Supramolecular and Biomacromolecular Enhancement of Metal-Free Magnetic Resonance Imaging Contrast Agents

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Materials

All chemicals were purchased from Sigma-Aldrich (St. Louis, MO), ThermoFisher Scientific (Pittsburgh, PA), Alfa Aesar (Ward Hill, MA), TCI America (Portland, OR), VWR International (Radnor, PA), and used without further purification.

Instrumentation

¹H and ¹³C NMR spectra were obtained using a 600 MHz Bruker Avance NMR spectrometer with residual solvent peaks as a reference for all NMR spectra. Thiophenol (10-20 eq) were added to samples containing aminoxyl radicals to reduce them to hydroxylamines so that the compound could be observed via NMR. ESI-MS were acquired using an Agilent 1100 HPLC with a PLRP-S column for separation and an ABSciex 4000 QTRAP system for detection. Size exclusion chromatography (SEC) was conducted using an Agilent 1100 HPLC with a Phenomenex PolySep-GFC-P Linear 300 × 7.8 mm column. Isothermal titration calorimetry (ITC) was conducted using a Malvern Microcal iTC200. Transmission electron microscopy (TEM) was conducted using a JEOL JEM-1400Plus transmission electron microscope. Fluorescence data were obtained using a BioTek Synergy H4 Hybrid microplate reader. EPR spectroscopy was performed using a Bruker EMX ER041XG X-band spectrometer with a Bruker ER 4119HS resonator. NMR relaxometry experiments were performed with a 43 MHz Magritek Spinsolve NMR spectrometer operating with a magnetic field strength of 1 T.

Synthesis



Scheme S1. Synthesis of 6.

Synthesis of Imidazole-1-sulfonyl azide hydrogen sulfate

NaN₃ (10 g, 154 mmol) was stirred in dry EtOAc (150 mL) at 0 °C, 0.5 h. Sulfuryl chloride (20.7 g, 12.4 mL, 153 mmol) was added dropwise while stirring was maintained. The resulting mixture was stirred at RT, 24 h. The reaction mixture was cooled to 0 °C in an ice bath. Imidazole (20 g, 294 mmol) was slowly added over 5 min. The resulting mixture was stirred at 0 °C, 5 h. A saturated NaHCO₃ solution (aq.) (300 mL) was added to the reaction mixture. The organic fraction was isolated, washed with H₂O (3×100 mL) and dried with MgSO₄. The organic fraction was filtered and the filtrate was collected. The resulting solution was cooled to 0 °C in an ice bath while stirring was maintained. H₂SO₄ (18 M, 8.4 mL, 151 mmol) was added dropwise over 5 min while vigorous stirring was maintained. The resulting solution was stirred vigorously at RT until colorless or white precipitate was formed. The reaction mixture was filtered and the feed was washed with EtOAc (0 °C). The feed was collected and solvent was removed under reduced pressure to yield the product as a white solid. Yield: 35.3 g, 85 %. ¹H NMR (600 MHz, DMSO-*d*₆) δ ppm 7.67 (s, 1 H), 8.01 (s, 1 H), 9.06 (s, 1 H), 10.43 (s, 1 H), 14.28 (s, 1 H). ¹³C NMR (150 MHz, DMSO-*d*₆) δ ppm 129.8, 134.4, 137.9.



Figure S1. ¹H NMR spectrum of imidazole-1-sulfonyl azide hydrogen sulfate. Asterisks indicate decomposition products.



Figure S2. ¹³C NMR spectrum of imidazole-1-sulfonyl azide hydrogen sulfate.

Synthesis of 6-Azidohexanoic acid (2)

Compound **1** (5.0 g, 25.6 mmol), and NaN₃ (4.998 g, 76.9 mmol) were stirred in DMF (20 mL) at 85 °C overnight. Upon cooling the reaction to RT, DCM (40 mL) was added to the reaction mixture and stirred. The reaction mixture was then washed with aqueous HCl (0.1 M, 3×20 mL) and dried with MgSO₄. The organic fraction was isolated and the solvent was removed under reduced pressure to yield the product as a clear pale yellow oil. Yield: 3.85 g, 96 %. ¹H NMR (600 MHz, CDCl₃) δ ppm 1.43 (quint, J = 7.2 Hz, 2 H), 1.61 (quint, J = 7.2 Hz, 2 H), 1.67 (t, J = 7.2 Hz, 2 H), 2.37 (quint, J = 7.2 Hz, 2 H), 3.27 (t, J = 6.4 Hz, 2 H). Found *m/z* (ESI-TOF) 158.0926. Calculated for C₆H₁₁N₃O₂ [M+H]⁺ 158.0930.



Synthesis of 2,5-Dioxopyrrolidin-1-yl 6-azidohexanoate (3)

Compound **2** (2.0 g, 12.7 mmol), *N*-hydroxysuccinimide (NHS) (4.395 g, 38.2 mmol), and 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide (EDC) (5.929 g, 38.2 mmol) were dissolved in DMF (15 mL) and stirred at RT, 48 h. DMF was then removed under reduced pressure. The remaining residue was dissolved in ethyl acetate (EtOAc) (25 mL). The organic layer was washed with H_2O (3×40 mL), saturated brine (3×40 mL), and dried with MgSO₄. The solvent was removed under reduced pressure to yield the crude product. The crude product was further purified via column chromatography (silica gel) with Hexanes:EtOAc (100:0-0:100). The fractions corresponding to the product were

combined and the solvent was removed under reduced pressure to yield the product as a clear pale yellow oil. Yield: 2.80 g, 87 %. ¹H NMR (600 MHz, CDCl₃) δ ppm 1.49 (quint, J = 6.8 Hz, 2 H), 1.63 (quint, J = 7.1 Hz, 2 H), 1.77 (t, J = 7.0 Hz, 2 H), 2.61 (quint, J = 7.1 Hz, 2 H), 2.82 (s, 4 H), 3.28 (t, J = 6.4 Hz, 2 H). Found *m/z* (ESI-TOF) 255.1092. Calculated for C₁₀H₁₄N₄O₄ [M+H]⁺ 255.1093.



Synthesis of 6-Azido-N-(1-oxyl-2,2,6,6-tetramethylpiperidin-4-yl)hexanamide (**4**) 4-Amino-2,2,6,6-tetramethylpiperidine-1-oxyl (2.0 g, 11.7 mmol), **3** (5.94 g, 23.3 mmol), and TEA (1.18 g, 11.7 mmol) were dissolved in dry (need not be anhydrous) DMF (25 mL). Potassium carbonate (1.61 g, 11.7 mmol) was added and the mixture was stirred at RT, OVN. DCM (50 mL) and H₂O (20 mL) were added and the reaction mixture was washed with H₂O (3×50 mL). The aqueous fraction was extracted with DCM (2×25 mL) and the organic fractions were combined. The organic fraction was washed with H₂O (3×50 mL) and dried with MgSO₄. The solvent was removed under reduced pressure. The crude product was further purified via column chromatography (silica) with DCM:MeOH (100:0 - 90:10). The solvent was removed under reduced pressure to yield the product as a red liquid. Yield: 6.52 g, 90 %. ¹H NMR (600 MHz, CDCl₃) δ ppm 0.90-2.30 (m, 26 H), 3.28 (t, 1 H). ¹³C NMR (150 MHz, CDCl₃) δ ppm 19.83, 25.15, 25.20, 26.44, 28.73, 36.62, 41.21, 45.57, 51.35. Found *m/z* (ESI-TOF) 312.2424. Calculated for C₁₀H₁₄N₄O₄ [M+H]⁺ 312.2400.





Synthesis of 4-((6-Aminohexyl)amino)-2,2,6,6-tetramethylpiperidin-1-oxyl (5)

Compound **4** (2.0 g, 6.4 mmol) was dissolved in Et₂O (100 mL) in ice bath, then LiAlH₄ (2.45 g, 64 mmol) was slowly added portionwise to the reaction solution. The reaction mixture was stirred at RT, OVN. The reaction mixture was cooled to 4 °C in an ice bath. H₂O (1.22 mL), followed by an aqueous NaOH solution (15% w/v, 1.22 mL), followed by H₂O (3.66 mL) were slowly added to the reaction mixture under stirring. Stirring was continued for 15 min. The reaction mixture was dried with MgSO₄ and stirred for 15 min. The reaction mixture was removed under reduced pressure. The organic fractions were combined. The solvent was removed under reduced pressure. The crude product was further purified via column chromatography (alumina) with DCM:MeOH (100:0 - 90:10). The solvent was removed under reduced pressure to yield the product as a light orange liquid. The crude compound was used without further purification. Yield: 1.27 g, 73 %. Found *m*/*z* (ESI-TOF) 272.2681. Calculated for C₁₅H₃₃N₃O [M+H]⁺ 272.2702.

Synthesis of 4-((6-Azidohexyl)amino)-2,2,6,6-tetramethylpiperidin-1-oxyl (6)

Compound 5 (2.0 g, 7.4 mmol) was dissolved in MeOH (50 mL) and the reaction solution was cooled to 4 °C in an ice bath. 1H-Imidazole-1-sulfonyl azide hydrogen sulfate (2.21 g, 8.1 mmol), CuSO₄ · 5H₂O (0.02 g, 0.074 mmol), and K₂CO₃ (2.04 g, 14.8 mmol) were added and the reaction mixture was stirred at RT, OVN. The solvent was removed under reduced pressure. H₂O (25 mL) was added to the remaining residue and the resulting mixture was filtered. The feed was washed with H₂O (25 mL) and EtOAc (25 mL). The filtrate was collected and H₂O (25 mL) was added. The organic fraction was collected. The aqueous fraction was extracted w/ EtOAc (2×25 mL) and the organic fractions were combined. The combined organic fraction was washed with NaHCO₃ (ag.) (4% w/v, 2×30 mL), and saturated brine (2×30 mL). The organic fraction was collected and dried with MqSO₄. The solvent was removed under reduced pressure to yield the crude product. The crude product was purified via column chromatography (alumina) with DCM:MeOH (100:0 - 90:10). The solvent was removed under reduced pressure to yield the product as a red liquid. Yield: 1.84 g, 84 %. In order to achieve high purity product, further purification was performed by preparative high performance C18 chromatography. 200 mg of product was purified by using a linear gradient elution of ACN:H₂O (40:60) with flow rate of 30 ml/min during total run time of 60 min. Peak fractions were collected according to chromatogram at the maximum detection wavelength of 210 nm. Solvent was removed under reduced pressure to yield product as a green liquid. ¹H NMR (600 MHz, CDCl₃) δ ppm 1.15-20 (m, 12 H), 1.41 (m, 4 H), 1.62 (m, 4 H), 1.87 (m, 4 H), 3.17 (m, 1 H), 3.27 (t, 2 H), 3.65 (t, 2 H). ¹³C NMR (150 MHz, CDCl₃) δ ppm 20.45, 20.47, 25.21, 26.32, 27.76, 28.62, 36.29, 39.38, 42.80, 51.28, 67.32, 67.97. Found m/z (ESI-TOF) 298.2610. Calculated for C₁₅H₃₃N₃O [M+H]⁺ 298.2607.





S10

Isothermal Titration Calorimetry



Figure S9. ITC data for **6** at 25 °C in 10 mM sodium phosphate buffer (pH 7.0). In all titrations, CB[8] was 50 μ M and 6 concentration in two experiment was 400 μ M, while it was 500 μ M in the third. The upper panel shows the overlaid, SVD-corrected thermograms for the experiments. The middle panel shows the respective isotherms and the final parameters. The symbols represent the integrated heats of injection from the top panel (with error estimates from NITPIC), and the lines result from the global fit of the three data sets. The bottom panel shows the residuals between the data and the fit lines. The K_d value for the CB[8] **6** complex was determined to be 5.8 × 10⁻⁷ [4.1 × 10⁻⁷, 7.9 × 10⁻⁷]^a M. The enthalpy and entropy values were determined to be -4.5 [-4.7, -4.3] kcal/mol and 13.4 [12.1, 14.8] cal/mol.K respectively. The data were integrated, globally analyzed, and illustrated using NITPIC, SEDPHAT, and GUSSI, respectively. ^a Numbers in brackets represent the 68.3% confidence interval as determined using error-surface projection.

Protocol for Expression of TMV

TMV particles were isolated from Nicotiana benthamiana plants. Tobacco plants were grown, infected with a solution of TMV from a stock source, collected (~10 d after infection), and stored at -80 °C until needed. The leaves (~100 g) were blended with cold (4 °C) extraction buffer (KP buffer (0.1 M, 1000 mL, pH 7.4) with 2-mercaptoethanol (0.2% (v/v)), followed by thorough grinding with a mortar and pestle. The mixture was filtered through cheese loth to remove the plant solids, and the filtrate centrifuged at 11,000 $\times q$ (4 °C, 20 min). The supernatant was filtered through cheesecloth again, and an equal volume of 1:1 chloroform/1-butanol mixture was added and stirred (4 °C. 30 min). The mixture was centrifuged at 4500 $\times g$ for 10 min. The aqueous phase was collected, followed by the addition of NaCI (final concentration of 0.2 M), PEG 8000 (8% (w/w)), and Triton X-100 surfactant (1% (w/w)). The mixture was stirred on ice for 30 min and stored (4 °C, 1 h). The solution was centrifuged at 22,000 ×g (4 °C, 15 min). The supernatant was discarded, and the pellet resuspended in KP buffer (0.1 M, pH 7.4) (4 °C, OVN). The supernatant was carefully layered on a 40% (w/v) sucrose gradient (that had undergone at least one freeze-thaw cycle to create a moderate sucrose gradient) in KP buffer (0.01 M, pH 7.4) in ultracentrifuge tubes and centrifuged in a swing bucket rotor for 2 h at 96,000 ×g. An LED light positioned under the transparent centrifuge tube was used to illuminate the colloidal suspension, which appears blue from Mie scattering. The light-scattering region was collected and centrifuged at 360,562 $\times g$ for 1.5 h. The supernatant was discarded, and the pellet resuspended in KP buffer (0.01 M, pH 7.4) (4 °C, OVN). The solution was portioned equally into microcentrifuge tubes and centrifuged at 15,513 ×g for 15 min. The supernatant was collected as the final TMV solution. UV-Vis measurements were taken at 260 nm (RNA) and 280 nm (protein). A ratio of A260/A280 around 1.23 indicates intact TMV. Using the Beer-Lambert Law with $\varepsilon = 3.0 \text{ cm}^{-1} \text{ mg}^{-1} \text{ ml}$ the concentration of the solution was determined.

Bioconjugation of TMV

Synthesis of TMV-Aky

Solutions of 3-ethynylaniline in acetonitrile (0.68 M, 75 μ L) and NaNO₂ (aq.) (3.0 M, 25 μ L) were added to a cold (4 °C) solution of p-toluenesulfonic acid (aq.) (0.3 M, 400 μ L) and mixed well. The resulting solution was mixed in light-free conditions (4 °C, 1 h) to form the diazonium salt. A solution of TMV (20 mg/mL, 100 μ L, 0.1 μ mol) was diluted in borate buffer (0.1 M, pH 8.8, 862 μ L) and the resulting solution was chilled to 4 °C. The diazonium salt solution (70 eq per coat protein of TMV, 76 μ L) was added to the solution of TMV and the resulting solution was mixed in light-free conditions (4 °C, 45 min). The resulting product was purified via either size exclusion chromatography using a GE Healthcare PD-10 Desalting Column or centrifuge filtration using an EMD Millipore Amicon Ultra Centrifugal Filter Unit (10,000 MW Cutoff) (4,303 ×g).

Synthesis of TMV-6

Compound **6** (1.7 mg, 5.7 µmol) was dissolved in DMSO (1 mL). Cold (4 °C) KP buffer (0.1 M, 3 mL, pH 7.4) was added to the resulting solution and mixed well. A cold (4 °C) solution of TMV-Aky (20 mg/mL, 100 µL, 0.1 µmol) in KP buffer (0.1 M, pH 7.4) was added to the resulting solution and mixed well. An aqueous solution of copper sulfate pentahydrate (0.1 M, 10 µL) was added to the resulting solution and mixed well. An aqueous solution of sodium ascorbate (0.2 M, 10 µL) was added to the resulting solution and mixed well. An aqueous solution of sodium ascorbate (0.2 M, 10 µL) was added to the resulting solution and mixed well. An aqueous solution of sodium ascorbate (0.2 M, 10 µL) was added to the resulting product was purified via either size exclusion chromatography using a GE Healthcare PD-10 Desalting Column or centrifuge filtration using an EMD Millipore Amicon Ultra Centrifugal Filter Unit (10,000 MW Cutoff) (4,303 ×g).

Fluorescence and EPR Kinetics Experimental Details

Fluorescence titrations of TMV-**6** into CB[8] \Box PF were performed using Greiner 384-well, black, flat-bottomed plates. Solutions of TMV-**6** were prepared by serial dilutions of a stock solution of TMV-**6** (200 µM in terms of TEMPO) in sodium phosphate buffer (0.01 M, pH 7.0). TMV-**6**+CB[8] \Box PF solutions were prepared by mixing the appropriate TMV-**6** (20 µL) solution with the solution of CB[8] \Box PF (0.6 µM, 10 µL). This resulted in solutions with final TMV-**6** concentrations from 0-20 µM and a final CB[8] \Box PF concentration of 0.2 µM. The solutions were mixed by pipetting before reading the fluorescence intensities on the plate reader (top reading mode; 400 nm excitation, 10 nm bandwidth; 510 nm emission, 20 nm bandwidth). Z-depth and gain were optimized on the first scan and then exact values were used in subsequent scans. For the titrations of native TMV (nTMV) into CB[8] \Box PF, all methods and parameters were identical to the titrations of TMV-**6** into CB[8] \Box PF, all methods and parameters were identical to the titrations of TMV-**6** into CB[8] \Box PF, all methods and parameters were identical to the titrations of TMV-**6** into CB[8] \Box PF, except for the use of nTMV instead of TMV-**6**. For the titrations of TMV-**6** into CB[8] \Box PF, except for the use of nTMV instead of TMV-**6**. For the titrations of TMV-**6** into CB[8] \Box PF, except for the use of nTMV instead of TMV-**6**. For the titrations of TMV-**6** into CB[8] \Box PF, except for the use of nTMV instead of TMV-**6**. For the titrations of TMV-**6** into CB[8] \Box PF, except for the use of nTMV instead of TMV-**6**. For the titrations of TMV-**6** into CB[8] \Box PF, except for the use of nTMV instead of TMV-**6**. For the titrations of TMV-**6** into CB[8] \Box PF, except for the use of nTMV instead of TMV-**6**. For the titrations of TMV-**6** into CB[8] \Box PF.

Since no other significant interactions between TMV, **6**, CB[8], and PF were observed (**Figure S10, S11**) and assuming the conservation of mass, the relationship and equilibria of the titration components can be described by the following equation:

 $[CB[8] \cdot PF] + [6] \rightleftharpoons [CB[8]] + [PF] + [6] \rightleftharpoons [CB[8] \Box 6] + [PF]$ (Eq. 1)

Therefore, the two dissociation constants, K_a for the complex consisting of CB[8] and PF and K_b for the complex consisting of CB[8] and **6** can be represented by the following equations:

$$K_{a} = \frac{[CB[8]][PF]}{[CB[8] \cdot PF]}$$
(Eq. 2)

$$K_{\rm b} = \frac{[\rm CB[8]][6]}{[\rm CB[8]\square 6]} \tag{Eq. 3}$$

Equations 1-3 can then be combined to form the following cubic equation:

$$\begin{split} [CB[8]]^3 + a \cdot [CB[8]]^2 + b \cdot [CB[8]] + c = 0 \\ \textbf{(Eq. 4)} \end{split}$$

where

$$a = K_a + K_b + [PF]_0 + [6]_0 - [CB[8]]_0$$
 (Eq. 5)

$$b = K_{b}([PF]_{0} - [CB[8]]_{0}) + K_{a}([6]_{0} - [CB[8]]_{0}) + K_{a}K_{b}$$
(Eq. 6)

$$c = K_a K_b [CB[8]]_0$$
 (Eq. 7)

and $[PF]_0$, $[6]_0$, and $[CB[8]]_0$ denote the total concentration of each respective compound. The change in the observed fluorescence intensity can be directly linked to the binding constants K_a and K_b by solving Equation 4 for the real root. The relationship between the observed fluorescence intensities and the binding constants are described by the equation:

$$F = F_{Min} + (F_{Max} - F_{Min}) \frac{2 \cdot \sqrt{(a^2 - 3b)} \cdot \cos \frac{\theta}{3} - a}{3K_a + \left[2 \cdot \sqrt{(a^2 - 3b)} \cdot \cos \frac{\theta}{3} - a\right]}$$
(Eq. 8)

where

$$\theta = \cos^{-1} \cdot \frac{-2a^3 + 9ab - 27c}{2 \cdot \sqrt{(a^2 - 3b)^3}}$$
(Eq. 9)

and F, F_{Min} , and F_{Max} denote the observed fluorescence intensity at any given point in the titration, the minimum observed fluorescence intensity during the titration, and the maximum observed fluorescence intensity during the titration, respectively. Upon fitting Equation 8 to the observed fluorescence intensities, the K_d value for the CB[8] \Box TMV-**6** complex was determined to be 3.8 ± 0.5 × 10⁻⁷ M.



Figure S10. Fluorescence titration data for control experiment with nTMV and CB[8] \Box PF. nTMV (0-20 µM in terms of TMV coat protein) was titrated into solutions of CB[8] \Box PF (0.2 µM). Since no significant changes in fluorescence were observed, it is demonstrated that TMV does not compete with **6** to bind inside the cavity of CB[8].



Figure S11. Fluorescence titration data for control experiment with TMV-6 and PF. TMV-6 (0-20 μ M in terms of TEMPO) was titrated into solutions of PF (0.2 μ M). Since no

significant changes in fluorescence were observed, it is demonstrated that TMV does not quench the fluorescence of **6**.



Figure S12. Fluorescence titration data for TMV-**6**. TMV-**6** (0-20 μ M in terms of TEMPO) was titrated into solutions of CB[8] \Box PF (0.2 μ M). The K_d value for the CB[8] \Box TMV-**6** complex was determined to be 3.8 ± 0.5 × 10⁻⁷ M.

EPR Spectroscopy

A solution of TMV-6 (2.6 mg/mL which corresponds to ~1 mM concentration of TEMPO) and sodium ascorbate (10 mM) in KP buffer (0.1 M, pH 7.4) was freshly prepared with sodium ascorbate being added last. The resulting solution was drawn into a glass capillary tube (1 mm diameter). The capillary tube was then placed inside a quartz EPR tube (4 mm diameter). An EPR spectrum for this sample was collected over 2 h at 10 min intervals. An EPR spectrum was obtained in an identical method with a solution of TMV-6 (2.6 mg/mL which corresponds to ~1 mM in term of TEMPO moieties), CB[8] (10 eq per TEMPO moieties), and sodium ascorbate (10 mM) in KP buffer (0.1 M, pH 7.4). This solution was also freshly prepared with sodium ascorbate being added last.

All EPR measurements were obtained using the following instrumental conditions:

-Microwave Power: 4.54 mW

-Microwave Frequency: 9.38 GHz

-Modulation Frequency: 100 kHz

- -Modulation Amplitude: 0.4 mT (4 G)
- -Temperature: 298 K
- -Center Field: 334 mT (3340 G)

-Sweep Range: 8 mT (80 G)

Table S1: Kinetics of the reduction of nitroxides with excess of sodium ascorbate. Numerical fits to pseudo-first order rate equation (k') for the relaxometric data of the reaction.

Agent	Reduction with ascorbate k' (×10 ⁻⁵ s ⁻¹)	Reference
TMV-6 with CB[8]	2.0	This work
exTEMPO-TMV,	170.0	1
TEMPO-conjugated branched-bottle brush polymer*	791.0	2
Chex-MIM*	37.9	3
P1*	27.0	3
Dendrimer*	57.8	4
TEMPOL*	633.3	5
BASP-ORCA1*,†	36.6	6
BASP-ORCA3*,††	38.2	7

*Determined with the integrated peak height (IPH) EPR data and for the initial kinetic fit (<1 hour).

[†] late kinetics: 6.72 ×10⁻⁵ s⁻¹

⁺⁺ late Kinetics: 5.755 ×10⁻⁵ s⁻¹

Relaxometry

Both longitudinal and transversal relaxation times were determined using 43 MHz Magritek Spinsolve NMR spectrometer operating with a magnetic field strength of 1 T. Relaxivity was obtained using linear regression analysis of the relaxation rates of four solutions (0 – 0.14 mM). The NMR measured all samples at 310 K.

Table S2. Comparison of relaxivity values between contrast agents. *Direct comparison of relaxivity rates at different field strengths is difficult as r_1 values are depressed and r_2 values enhanced at higher fields. These values are included for completeness and to acknowledge the contributions of others in this area.

Contrast Agent (CA)	CA per Particle	<i>r</i> ₁ per CA (mM⁻¹⋅s⁻¹)	<i>r</i> ₂ per CA (mM⁻¹⋅s⁻¹)	r₁ per Particle (mM⁻¹⋅s⁻¹)	r₂ per Particle (mM⁻¹⋅s⁻¹)	<i>r</i> ₂ / r ₁	Field (T)*	ref
TMV-6	~2130	2.8 ± 0.1	10.3 ± 0.1	~5964	~21939	3.7	1	This work
TMV-6+CB[8]	~2130	1.9 ± 0.1	3.1 ± 0.1	~4047	~6603	1.6	1	This work
TEMPO-NH ₂	1	0.6 ± 0.1	2.0 ± 0.1	0.6 ± 0.1	2.0 ± 0.1	3.3	1	This work
TEMPO-NH ₂ +CB[8]	1	0.2 ± 0.1	0.2 ± 0.1	0.2 ± 0.1	0.2 ± 0.1	1	1	This work
Gd-DOTA	1	3.0	5.0	3.0	5.0	1.7	1	8
exTEMPO-TMV	~2130	1.5 ± 0.1	4.7 ± 0.1	~3195	~10011	3.13	1.5	1
inTEMPO-TMV	~3919	0.4 ± 0.1	1.7 ± 0.1	~1567.6	~6662.3	4.25	1.5	1
3-CP	1	0.15	0.17	0.15	0.17	1.13	7	6
Chex-MM	N/A	0.21	0.3	N/A	N/A	1.42	7	3
Chex-dendrimer	N/A	0.44	0.86	N/A	N/A	1.95	7	4
Chex-bottlebrush	N/A	0.32	0.82	N/A	N/A	2.56	7	3
BASP-ORCA1	N/A	0.41	4.67	N/A	N/A	11.39	7	6
BASP-ORCA3	N/A	0.63	4.62	N/A	N/A	7.33	7	7
Dy-DTPA- PcHexPh2	1	0.11	3	0.11	3	27	7	9

MRI In Vivo Studies

All animal procedures were reviewed by the UT Southwestern IACUC committee and accepted under protocol # 2016-101780. Mice were placed under anesthesia and a heater was used to keep the temperature around the mice at 30 °C for the duration of the study. Each mouse was injected intramuscularly with 50 μ L of TMV-6 without CB[8] and TMV-6 with CB[8]. The mice were placed in a 9.4 T Varian MRI scanner and the bladder was positioned to be in the center. 3D T1-weighted gradient echo multi slice scans were taken before injection (*TE* = 4.00 ms and *TR* = 256.92 ms, Matrix = 128 × 138 × 128) and at 1 min, 30 min, and 2 h after injection.

Modeling

The molecular dynamics (MD) simulations included one TEMPO molecule, one CB[8] molecule, 1877 water molecules, and one chloride anion in the unit cell under periodic boundary conditions. The force field parameters for CB[8] were obtained from CGenFF^{10, 11} using the online server at https://cgenff.paramchem.org. The force field parameters for TEMPO were obtained from the SLH moiety in work by Sezer *et al.*¹² The TIP3P water

model was used. Note that the TIP3P water model was found to yield better agreement with experimental cucurbituril-guest binding enthalpies than competing water models such as TIP4P-Ew.¹³



Figure S13. The free energy profile as a function of the insertion depth of the TEMPO ring in the CB[8] cavity.

All simulations were run using the NAMD software package¹⁴ with the following parameter choices: temperature 300 K enforced with a Langevin thermostat with damping parameter 1.0 ps⁻¹; pressure 1 atm enforced with a Langevin barostat with a period of 100 fs and a decay time of 50 fs; cutoff distance 12 Å for the van der Waals interactions and the changeover from real space to reciprocal space for the electrostatic interactions; time step 1.0 fs; particle mesh Ewald grid spacing of 1 Å.



Figure S14. Radial distribution functions and their integrals for the distance between the TEMPO oxygen radical and water hydrogen and oxygen atoms.

Three simulations were run, namely an equilibrium simulation of 100 ns, an adaptive biasing force simulation of 100 ns, and an umbrella sampling simulation of 100 ns. The equilibrium simulation quantifies, among other things, the accessibility of the TEMPO oxygen radical to solvent water molecules. This data is shown in Figure S14. We see that

water hydrogen atoms (black line) are found preferentially about 2 Angstroms from the TEMPO oxygen radical, and water oxygen atoms (red line) are found preferentially about 3 Angstroms from the TEMPO oxygen radical. In terms of numbers, the green and blue curves in Figure S14 show that, on average, one water hydrogen and one water oxygen are found within 2.6 and 3.2 Angstroms, respectively, of the TEMPO oxygen radical. A water molecule including this hydrogen and oxygen atom is shown in Figure S15. This water molecule is surrounded by other solvent water molecules, thus allowing exchange to generate the MRI contrast. In addition, due to the CB[8] cavity, we see that the radial distribution functions do not plateau until about 15 Angstroms.



Figure S15. Representative snapshot from the equilibrium MD simulation showing the location of the TEMPO molecule with respect to CB[8] and the TEMPO oxygen radical's access to solvent water. Only one solvent water molecule is shown.

The two free energy simulations quantify the CB[8]—TEMPO host—guest binding free energy and also show exactly where the TEMPO molecule prefers to sit in the CB[8] host cavity. The data is shown in Figure S13. We can notice two main observations. First, the equilibrium position of the TEMPO ring is about 0.9 Å above the plane of the CB[8] ring. Second, the binding free energy is very strong at over 20 kcal/mol. Previous literature suggests that computational methods typically overestimate the binding free energy for cucurbit[n]uril host-guest systems¹⁵ but nonetheless the CB[8]—TEMPO association is clearly very strong.

Although we do not attempt to decompose the binding free energy into contributions from separate factors, we note that previous studies have attributed significant effects from the change in solvation of the ammonium unit upon binding,¹⁶ and from the release of water molecules inside the CB[8] cavity upon binding.¹⁷

For the binding free energy calculation, we used five collective variables to control the insertion of TEMPO into the CB[8] cavity and ensure reversibility of the transformation. The first two collective variables have no effect on the energy, the 3rd and 4th ones do have a minor effect on the energy, and the 5th one is the reaction coordinate. The 1st collective variable constrains the center of mass of CB[8] to the origin. The 2nd collective variable constrains the plane of the CB[8] ring to the x-y axis. These two collective variables have no effect on the system properties since periodic boundary conditions are

used; their purpose is to make the choice of reaction coordinate simpler. The 3rd collective variable weakly constrains the center of mass of the TEMPO ring to the z-axis. This is done so that the TEMPO molecule does not drift sideways when it is separated from CB[8]. The 4th collective variable does not allow the terminal carbon atom in the TEMPO tail chain to be more than 3 Å below the center of mass of the TEMPO ring. This is done to prevent the TEMPO molecule from rotating 180 degrees which would otherwise potentially let it insert backwards after being separated from CB[8]. Although the entropic cost of the 3rd and 4th collective variable constraints could be estimated analytically, we simply neglected their contribution to the binding free energy. The 5th collective variable is defined as the z-distance between the center of mass of CB[8] and the center of mass of the TEMPO ring. This is our reaction coordinate for measuring the binding free energy. For the umbrella sampling run, it was controlled using 40 umbrellas between reaction coordinate values of -3 and +8 with a spring constant of 10 kcal/mol/Å² over a 100 ns simulation. For the ABF run we used the default values. We also computed the binding free energy, or at least the accessible portion, from the equilibrium simulation. This was done by taking kT times the negative of the logarithm of the normalized histogram of the reaction coordinate values visited during the equilibrium simulation.

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