TWIN 1 0 0 0 -1 0 0 0 -1, BASF 0.41277). The main molecule and the two acetonitrile molecules are located on a mirror plane (half molecules are refined).

(2) Crystal data for **2b+methylene chloride** at 100 K: C₅₁H₄₆Br₄Cl₆N₄ (C₄₈H₄₀N₄ + 3 x CH₂Cl₂), 1247.26 gmol⁻¹, monoclinic, P2₁/c, a = 14.003(3) Å, b = 28.119(5) Å, c = 13.132(3) Å, β = 92.886(5)°, V = 5163.9(17) Å³, Z = 4, \( \rho_{\text{calcld}} = 1.604 \text{ Mg/m}^3 \), \( R_1 = 0.0699 \) (0.1066), \( \text{wR}_2 = 0.1584 \) (0.1774), for 6813 reflections with I>2σ(I) (for 9700 reflections [Rint: 0.1357] with a total measured of 36088 reflections), goodness-of-fit on \( F^2 = 1.046 \), largest diff. peak (hole) = 1.664 (-1.311) e Å⁻³. The crystals of this sample were of poor quality and are mostly twinned. A best data set could not be obtained. The structure contains three molecules of methylene chloride.

(3) Crystal data for **2c+acetonitrile** at 100 K: C₅₈H₄₉N₁₁ (C₅₂H₄₀N₈ + 3 x ACN), 900.08 gmol⁻¹, tetragonal, P4/n, a = 11.2807(19) Å, c = 18.779(6) Å, V = 2389.7(10) Å³, Z = 2, \( \rho_{\text{calcld}} = 1.251 \text{ Mg/m}^3 \), \( R_1 = 0.0601 \) (0.1003), \( \text{wR}_2 = 0.1502 \) (0.1718), for 1901 reflections with I>2σ(I) (for 2885 reflections [Rint: 0.0433] with a total measured of 25841 reflections), goodness-of-fit on \( F^2 = 1.057 \), largest diff. peak (hole) = 0.366 (-0.545) e Å⁻³. This structure crystallizes with the main molecule centered on a fourfold rotation axes (one fourth of molecule is refined) and also with three acetonitrile molecules of the same axes. The hydrogen atoms of the acetonitrile molecules are disordered around the fourfold rotations axis.

(4) Crystal data for **2d+acetonitrile** at 100 K: C₅₄H₄₉N₁₁O₈ (C₄₈H₄₀N₈O₈ + 3 x ACN), 980.04 gmol⁻¹, monoclinic, P2₁/m, a = 10.7827(4) Å, b = 20.7050(8) Å, c = 10.9310(4) Å, β = 96.3250(10)°, V = 2425.55(16) Å³, Z = 2, \( \rho_{\text{calcld}} = 1.342 \text{ Mg/m}^3 \), \( R_1 = 0.0534 \) (0.0666), \( \text{wR}_2 = 0.1545 \) (0.1655), for 11507 reflections with I>2σ(I) (for 14224 reflections [Rint: 0.0299] with a total measured of 49543 reflections), goodness-of-fit on \( F^2 = 1.077 \), largest diff. peak (hole) = 0.811 (-1.060) e Å⁻³. This structure crystallizes with the main molecule and three acetonitrile molecules on a mirror plane (half molecules are refined). One of the acetonitrile molecules is disordered in two positions. The hydrogen atoms of the acetonitrile molecules are disordered around the mirror plane.

(5) Crystal data for **2f+dimetylformamide** at 100 K: C₅₅H₅₉N₅O₅ (C₅₂H₅₂N₄O₄ + 1 x DMF), 870.07 gmol⁻¹, monoclinic, Cc, a = 17.5204(9) Å, b = 13.0497(6) Å, c = 20.7704(11) Å, \( \beta = 105.619(3)^\circ \), V = 4573.5(4) Å³, Z = 4, \( \rho_{\text{calcld}} = 1.264 \text{ Mg/m}^3 \), \( R_1 = 0.0362 \) (0.0384), \( \text{wR}_2 = 0.0935 \) (0.0959), for 10839 reflections with I>2σ(I) (for 11324 reflections [Rint: 0.0234] with a total measured of 46747 reflections), goodness-of-fit on \( F^2 = 1.080 \), largest diff. peak (hole) = 0.480 (-0.184) e Å⁻³. This compound crystallized always as multi component crystals. The measured data corresponded to a two component crystal which was processed simultaneously using APEX v2.1-4 for data integration and TWINABS for the absorption correction.[4,5] The R₁-value was lowered using this procedure from 11.40 % to 7.6 %. This structure crystallizes with the main molecule, the tetraethyl ammonium cation and the chlorine anion on a mirror plane (half molecules are refined).

Crystal data for **2g+acetonitrile** at 100 K: The crystal data obtained for **2g** confirmed the structure expected and are identical to the crystal data for the structure described as complex B in C. J. Woods et. al.[3]. Consequently, the cif file is not deposited.

(6) Crystal data for **TEA Cl@2d** at 100 K: 1/2 C₅₆H₆₀Cl₁N₉O₈ (This structure does not contain solvent), 511.29 gmol⁻¹, monoclinic, P2₁/m, a = 10.8193(11) Å, b = 21.260(2) Å, c = 11.2847(11) Å, \( \beta = 105.649(6)^\circ \), V = 2499.4(4) Å³, Z = 4, \( \rho_{\text{calcld}} = 1.359 \text{ Mg/m}^3 \), \( R_1 = 0.0760 \) (0.1374), \( \text{wR}_2 = 0.1717 \) (0.1996), for 6545 reflections with I>2σ(I) (for 12171 reflections [Rint: 0.0997] with a total measured of 47335 reflections), goodness-of-fit on \( F^2 = 0.949 \), largest diff. peak (hole) = 0.810 (-0.737) e Å⁻³. This compound crystallized always as multi component crystals. The measured data corresponded to a two component crystal which was processed simultaneously using APEX v2.1-4 for data integration and TWINABS for the absorption correction.[4,5] The R₁-value was lowered using this procedure from 11.40 % to 7.6 %. This structure crystallizes with the main molecule, the tetraethyl ammonium cation and the chlorine anion on a mirror plane (half molecules are refined).
(7) Crystal data for **TBA Cl@2d** at 100 K: C_{68}H_{84}Cl_{9}N_{9}O_{8} (C_{64}H_{76}Cl_{1}N_{9}O_{8} + 4 x CH_{2}Cl_{2}), 1474.49 gmol^{-1}, monoclinic, \( P2_1/c \), \( a = 17.3488(3) \) Å, \( b = 21.8818(5) \) Å, \( c = 20.6886(4) \) Å, \( \beta = 112.6090(10) \)°, \( V = 7250.3(3) \) Å\(^3\), \( Z = 4 \), \( \rho_{\text{calcd}} = 1.351 \) Mg/m\(^3\), \( R_1 = 0.0557 \) (0.0884), \( wR_2 = 0.1377 \) (0.1569), for 16392 reflections with \( I > 2\sigma(I) \) (for 24051 reflections \( [R_{\text{int}}: 0.0325] \) with a total measured of 44390 reflections), goodness-of-fit on \( F^2 = 1.024 \), largest diff. peak (hole) = 0.978 (-0.747) e Å\(^{-3}\). The methylene chloride molecules contained in this crystal are partially disordered.

(8) Crystal data for **TMA Cl@2g** at 100 K: \( 1/4 \) C_{62}H_{68}Cl_{5}N_{5}O_{8} (C_{60}H_{64}Cl_{1}N_{5}O_{8} + 2 x CH_{2}Cl_{2}), 1188.46 gmol^{-1}, tetragonal, \( P4/ncc \), \( a = 17.793(3) \) Å, \( c = 20.080(7) \) Å, \( V = 6357(3) \) Å\(^3\), \( Z = 4 \), \( \rho_{\text{calcd}} = 1.242 \) Mg/m\(^3\), \( R_1 = 0.0600 \) (0.0972), \( wR_2 = 0.1513 \) (0.1859), for 2639 reflections with \( I > 2\sigma(I) \) (for 3788 reflections \( [R_{\text{int}}: 0.0493] \) with a total measured of 61296 reflections), goodness-of-fit on \( F^2 = 1.040 \), largest diff. peak (hole) = 0.693 (-0.679) e Å\(^{-3}\). This structure crystallizes with the main molecule, the tetramethyl ammonium cation and the chloride anion centered on a fourfold rotation axes (a quart of molecule is refined). One of the carbon atoms and the nitrogen atom of the tetramethyl ammonium cation are sitting on the fourfold rotation axis. The three additional carbon atoms of the cation are disordered in two positions with an occupancy of 0.375 atoms for each position. Once the symmetry of the fourfold rotation axes is applied, eight positions are possible for this two disordered atoms, which gives the expected total of three atoms. The methylene chloride molecules contained in this crystal are disordered in two positions with an occupation ratio of 50:50.

(9) Crystal data for **TMA Cl\bullet2e** at 100 K: C_{112}H_{44}Cl_{1}N_{9}O_{12} (2 x C_{48}H_{44}N_{4}O_{4} + N(CH_{3})_{4}^{+} + Cl^{-} + 4 x (CH_{3})_{2}CO), 1823.65 gmol^{-1}, monoclinic, \( P2/c \), \( a = 13.2426(10) \) Å, \( b = 10.9831(10) \) Å, \( c = 32.487(3) \) Å, \( \beta = 94.644(2) \)°, \( V = 4709.5(7) \) Å\(^3\), \( Z = 2 \), \( \rho_{\text{calcd}} = 1.286 \) Mg/m\(^3\), \( R_1 = 0.0883 \) (0.1154), \( wR_2 = 0.2293 \) (0.2289), for 6652 reflections with \( I > 2\sigma(I) \) (for 9034 reflections \( [R_{\text{int}}: 0.0555] \) with a total measured of 30380 reflections), goodness-of-fit on \( F^2 = 1.048 \), largest diff. peak (hole) = 1.356 (-0.876) e Å\(^{-3}\). The elementary cell contains one molecule of 2g, a half tetramethyl ammonium cation, a half chlorine anion and two molecules of acetone which are located on disordered positions. The nitrogen atom of the cation and the chlorine anion are sitting on a special position (twofold rotation axis). One of the phenol rings of 2g is disordered in two positions with a ratio of 53:47.

![Scheme S1](image)

**Scheme S1.** Molecular structures of the receptors 2 used in this study.
**Isothermal Titration Calorimetry experiments.** Titrations between tetrabutylammonium chloride TBA·Cl (guest) and the hosts 2c, 2d and 1 were carried out by adding small aliquots (5 μL) of an acetonitrile solution of the guest into a solution of the host in the same solvent. The solution of the guest was approximately seven times more concentrated than that of the host ([2c]=0.85 mM, [2d]=0.56 mM, [1]=0.6 mM. The association constants and the thermodynamic parameters were obtained from the fit of the titration data to a simple 1:1 binding model using the Microcal ITC Data Analysis module.

**Figure S1.** Top – Trace shows raw data for the titration of TBACl into host (left 2c, right 2d). Titration was performed at 25 °C. Bottom – Binding isotherm of the calorimetric titration shown on top. The enthalpy of binding for each injection is plotted against the concentration of guest in the cell. The continuous line represents the least-squares-fit of the data to a single-site binding model.
Figure S2. Top – Trace shows raw data for the titration of TBACl into host (1). Titration was performed at 25 °C. Bottom – Binding isotherm of the calorimetric titration shown on top. The enthalpy of binding for each injection is plotted against the concentration of guest in the cell. The continuous line represents the least-squares-fit of the data to a single-site binding model.
1H NMR Titrations

All titrations were carried out on a Bruker 500MHz spectrometer, at 298K, in CD$_3$CN. The association constants were determined using 1-3 mM solutions of 2 in CD$_3$CN at 298 K, and adding aliquots of a solution of the corresponding salt, approximately 10 times more concentrated, in the same solvent. The concentration of the receptor was maintained constant throughout the titration. The association constants between calixpyrrole 2a, 2f, 2g and the chloride anion were determined by simple integration in the 1H NMR spectrum of the signals corresponding to the protons of pyrroles NHs of the free species (7.90 ppm 2a, 7.89 ppm 2f and 8.01 ppm 2g) and that corresponding signals of the same protons in the complexed species (11.36, 11.35 and 11.25 ppm respectively) under the presence of different amounts of guest. The reported values of the association constants are the average of at least 3 different host-guest ratios. Similar values were obtained using the integration areas of other proton signals. For receptor 2e, the complexation of TBACl showed a fast exchange regime in the NMR timescale. The association constant between 2e and the chloride anion was determined as $K_a = 1.4 \times 10^3$ M$^{-1}$ by monitoring the chemical changes of the protons resonating at 6.90 ppm (hydroxy) and 1.85 ppm (methyl) in the 1H NMR spectrum as incremental amounts of the guest were added. The value of the association constant was calculated using the software SPECFIT which uses a global analysis system with expanded factor analysis and Marquardt least-squares minimization to obtain globally optimized parameters. The data were fitted to a simple 1:1 binding model.

![Figure S3. NMR titration of 2c ([2c]= 1.34 mM) with TBACl in CD$_3$CN at 298K. a) 2c. b) 2c + 0.55 eq. TBACl.](image-url)
Figure S4. : NMR titration of 2f ([2f] = 1.10 mM) with TBACl in CD$_3$CN at 298K. a) 2f. b) 2f + 6 eq. TBACl. c) Zoom into the aromatic region of b).

Figure S5. : NMR titration of 2g ([2g] = 1.30 mM) with TBACl in CD$_3$CN at 298K. a) 2g. b) 2g + 1.7 eq. TBACl.
Figure S6. NMR titration of 2d ([2d] = 1.17 mM) with TBACl in CD$_3$CN at 298K. a) 2d. b) 2d + 0.55 eq. TBACl.

Figure S7. NMR titration of 2e ([2e] = 1.50 mM) with TBACl in CD$_3$CN at 298K. a) 2e. b) 2e + 0.55 eq. TBACl. c) 2e + 1.2 eq. TBACl. d) 2e + 5 eq. TBACl.
Figure S8. Side view of the X-ray structure of the acetone adduct of the \textit{exo} chloride complex of receptor 2e (Cl\textsuperscript{−}(2e\textsubscript{2})). The solid state structure shows that the chloride ion is not included in the aromatic cavity. The chloride is bound to two hydroxyl groups of the calixpyrrole receptor. In the packing of the crystals (not shown) the chloride is also bound to other two hydroxyls of and adjacent calixpyrrole molecule. This solid state structure is in agreement with the observations of the \textsuperscript{1}H NMR titration presented above (Figure S7),

Figure S9. NMR titration of 2a ([2a]= 1.28 mM) with TBACI in CD\textsubscript{3}CN at 298K. a) 2a. b) 2a + 5 eq. TBACI.
Table S1. $^1$H NMR chemical shifts $\Delta \delta$ (ppm, $\delta_{\text{complex}} - \delta_{\text{host}}$) of calixpyrrole hosts 2a-g; Chemical shifts for the complex were obtained from the addition of an excess of TBACl to a host solution in CD$_3$CN at 298K.

**Table S1.**

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**ESI-MS experiments**

Negative-ion ESI mass spectrometric analyses were performed on a Waters LCT Premier mass spectrometer from Micromass Instruments (Manchester, UK) under the following conditions: Solvent: CH$_3$CN; source temperature: 100 °C; cone voltage:0; flow rate: 10uL/min; Capillary voltage: 0. Spectra were scanned over the mass range m/z 100-2000 and were recorded and processed using the MassLynx software (Micromass).

**Figure S10:** ESI-MS of 2f in TBACl solution.
Figure S11: ESI-MS of 2a in TBACl solution.

Figure S12: ESI-MS of 2g in TBACl solution.
Figure S13: ESI-MS of 2b in TBACL solution.

Figure S14: ESI-MS of 2d in TBACL solution.
Competitive binding assays were performed among different receptors. To an equimolecular solution containing the competing receptors was added 1 equivalent of TBACl. The obtained solution was directly injected in the mass spectrometer.

**Figure S15:** ESI-MS of an equimolar solution containing 2d, 2f, 2d and 1 equivalent of TBACl.

**Figure S16:** ESI-MS of an equimolar solution containing 2d, 1 and 1 equivalent of TBACl.
References


