

Supporting information

Conformational selection in anion recognition: cGMP-selective binding by a naphthalimide-functionalized amido-amine macrocycle

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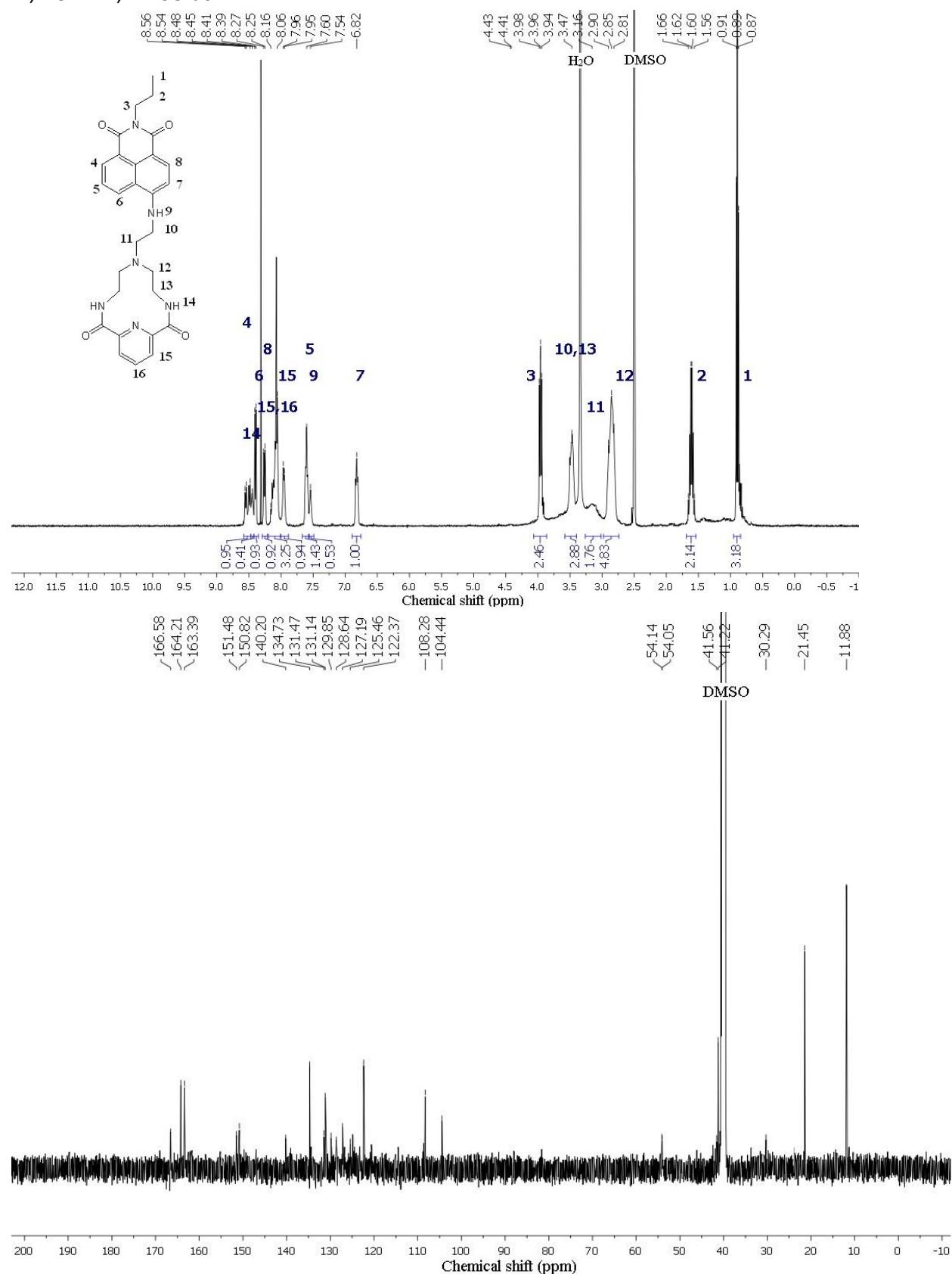
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1. NMR spectra

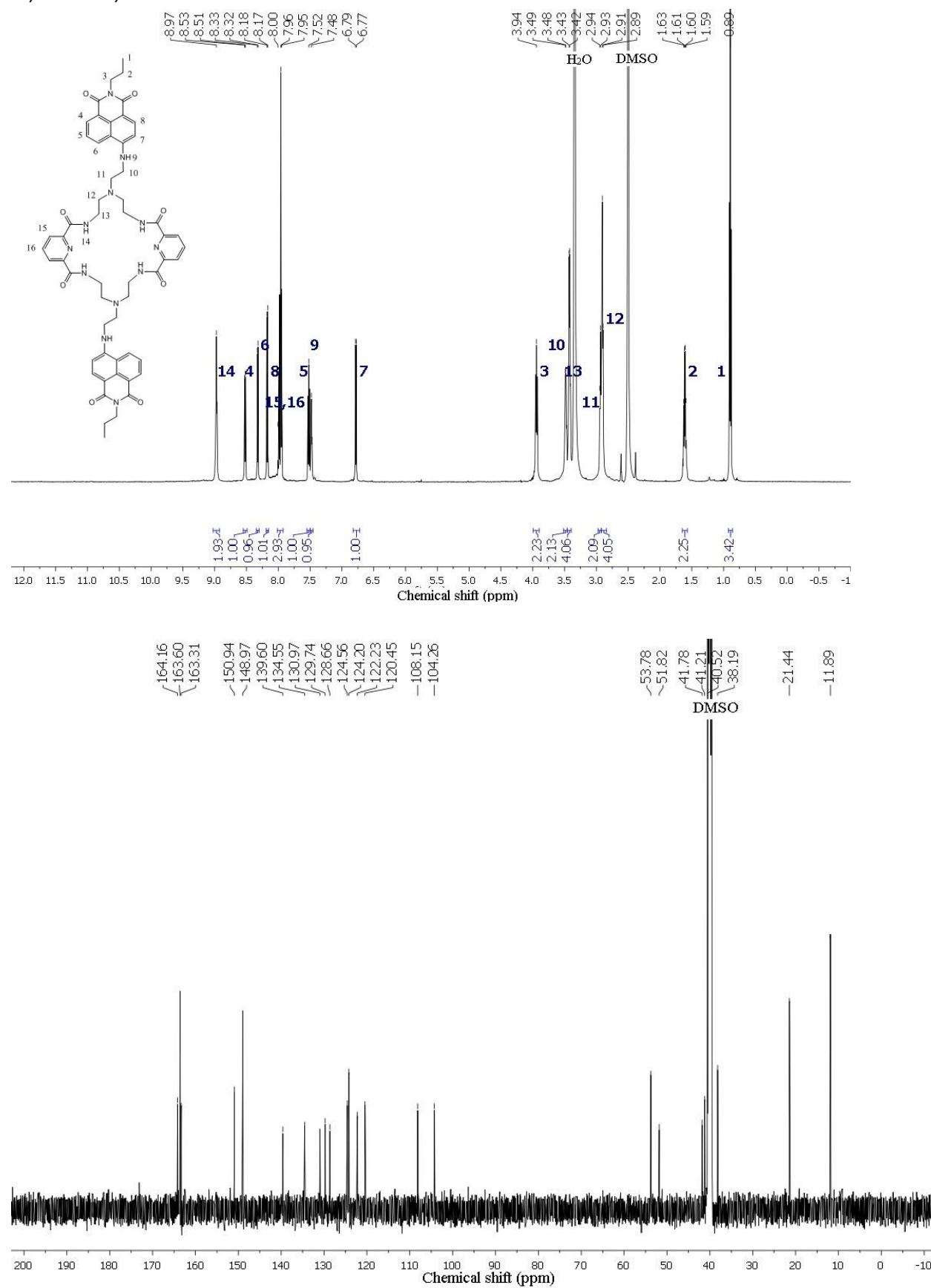
Compound 5

^1H , ^{13}C NMR, DMSO-*d*6



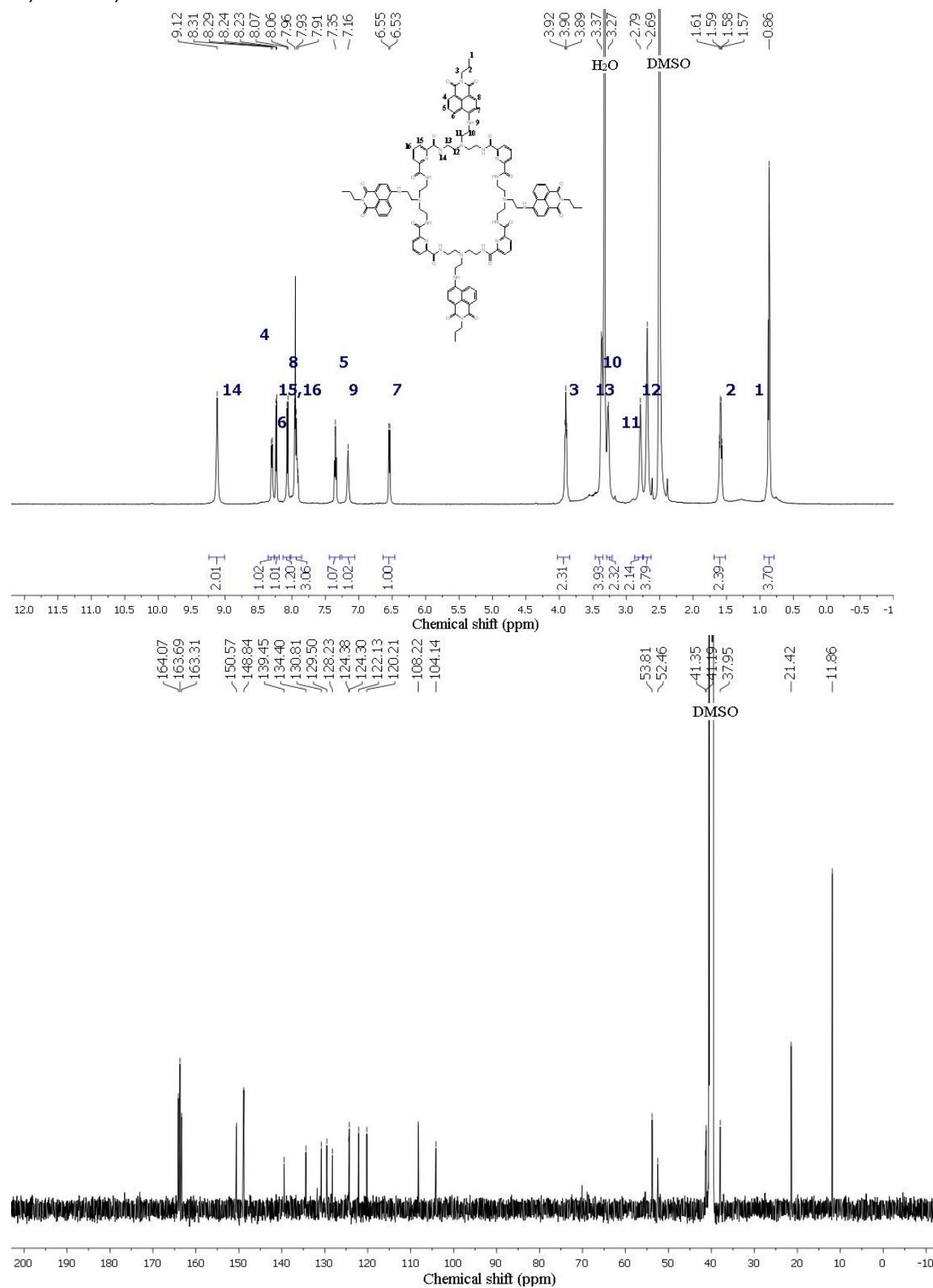
Compound 3

^1H , ^{13}C NMR, DMSO- d_6



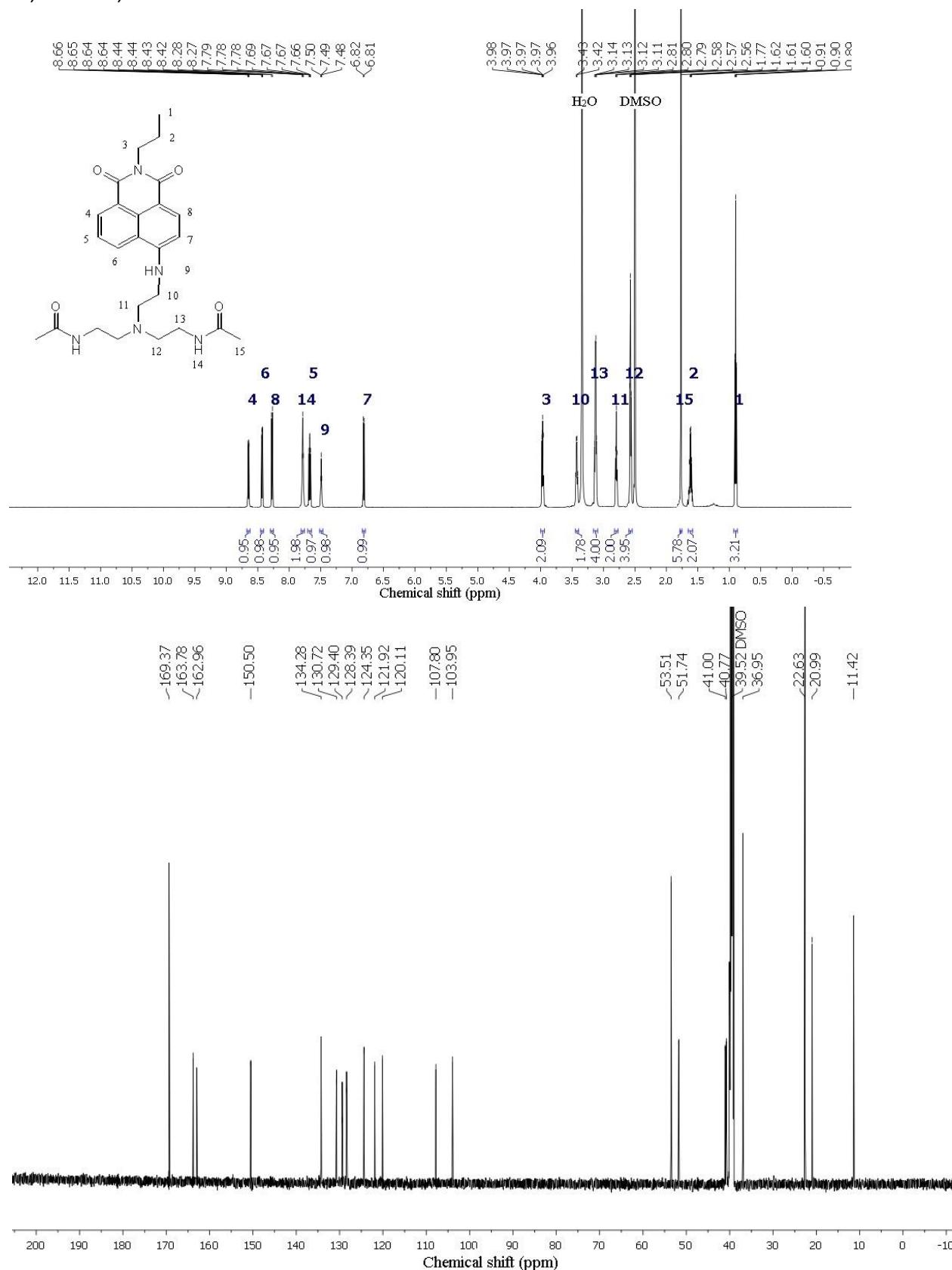
Compound 4

^1H , ^{13}C NMR, DMSO-*d*6



Compound 4

^1H , ^{13}C NMR, DMSO-*d*6



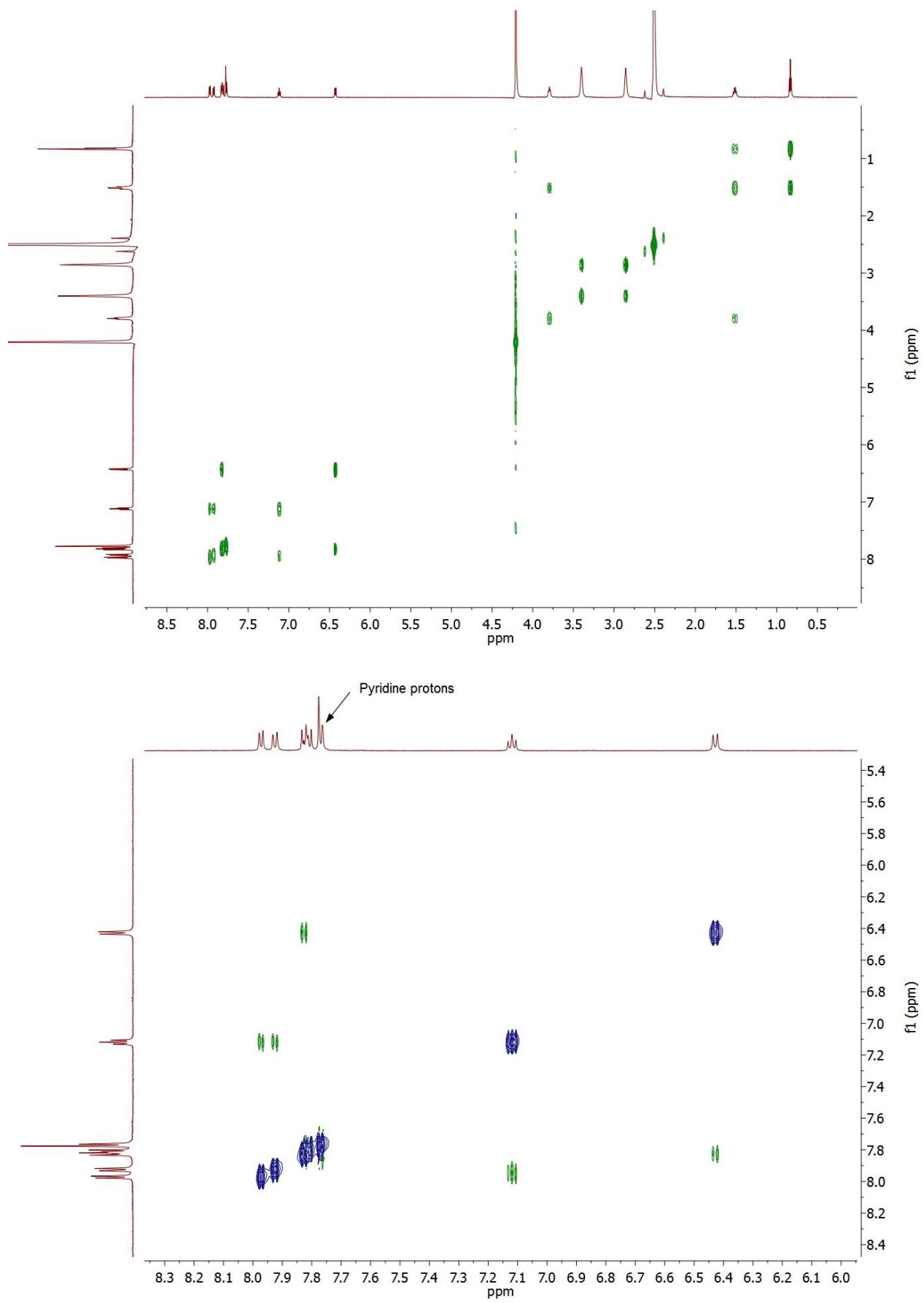


Figure S1. ^1H - ^1H COSY and ROESY of **3** measured in 7:3 DMSO- d_6 -D₂O.

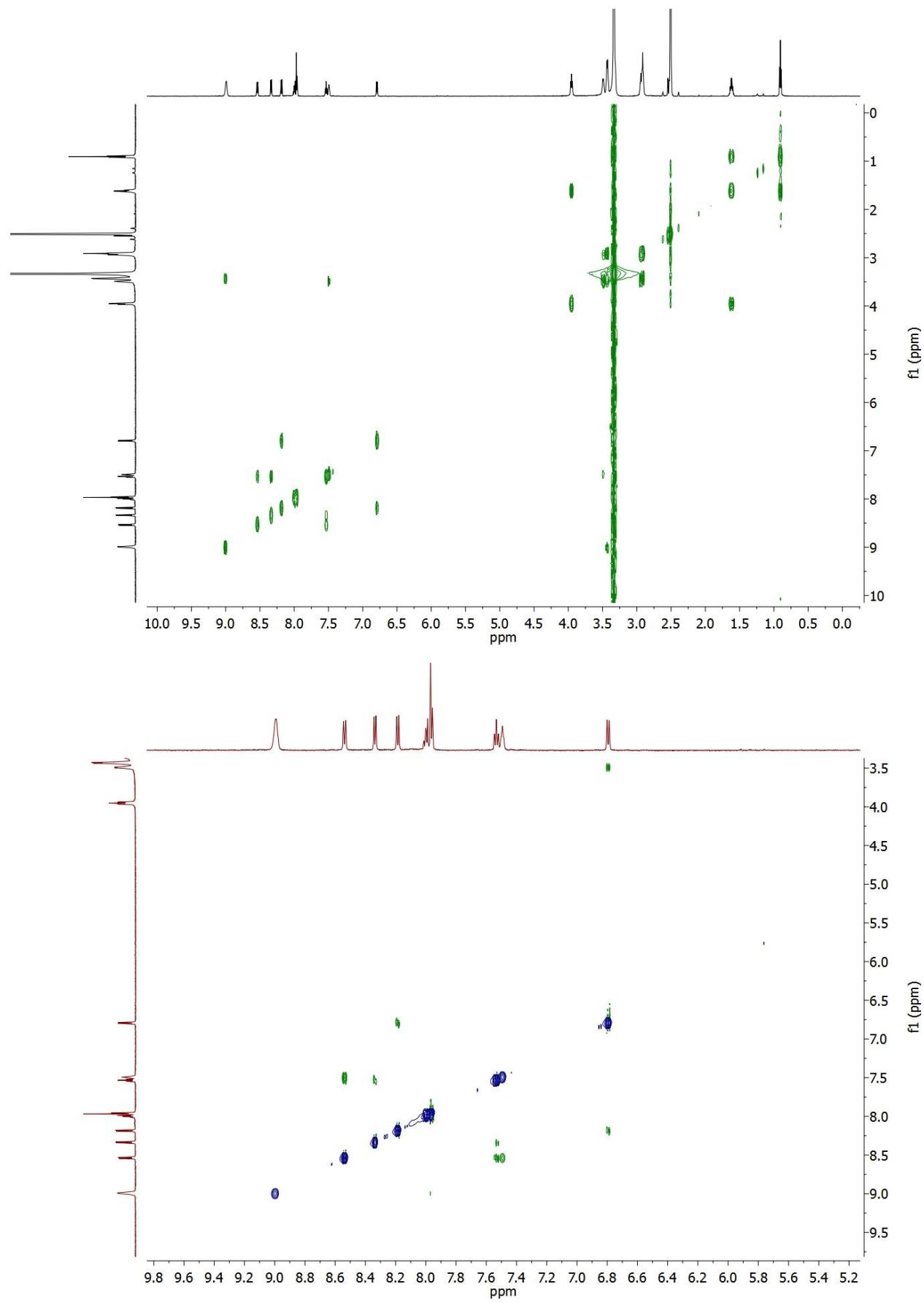


Figure S2. ^1H - ^1H COSY and ROESY of **3** measured in $\text{DMSO}-d_6$.

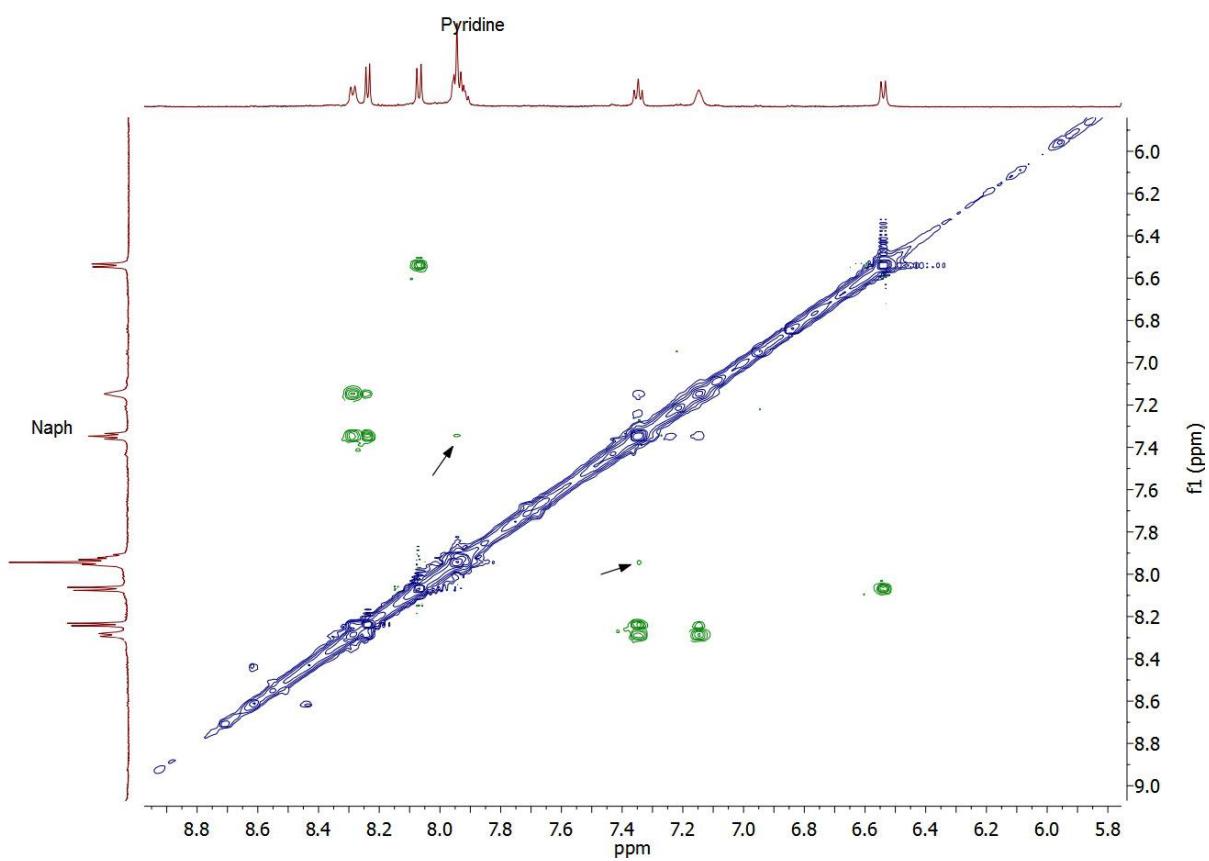
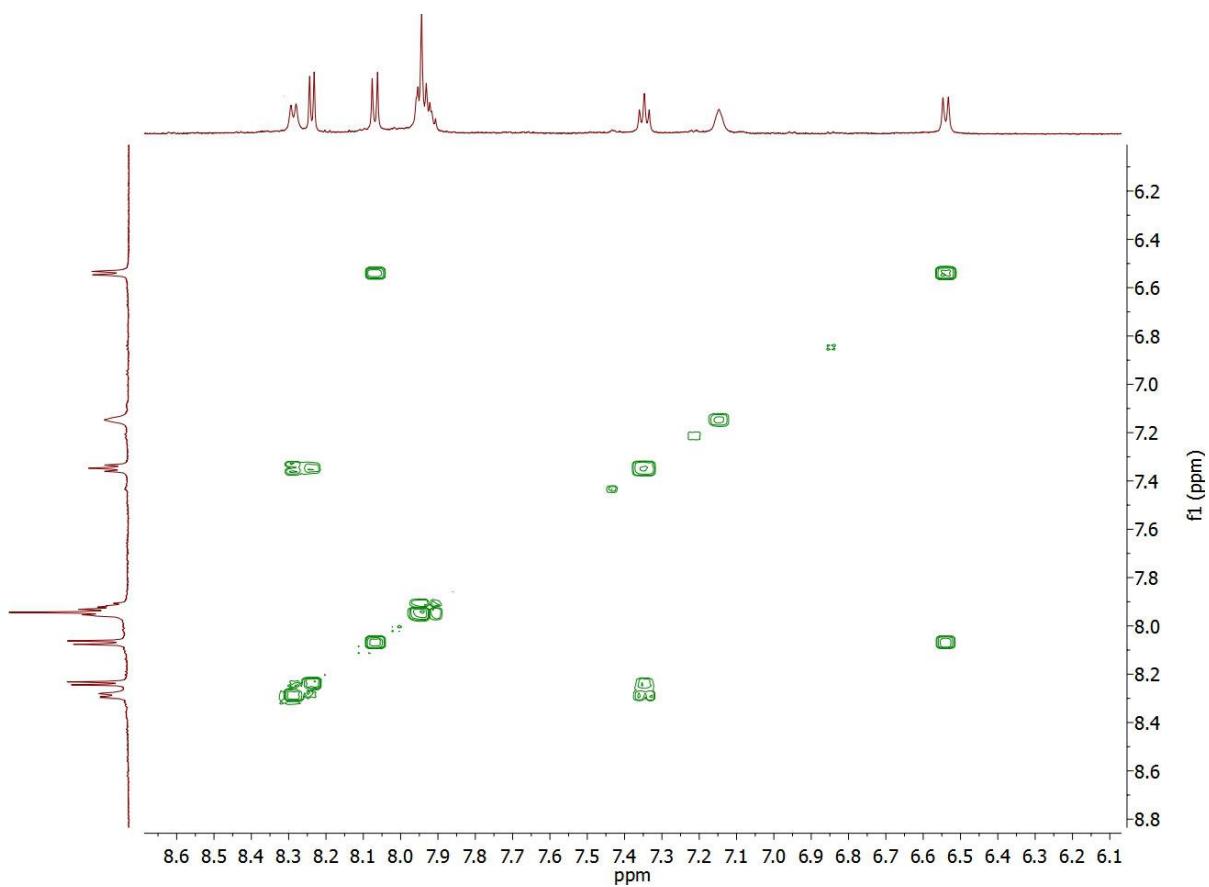


Figure S3. ¹H-¹H COSY and ROESY of **4** measured in DMSO-*d*₆.

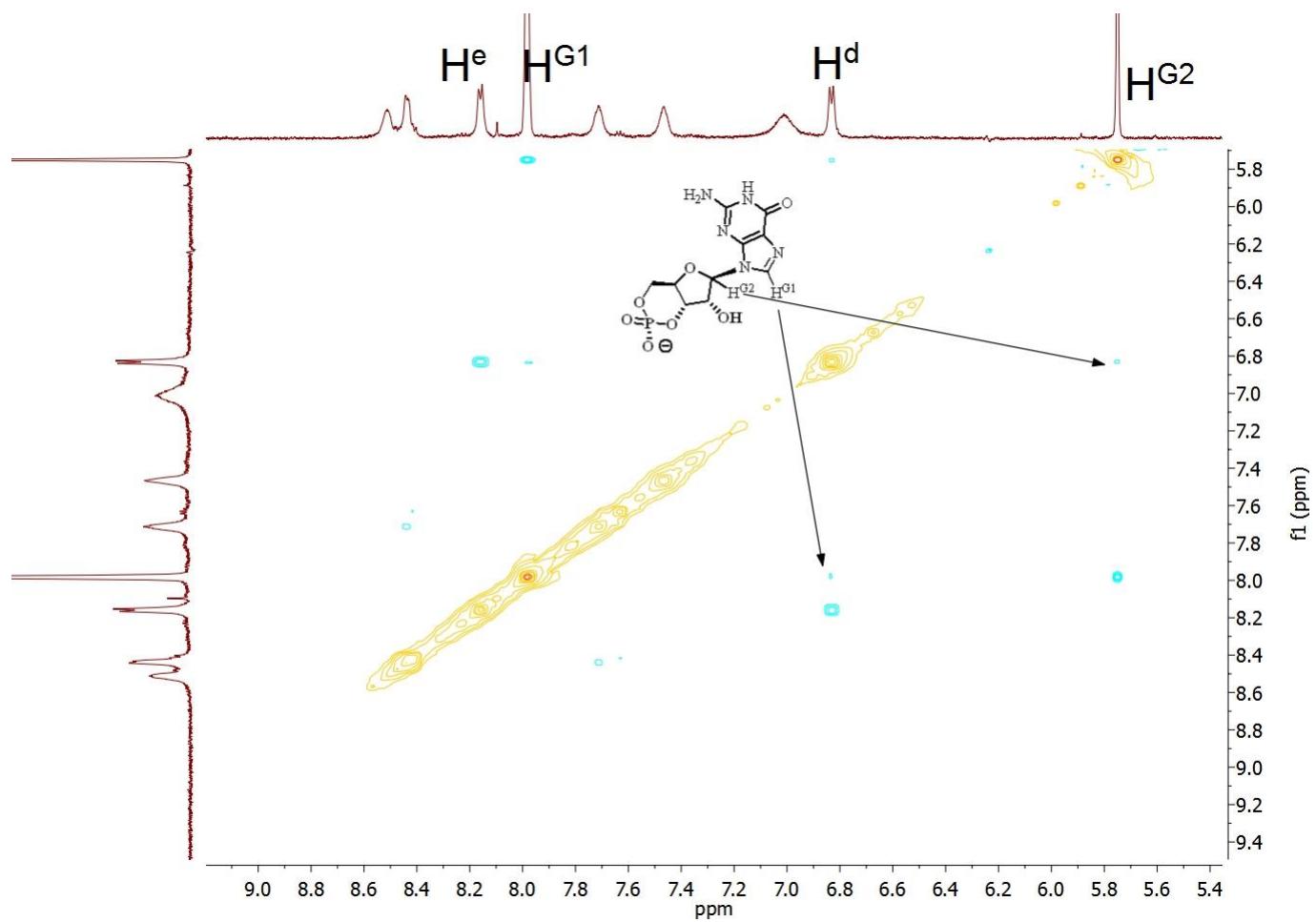


Figure S4. ¹H-¹H ROESY NMR of **3** with 5 equiv. cGMP and 5 equiv. HClO₄ measured in DMSO-*d*₆-D₂O (7:3) mixture.

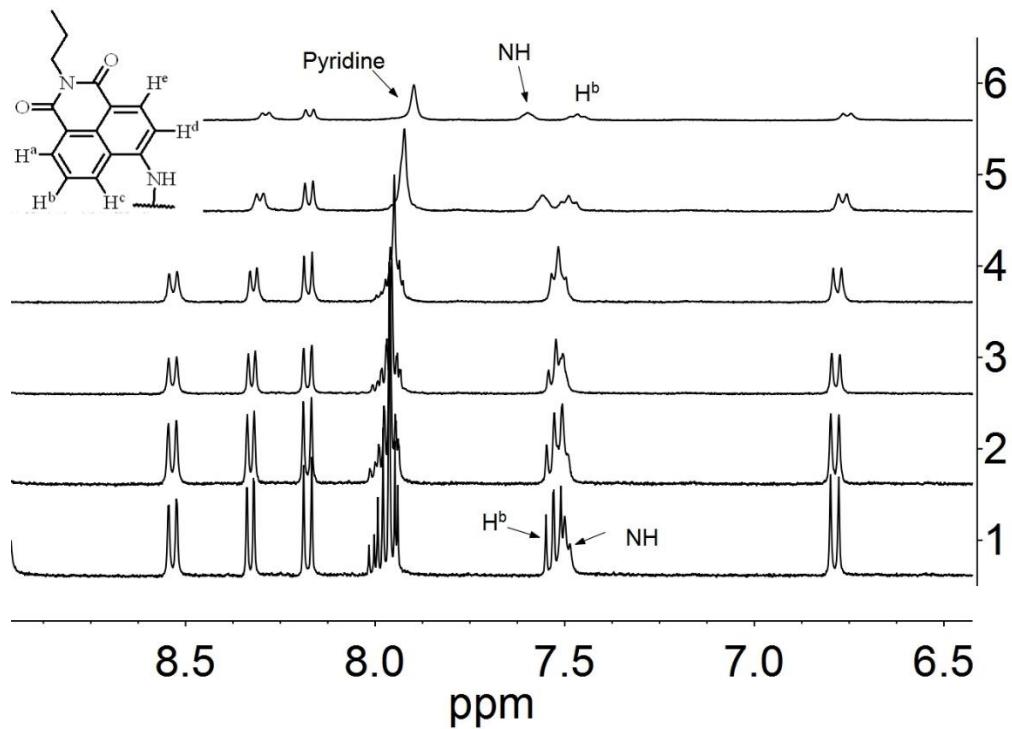


Figure S5. ^1H NMR of receptor **3** in the presence of TBAHSO₄ in DMSO-*d*6–D₂O mixture. Additions 1 to 5 are 0.25, 0.5, 1, 4 and 10 equiv of TBAHSO₄.

2. Atomic Force Microscopy (AFM) measurements

For AFM imaging, we prepared samples on polished Si wafers covered with a 100 nm thick oxide layer by spin-casting (1000 rpm, 60 s) an aqueous solution (pH 3.6, 50 mM acetate buffered with 2% DMSO addition) of **3** in the presence of 5 equiv of Na₂SO₄ or ATP. AFM measurements were performed at ambient conditions in the amplitude modulation mode (also known as tapping mode) using a NanoWizard II AFM (JPK Instruments AG, Berlin, Germany) and silicon cantilevers (Pointprobe NCH, NanoWorld AG, Neuchâtel, Switzerland) with a resonance frequency of typical 350 kHz and a tip radius of 8 nm as given by the manufacturer. The free amplitude A_0 was ≈ 60 nm and the amplitude setpoint $A/A_0 \approx 0.8$.

3. DFT calculations

Molecular modeling calculations were performed first using program “ORCA”. A BP86 functional which includes electron density gradient was used. def2-SVP basis set-atomic basis sets of grouped Gaussian functions were used to solve the Kohn–Sham equations. The criterion for convergence was a difference below 0.01 kcal/mol/Ångstrom in the energy between two sequential structures. The host-guest model structures were generated by combining a preoptimized structure of the receptor with the anion, followed by simultaneous optimization of the proposed structures. Searches for the relevant global minima were performed by calculating different anion-to-receptor coordination modes. In order to get more accurate energies, we performed single-point calculations for the received geometries, using the BP86 functional and def2-TZVP basis set.

Coordinates of complex **3**H₂²⁺•cGMP⁻:

O	-2.451873	6.143204	-1.441870
O	-6.478353	0.320873	-0.872045
O	-1.582951	-1.552375	2.366985
O	3.560320	2.817927	0.254097
O	5.092587	-1.141433	0.923536
O	4.327749	-3.750351	4.621533
O	-3.219701	1.421762	3.142008
O	0.091243	1.358320	6.327163
N	-2.210429	4.237957	-2.706734
H	-2.532207	3.263138	-2.825868
N	-4.212873	3.033522	-1.430970
N	-4.714933	0.536901	-2.325198
H	-3.930687	1.144242	-2.615807
N	-3.649843	-2.056936	-1.073262
H	-2.841008	-1.561591	-1.594277
N	-1.638274	-0.212746	0.502555
H	-1.056300	0.479480	0.016301
N	0.875376	0.590399	0.899427
N	2.173166	1.739286	-1.225589
H	1.529669	0.945042	-1.331081

N	0.884348	3.756010	-2.943983
H	0.438882	3.275181	-2.130280
N	-0.796517	-3.137465	-0.619254
H	-0.969026	-2.425655	-1.346783
N	4.716075	-2.468379	2.757461
N	1.308291	4.786666	0.014714
H	2.302227	4.790579	0.255749
N	-1.572542	1.409927	4.747423
C	-2.792421	4.987924	-1.719118
C	-3.869705	4.246891	-0.964947
C	-4.468599	4.829666	0.166366
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H	-5.958549	4.521788	1.725312
C	-5.851350	2.851225	0.333594
H	-6.636115	2.239929	0.800568
C	-5.187785	2.354256	-0.804206
C	-5.547298	0.986178	-1.341732
C	-4.863199	-0.765237	-2.941807
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H	-5.834699	-0.829406	-3.481333
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H	-5.758224	-1.970173	-1.361230
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C	-3.869663	-1.364937	0.259499
H	-3.583598	-2.058063	1.069372
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H	-3.462548	0.420032	1.339344
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C	0.357581	-0.220616	1.840736
C	1.029122	-0.534353	3.034451
H	0.555095	-1.222677	3.746744
C	2.274427	0.065472	3.275255
H	2.821206	-0.139655	4.206426
C	2.813069	0.922825	2.308741
H	3.786285	1.414079	2.428522
C	2.078358	1.138390	1.126499
C	2.675761	1.982041	0.038115
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H	0.133742	-6.043210	3.520659
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C	2.192177	-3.247687	1.692078
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H	-2.626944	2.613747	1.008181
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C	-0.292559	1.754149	5.228758
C	0.544814	2.615638	4.351885
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H	3.570219	4.222232	4.382488

C 2.184227 4.223268 2.725143
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 H 0.816523 -0.477383 -5.999655

FINAL SINGLE POINT ENERGY -4962.027996893603

4. Absorption and fluorescence titrations

The stock solutions of compounds **3**, **4** (10^{-5} M) in pH 3.6: 50 mM acetate buffer (2% DMSO vol.) were prepared in 50 ml volumetric flasks. The solutions of sodium salts (0.001 – 0.01 M) were prepared in the solution of compounds to keep the concentration of the compound constant throughout the titrations. The receptor solution in a 10mm cuvette (2.0 ml) was then titrated with the salt solution and each time the spectrum was recorded. Following setup parameters for fluorescent titration were used $\lambda_{\text{ex}}: 440 \text{ nm}$, slit 2/2, $\lambda_{\text{em}}: 480\text{-}680 \text{ nm}$. (For absorption titrations $\lambda_{\text{abs}}=320\text{-}550 \text{ nm}$). The resulting data was imported in HypSpec program and the data was fitted to obtain stability constants with anions.

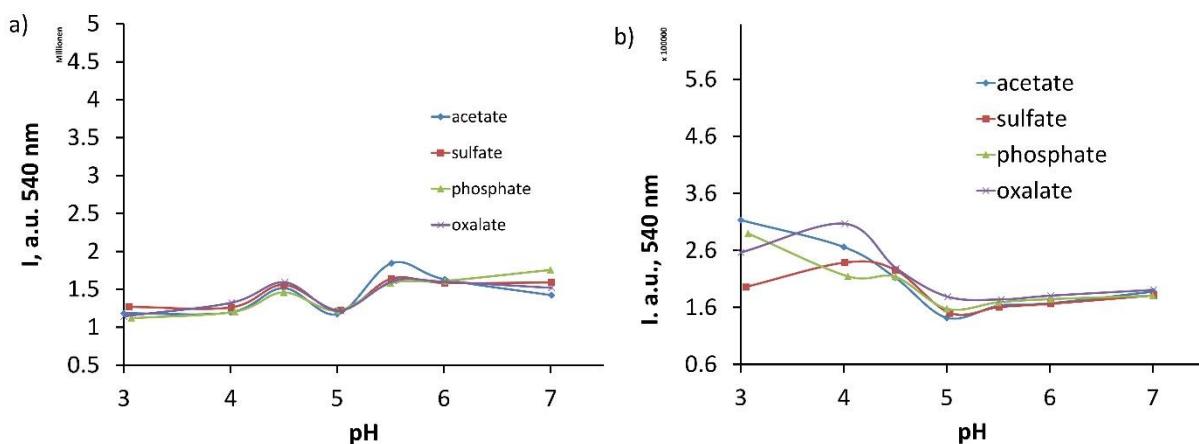


Figure S6. Fluorescence intensity of receptor a) **5** and b) **4** at 540 nm in the presence of an excess of different anions depending on the pH of the solution. Content of the solution with different pH values: 0.01 mM receptor in 50 mM NaOH/acetic acid mixtures containing 2% DMSO and 1 mM anions as sodium salts.

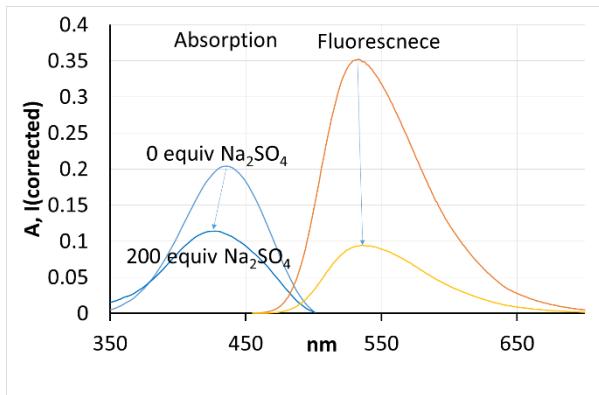


Figure S7. Corrected absorption and fluorescence spectra before and after addition of 200 equiv of Na_2SO_4 to **3**.

4.1 Binding constants with anions and nucleotides

Table S1. Binding constants, $\log\beta_{11}$ and $\log\beta_{12}$ of macrocycles **3** and **4** with anions determined by UV-Vis and fluorescence titrations (in parenthesis) in a 50 mM acetate buffer containing 2% (vol.) DMSO, pH 3.6, 23°C.

Anion/Receptor	3	4
Na_2SO_4	4.41 ± 0.02 (4.20 ± 0.03)	3.96 ± 0.05 $\log\beta_{12} = 7.00 \pm 0.05$

NaH ₂ PO ₄	4.23 ± 0.02 (4.10 ± 0.03)	4.79 ± 0.02 $\log\beta_{12} = 7.46 \pm 0.05$
Na ₂ C ₂ O ₄	4.25 ± 0.03 $\log\beta_{12} = 8.00 \pm 0.03$	5.49 ± 0.02 $\log\beta_{12} = 8.50 \pm 0.06$
NaClO ₄	3.03 ± 0.01	4.00 ± 0.03
NaNO ₃	2.83 ± 0.01	4.55 ± 0.03
NaCl	3.02 ± 0.01 (2.88 ± 0.01)	3.84 ± 0.04
NaBr	2.82 ± 0.01 (2.55 ± 0.01)	4.00 ± 0.03
Nal	2.54 ± 0.01 (2.24 ± 0.01)	3.58 ± 0.04

Table S2. Binding constants, $\log K_{11}$ of macrocycles **3** and **4** with nucleotides determined by UV-Vis and fluorescence titrations (in parenthesis). Conditions: 50 mM acetate buffer (2% DMSO, pH 3.6, 23°C); ex. 450 nm.

Nucleotide	receptor 3	receptor 4
AMP	4.40 ± 0.02 (4.10 ± 0.04)	3.29 ± 0.02 (2.97 ± 0.04)
cAMP	4.60 ± 0.01 (4.80 ± 0.01)	3.90 ± 0.02 (3.33 ± 0.02)
GMP	4.31 ± 0.01; (4.25 ± 0.01)	4.00 ± 0.03 (3.60 ± 0.02)
cGMP	4.91 ± 0.01 (4.80 ± 0.01)	4.20 ± 0.03 (3.55 ± 0.02)
CMP	4.35 ± 0.02	4.15 ± 0.02
TMP	4.32 ± 0.02	4.20 ± 0.02
UMP	4.38 ± 0.03	4.25 ± 0.02

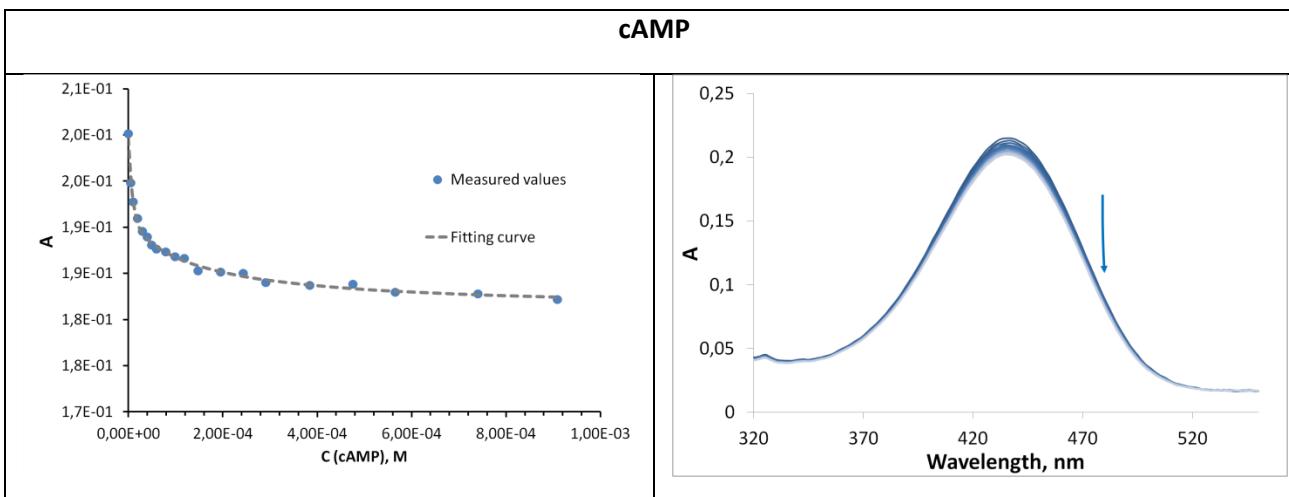
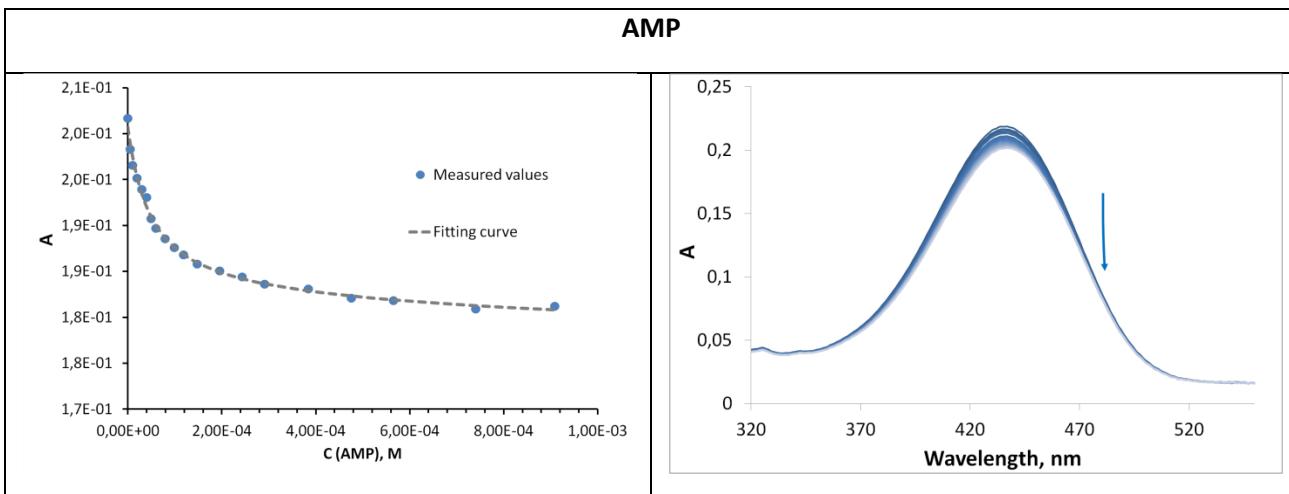
4.2. Photophysical properties of the compounds

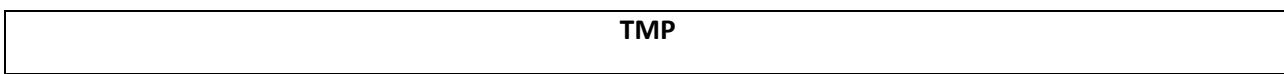
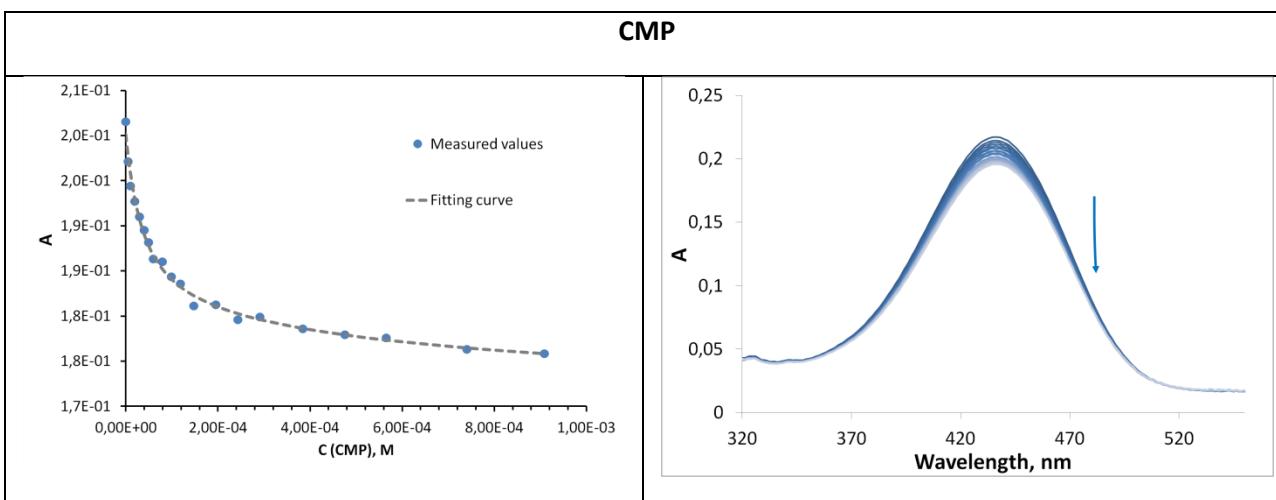
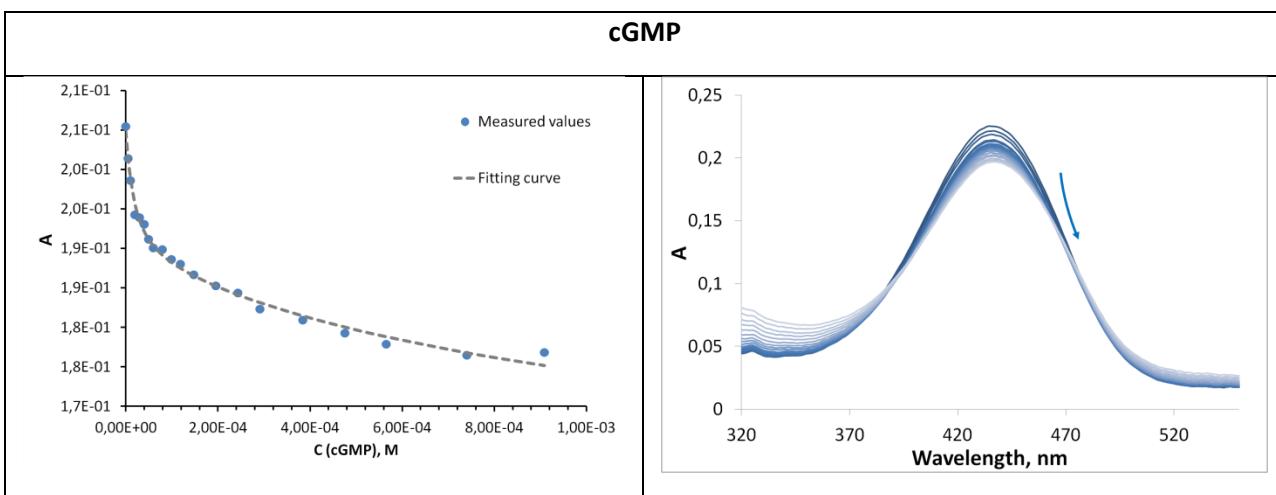
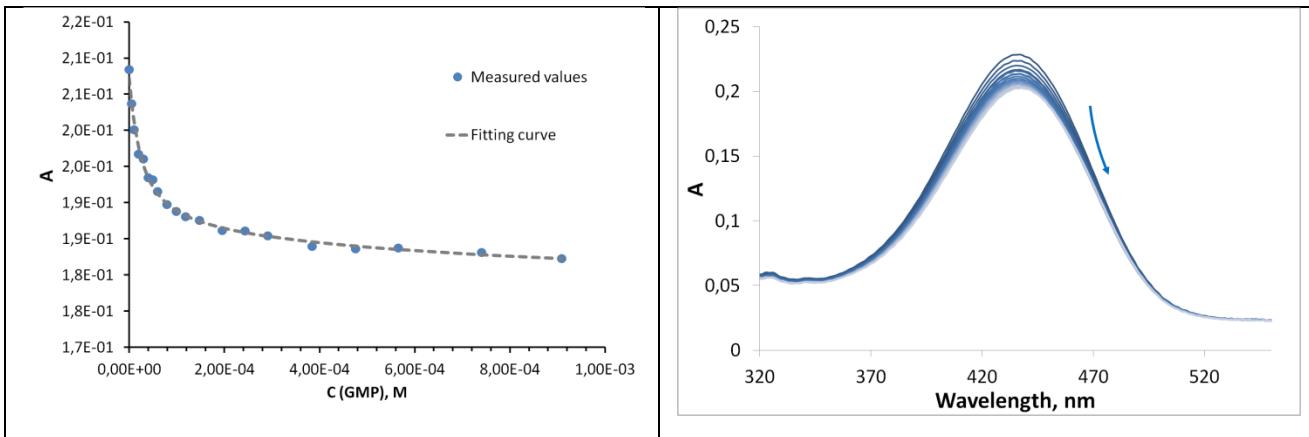
Table S3. Photophysical properties of the compounds determined in a 50 mM acetate buffer pH 3.6, at full-protonated state.

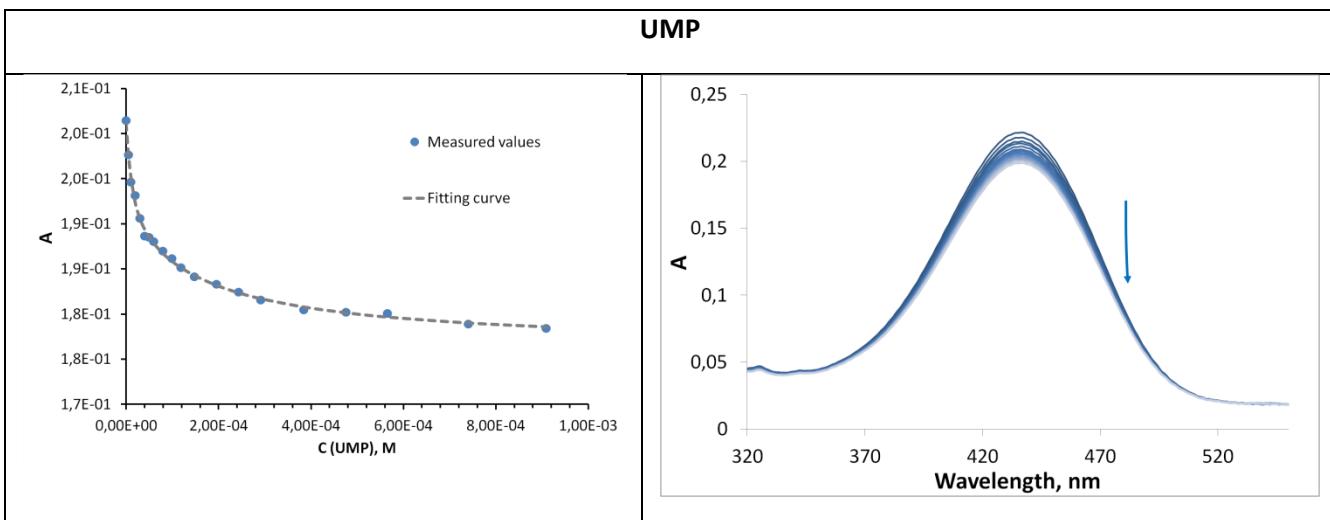
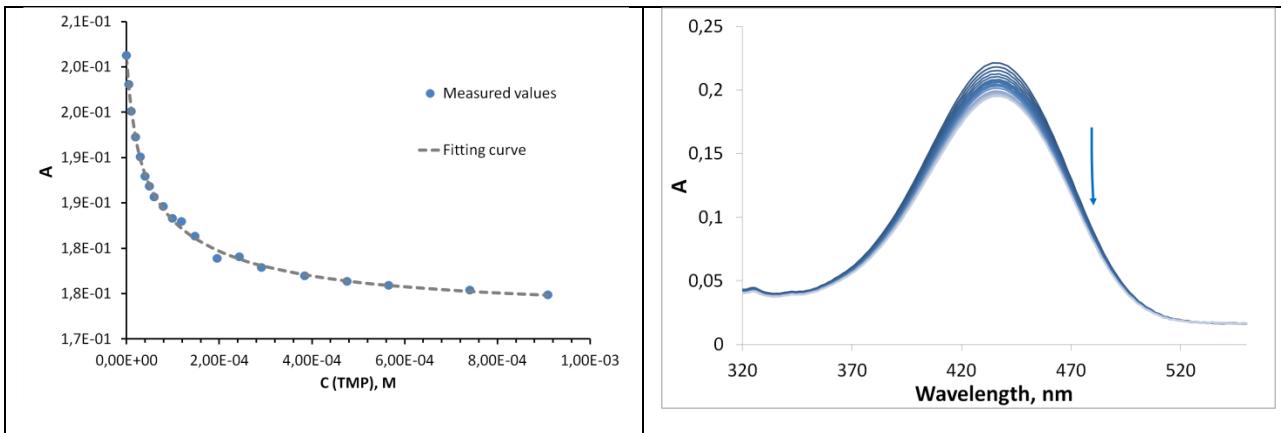
Compound	$\epsilon(\max)[\text{Lmol}^{-1}\text{cm}^{-1}]$	Absorption	Emission

		$\lambda_{\text{max}}, \text{nm}$	$\lambda_{\text{max}}, \text{nm}$
6	17010	430	528
3	20290	436	529
4	39690	441	534

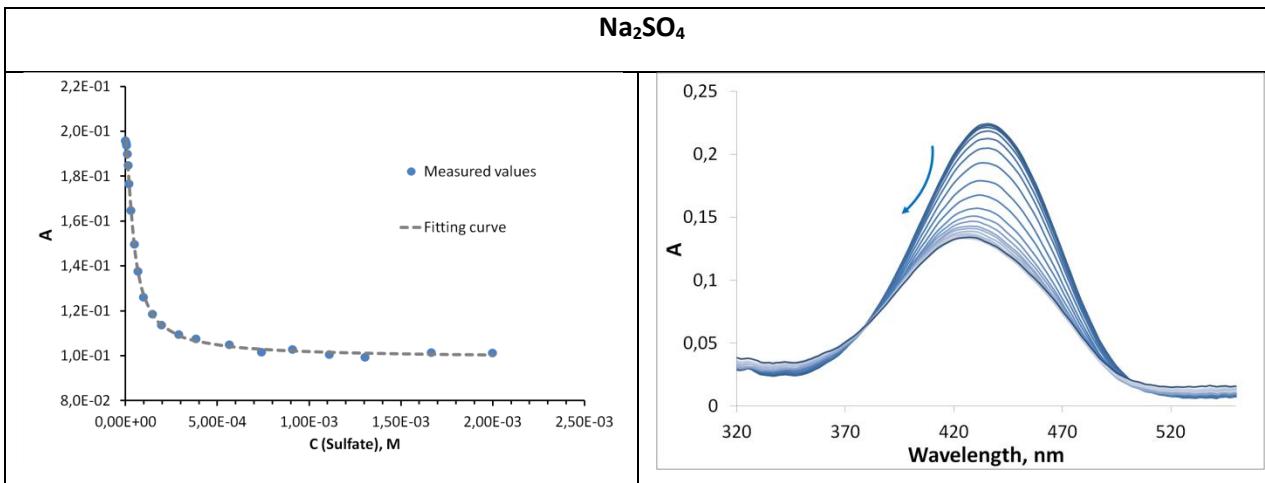
4.3. Absorption titration of 3 with nucleotides

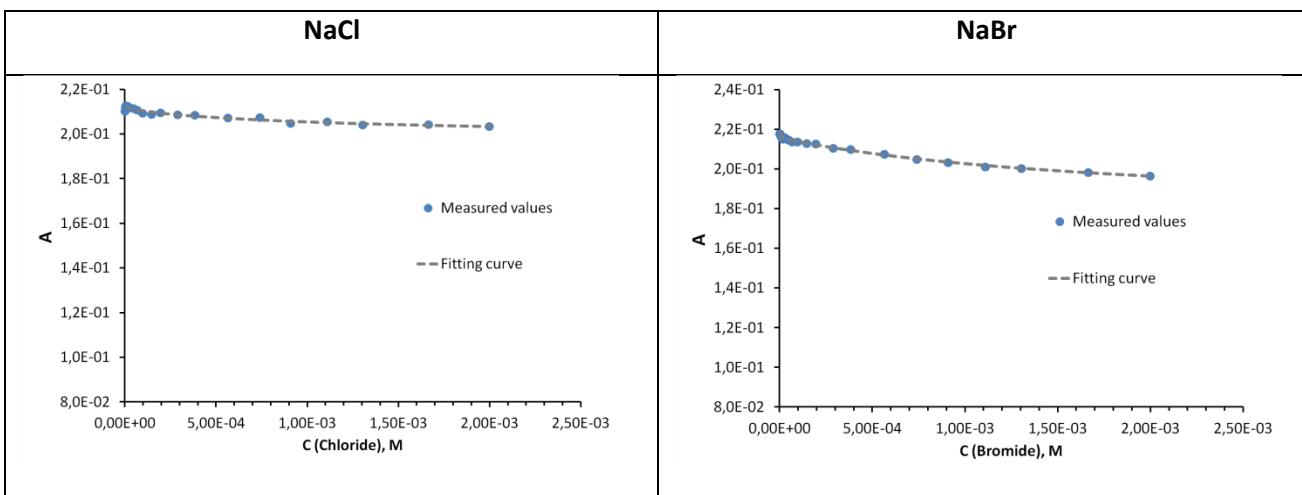
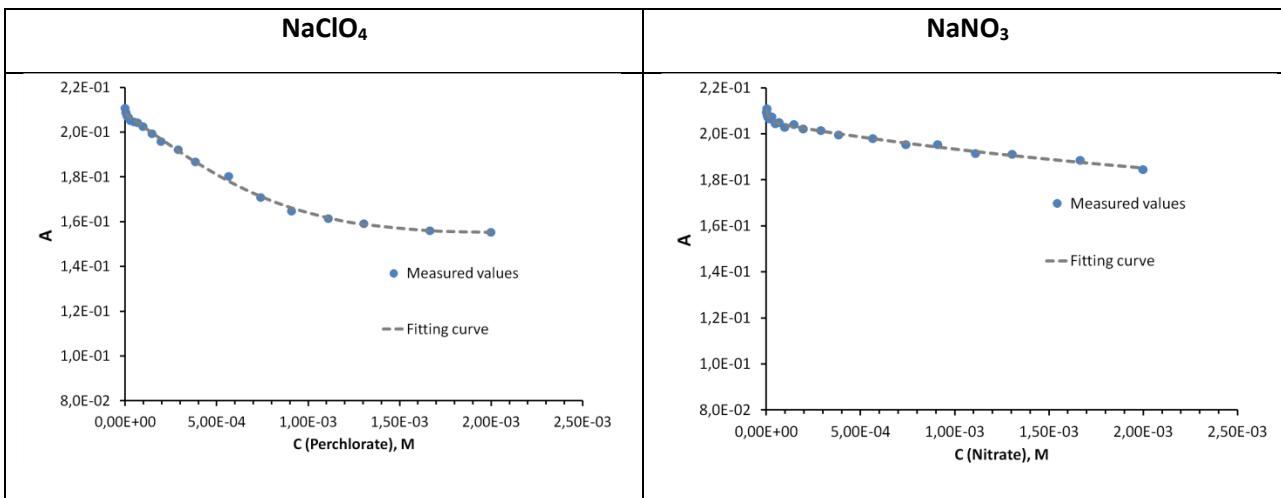
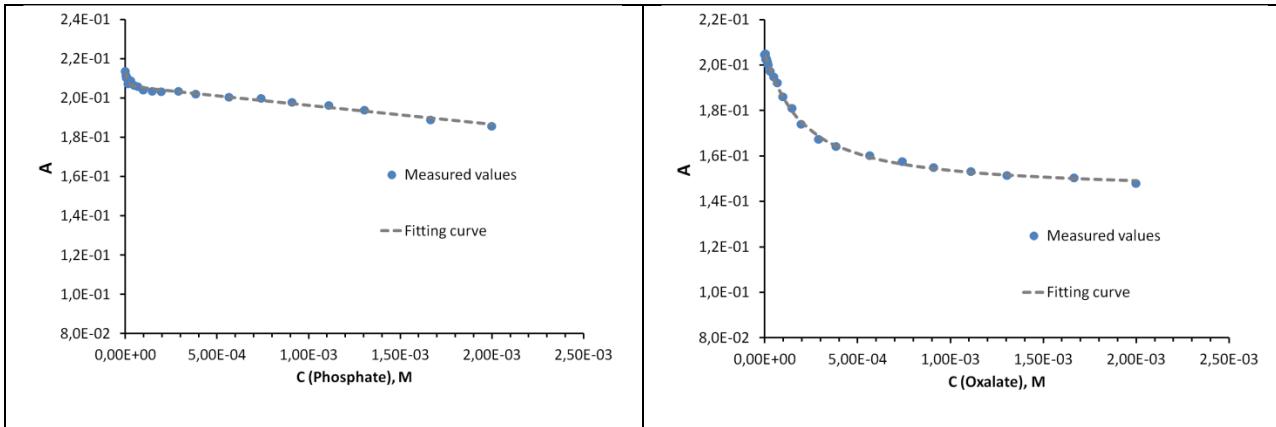


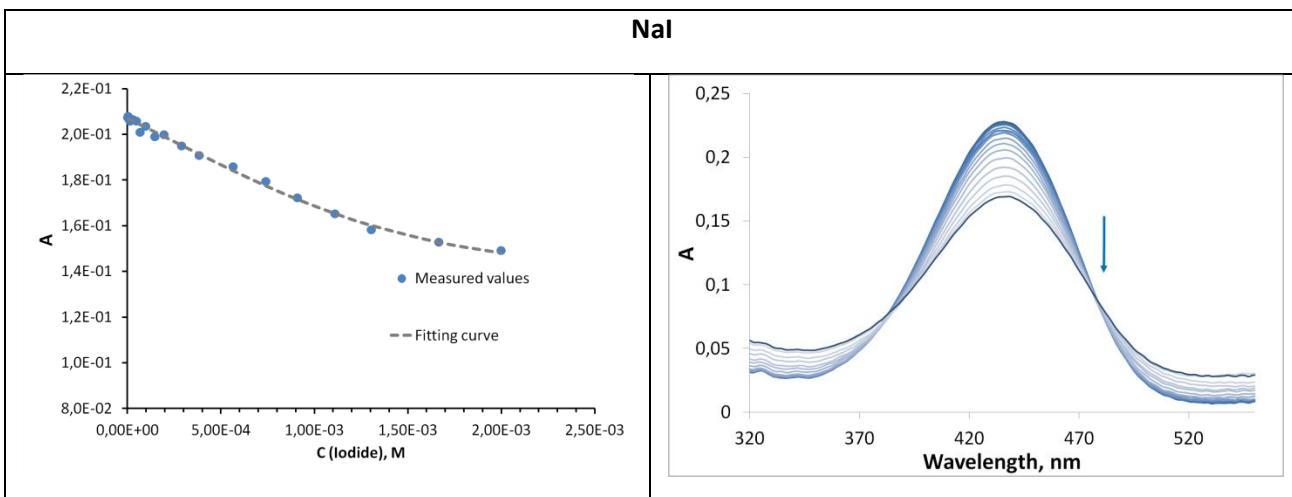
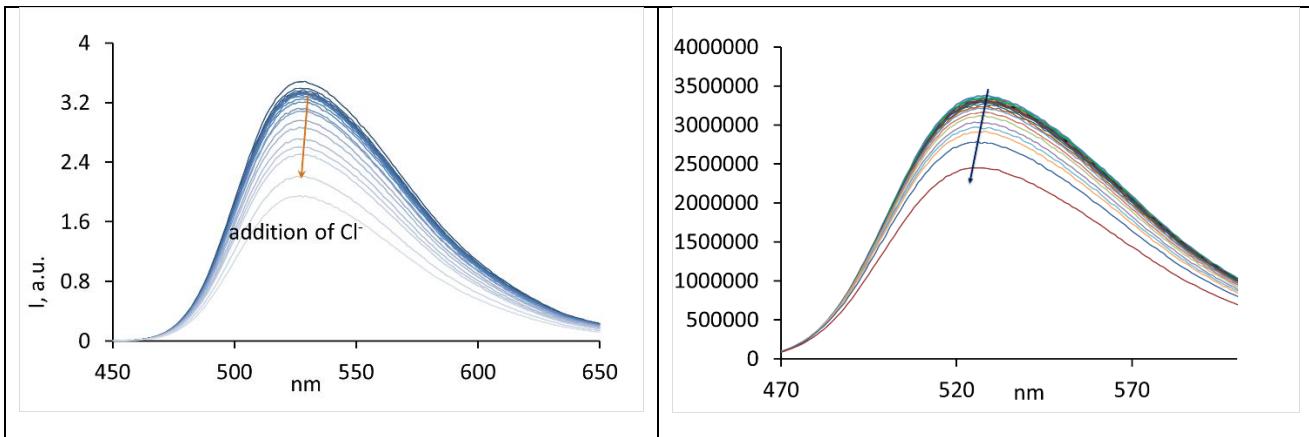




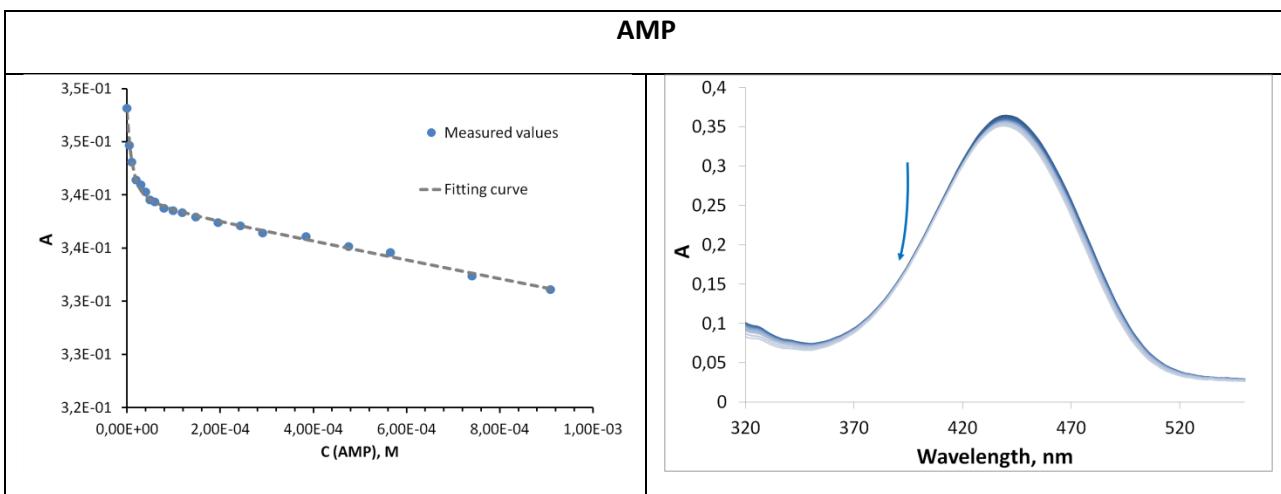
4.4. Absorption titration of 3 with anions

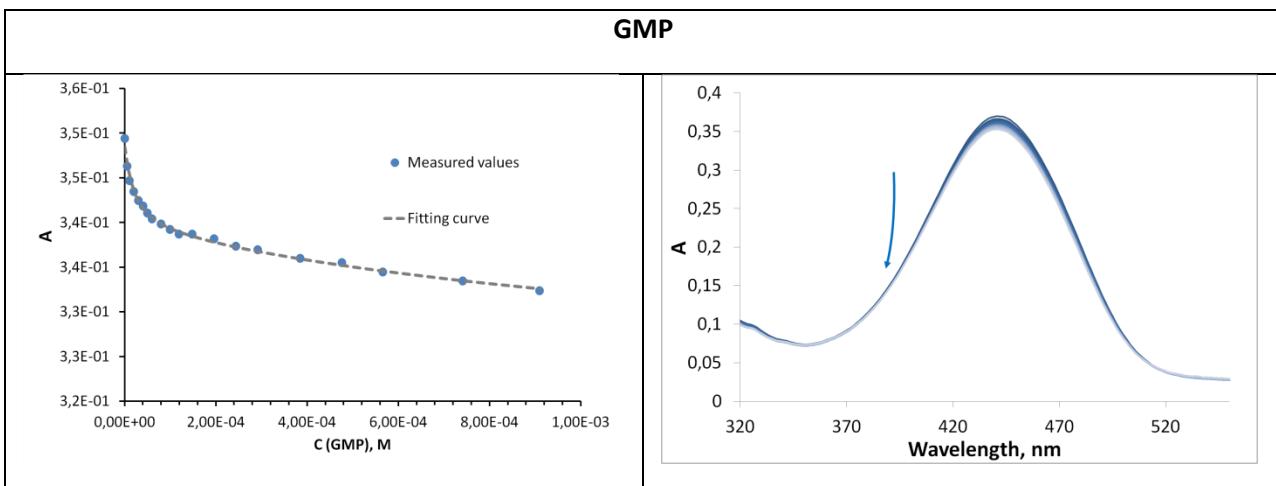
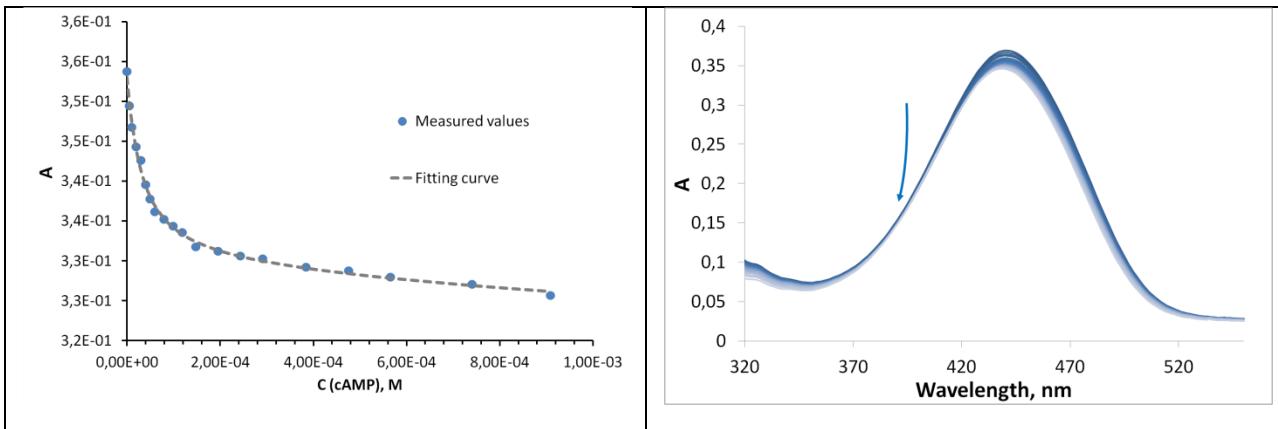


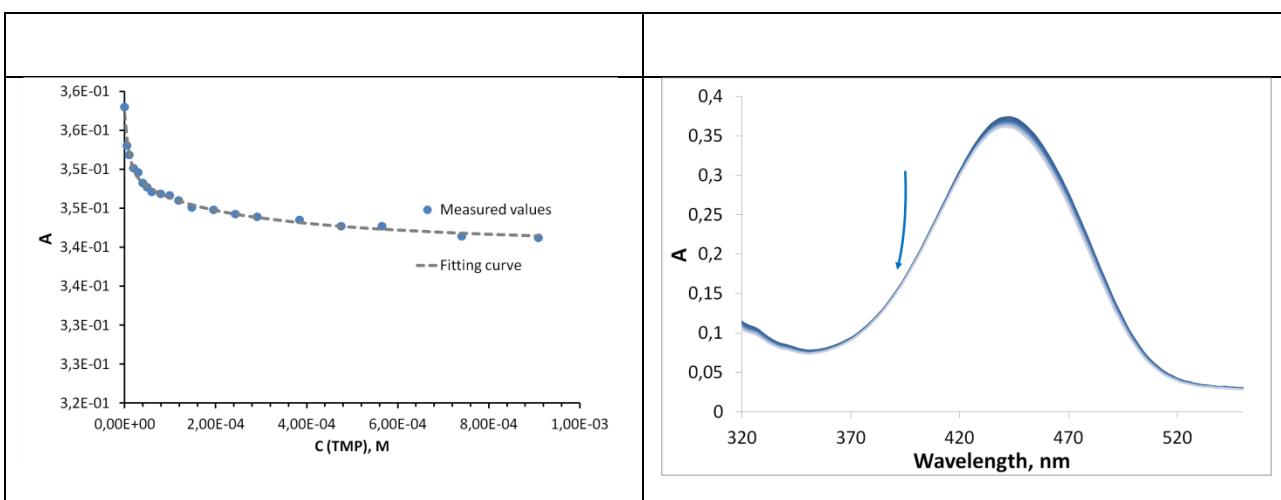
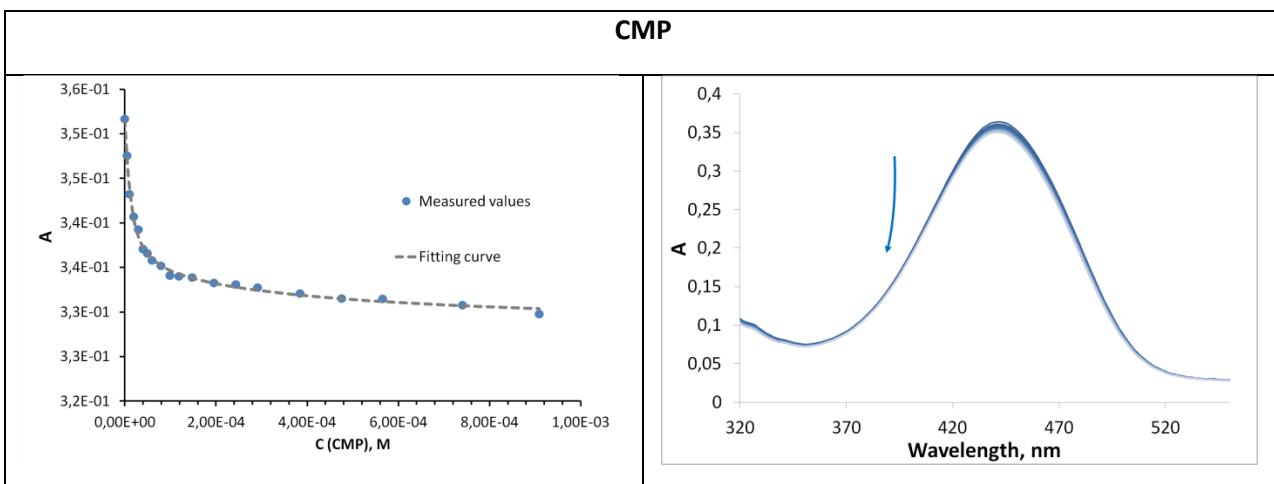
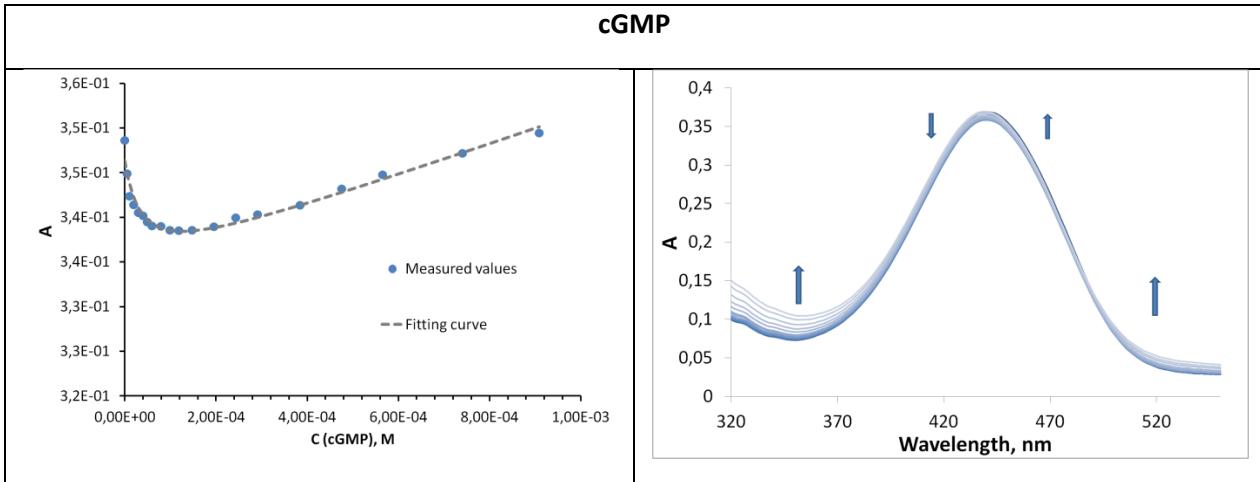


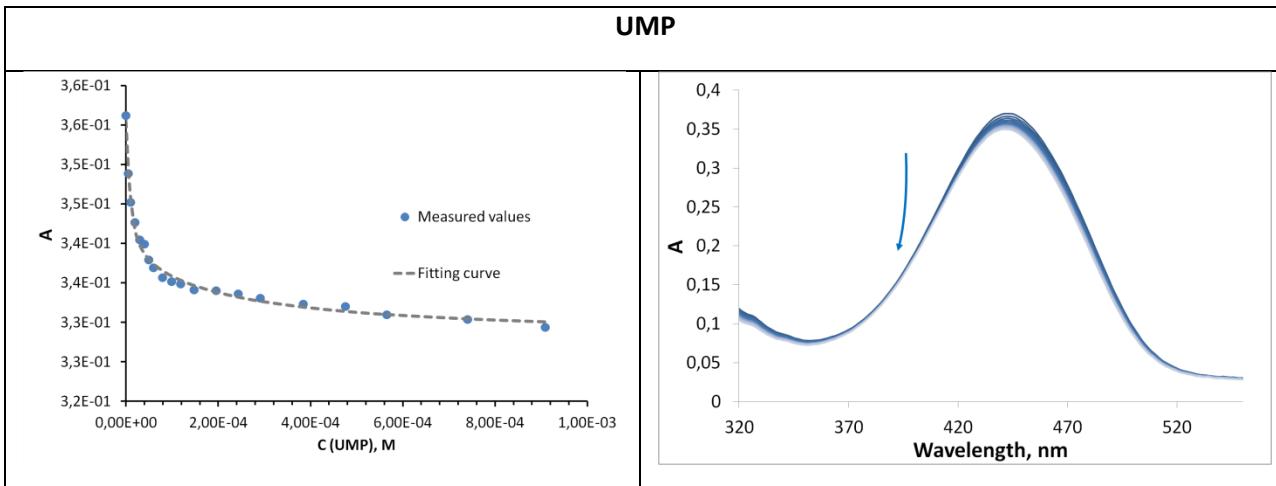


4.5. Absorption titration of 4 with nucleotides

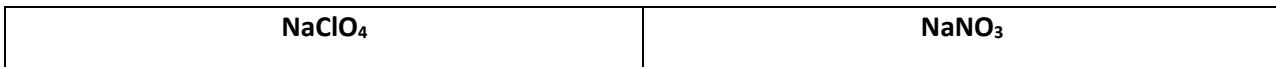
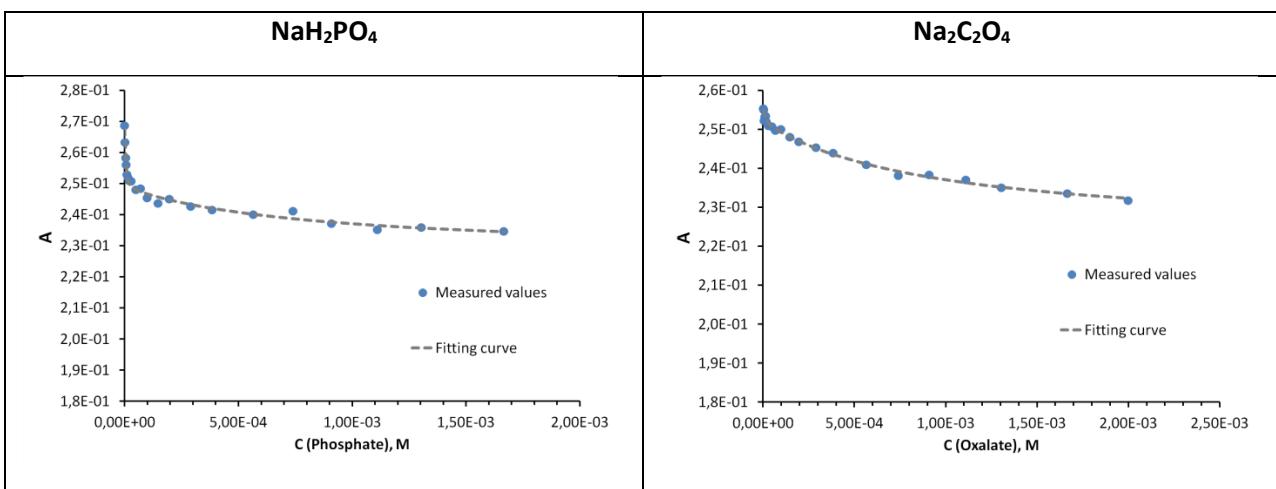
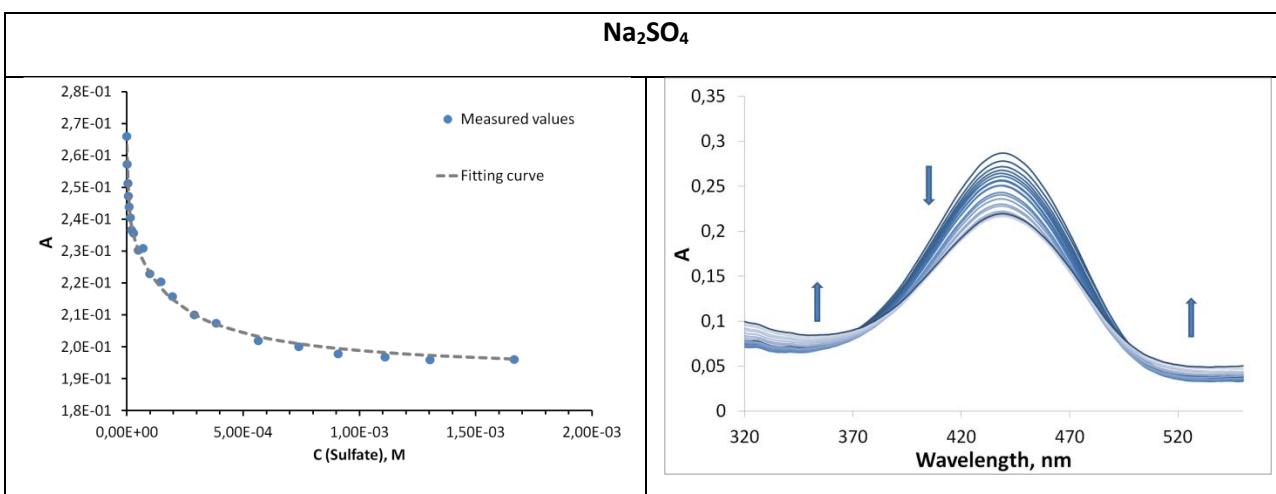


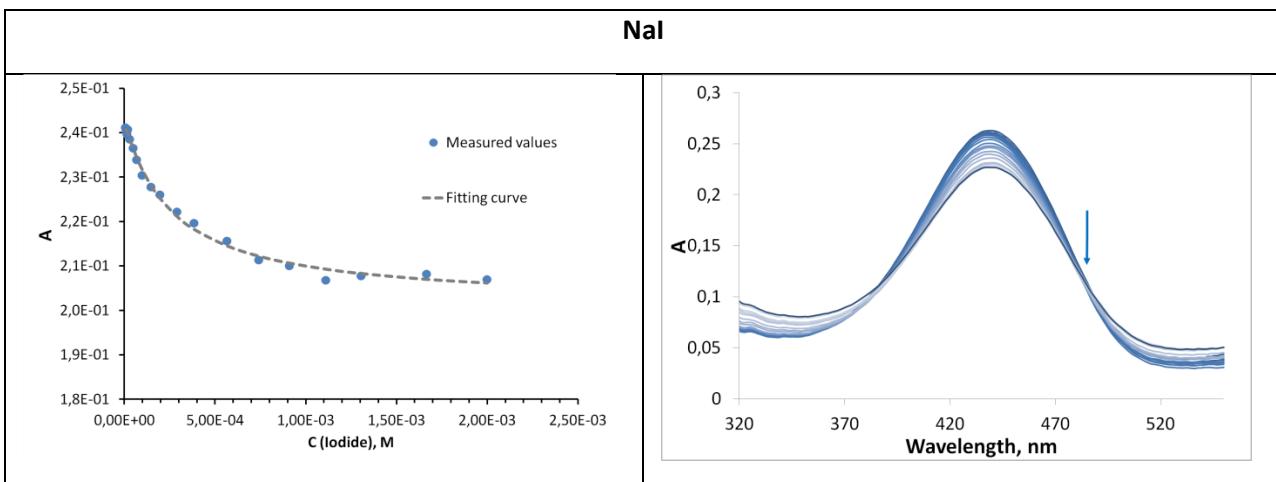
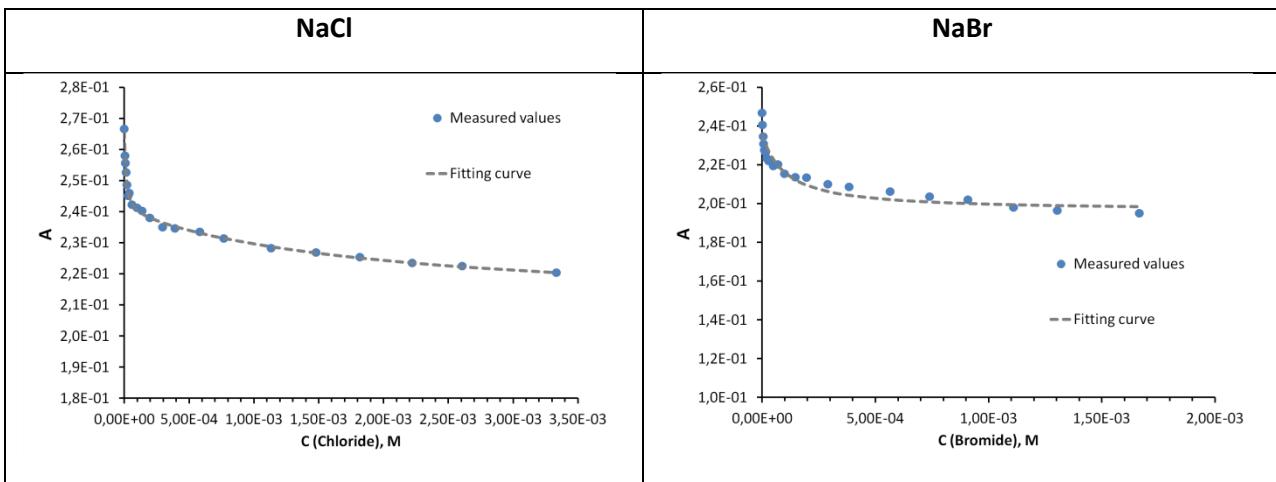
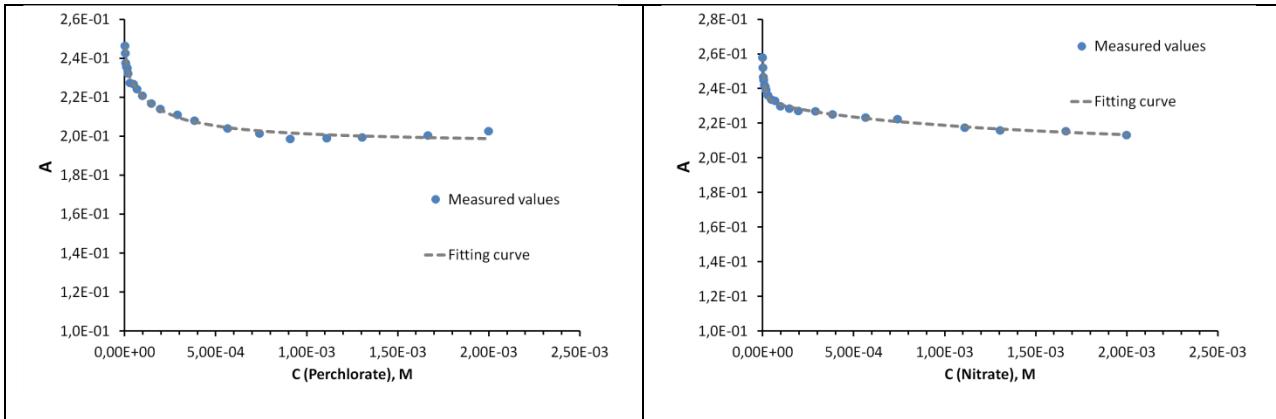






4.6. Absorption titration of 4 with anions





Job plots for the titrations experiments were constructed according to the classical method described by Cooper.¹ The second method to determine the stoichiometry is based on the best fit of the experimental data and described earlier by Jurczak.² The stock solution of compounds and anions with identical concentration (10^{-5} M) were mixed together producing different mol fractions of guest. Assuming that in this concentration range there is a linear relationship between absorbance intensity and concentration, one can predict the intensity of the receptor at each concentration as follows: $k = I_0/c_0$, where k is a coefficient; the predicted intensity I_c at concentration c will be $I_c = c*k$. The difference between the expected value and measured $D = I_{obs} - I_c$ is plotted versus mol fraction of the guest to find the maximum.

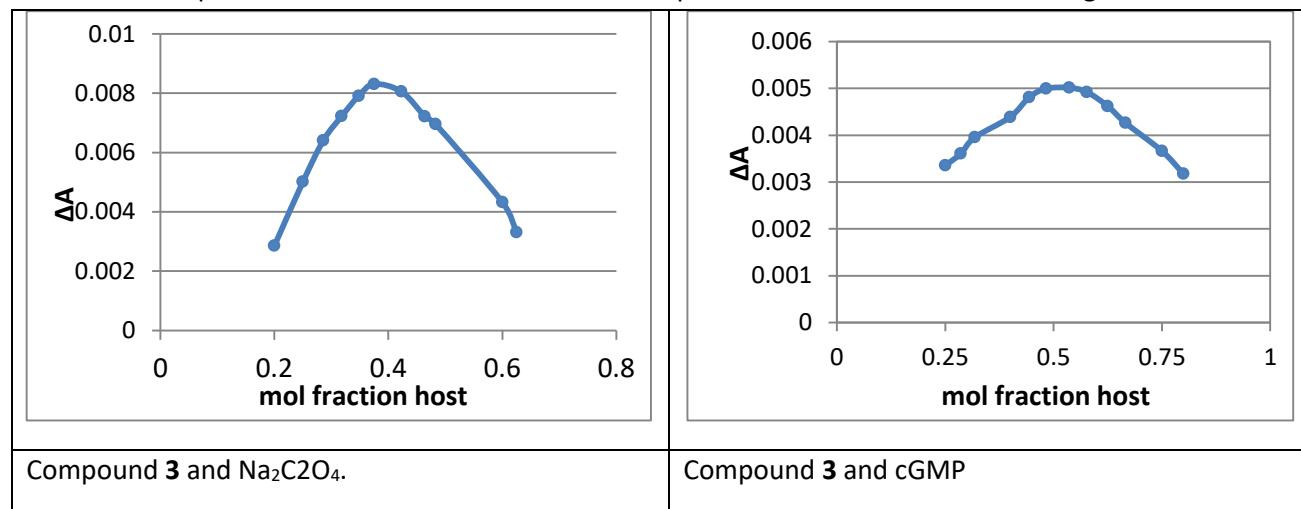


Figure S8. Selected Job plots.

4.7 Fluorescence titration of 4 with tetranucleotides

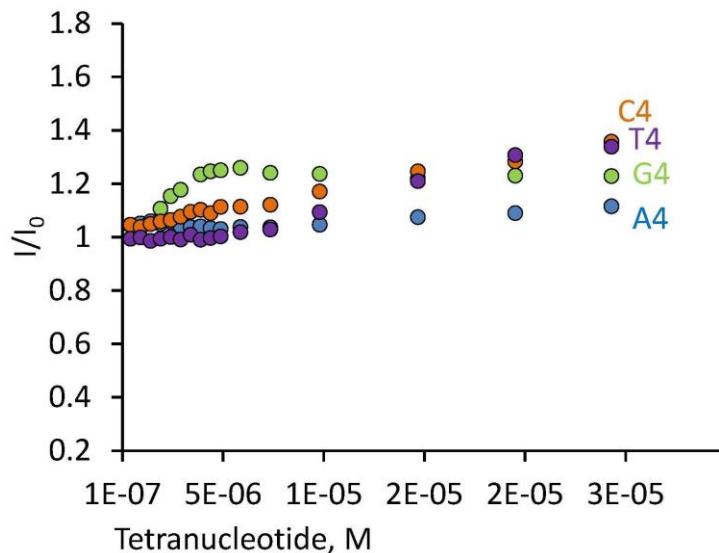


Figure S9. Changes in fluorescence intensity of **4** at 600 nm observed during the addition of tetranucleotides. Conditions: 50 mM acetate buffer (2% DMSO, pH 3.6, ex. 450 nm).

5. X-ray structure analysis.

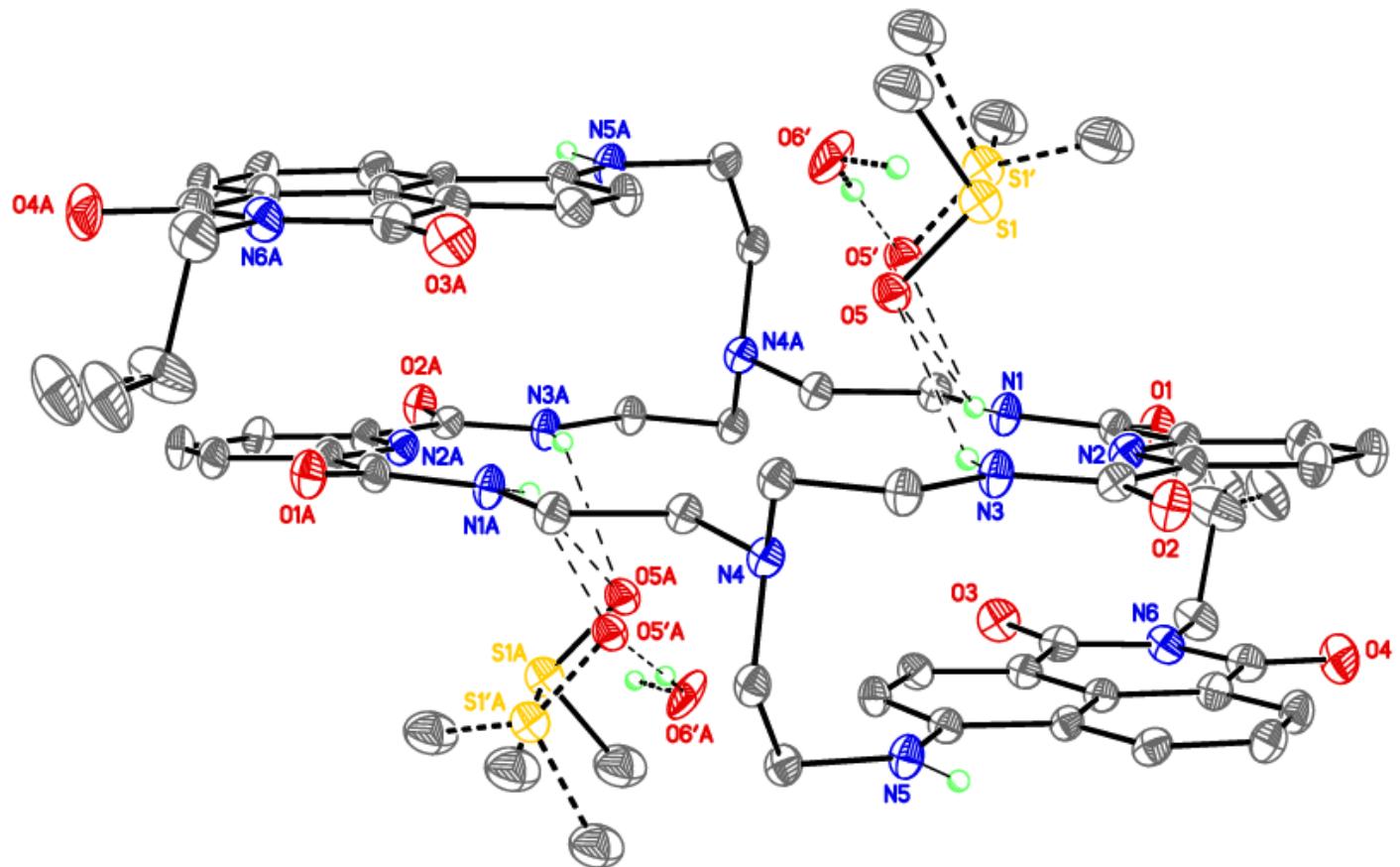
The single-crystal X-ray diffraction data for compounds **3**, $[\text{3H}_2]^{2+}[\text{SO}_4]^{2-}$, and **4** (from different solvents) were collected on the ‘Belok’ beamline of the National Research Center ‘Kurchatov Institute’ (Moscow, Russian Federation)

using a Rayonix SX165 CCD detector.³ In total, 720 frames were collected with an oscillation range of 1.0° in the φ scanning mode using two different orientations for each crystal. The semi-empirical correction for absorption was applied using the Scala program.⁴ The data were indexed and integrated using the utility iMOSFLM from the CCP4 software suite.^{3,5} For details, see Table 1. The structures were solved by intrinsic phasing modification of direct methods and refined by a full-matrix least-squares technique on F^2 with anisotropic displacement parameters for all non-hydrogen atoms. All investigated crystals contained solvate molecules of the corresponding solvents. The hydrogen atoms of the NH-groups as well as the solvate water and methanol molecules were localized in the difference-Fourier maps and included into the refinement within the riding model with fixed isotropic displacement parameters [$U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$, $1.2U_{\text{eq}}(\text{N})$, and $1.5U_{\text{eq}}(\text{O})$]. The other hydrogen atoms in all compounds were placed in calculated positions and refined within the riding model with fixed isotropic displacement parameters [$U_{\text{iso}}(\text{H}) = 1.5U_{\text{eq}}(\text{C})$ for the methyl groups and $1.2U_{\text{eq}}(\text{C})$ for the other groups]. All calculations were carried out using the SHELXTL program suite.⁶

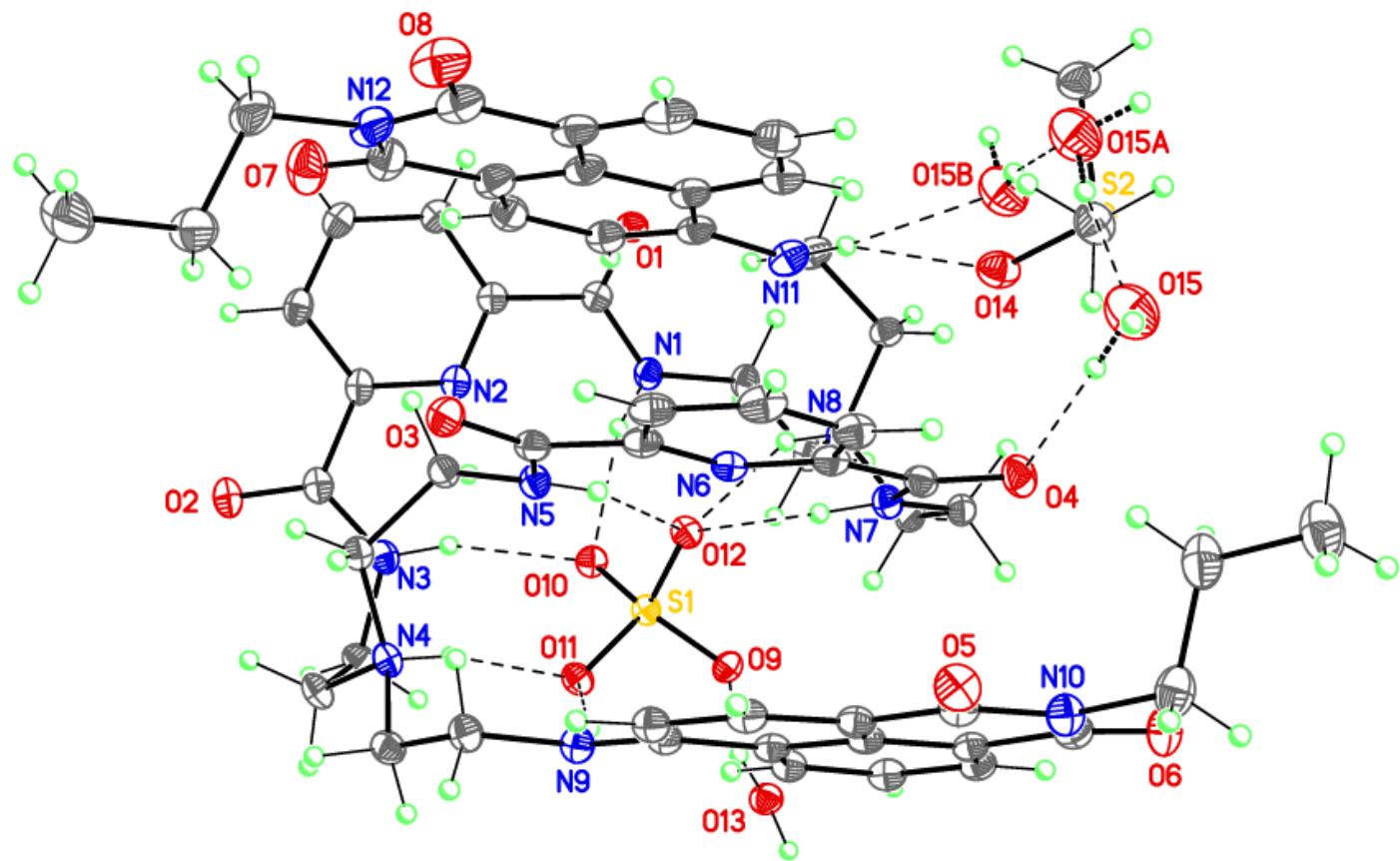
Table S2. Crystal data and structure refinement.

Compound	3 • 2DMSO • 0.3H₂O	[3H₂]²⁺[SO₄]²⁻ • ¾DMSO • ¼H₂O	4 • 3½DMSO • 2½CHCl₃	4 • 7¾CH₃OH • 1¼H₂O
Empirical formula	C ₆₀ H _{72.6} N ₁₂ O _{10.3} S ₂	C _{57.5} H ₇₀ N ₁₂ O _{14.5} S _{1.75}	C _{121.8} H ₁₄₅ N ₂₄ O _{19.8} S _{3.8} Cl _{6.6}	C _{119.75} H _{153.5} N ₂₄ O ₂₅
Formula weight	1190.82	1217.36	2617.82	2329.16
Temperature, K	100(2)	100(2)	100(2)	100(2)
λ , Å	0.96990	0.80246	0.96990	0.96990
Crystal system	Triclinic	Monoclinic	Triclinic	Triclinic
Space group	<i>P</i> $\bar{1}$	<i>C</i> 2/c	<i>P</i> $\bar{1}$	<i>P</i> $\bar{1}$
<i>a</i> , Å	11.232(2)	48.205(10)	13.580(3)	14.357(3)
<i>b</i> , Å	11.984(2)	10.714(2)	15.990(3)	15.749(3)
<i>c</i> , Å	12.359(3)	23.955(5)	16.320(3)	30.441(6)
α , deg.	93.83(3)	90	75.75(3)	84.29(3)
β , deg.	115.42(3)	117.53(3)	83.99(3)	77.01(3)
γ , deg.	94.22(3)	90	65.84(3)	63.61(3)
<i>V</i> , Å ³	1489.5(7)	10971(5)	3133.9(14)	6008(3)
<i>Z</i>	1	8	1	2
<i>D</i> _{calc} , g·cm ⁻³	1.328	1.474	1.387	1.287
Absorption coefficient, μ	0.358	0.230	0.677	0.193
<i>F</i> (000)	631	5144	1375.2	2480
Crystal size, mm	0.03×0.10×0.20	0.05×0.05×0.10	0.10×0.15×0.20	0.03×0.15×0.20
θ range for data collection	2.34 – 38.49	3.16 – 30.89	1.76 – 38.42	3.17 – 38.59
Index ranges	-13 < <i>h</i> < 14 -15 < <i>k</i> < 14 -15 < <i>l</i> < 11	-61 < <i>h</i> < 61 -13 < <i>k</i> < 13 -30 < <i>l</i> < 30	-17 < <i>h</i> < 16 -20 < <i>k</i> < 18 -20 < <i>l</i> < 19	-18 < <i>h</i> < 18 -19 < <i>k</i> < 19 -38 < <i>l</i> < 38

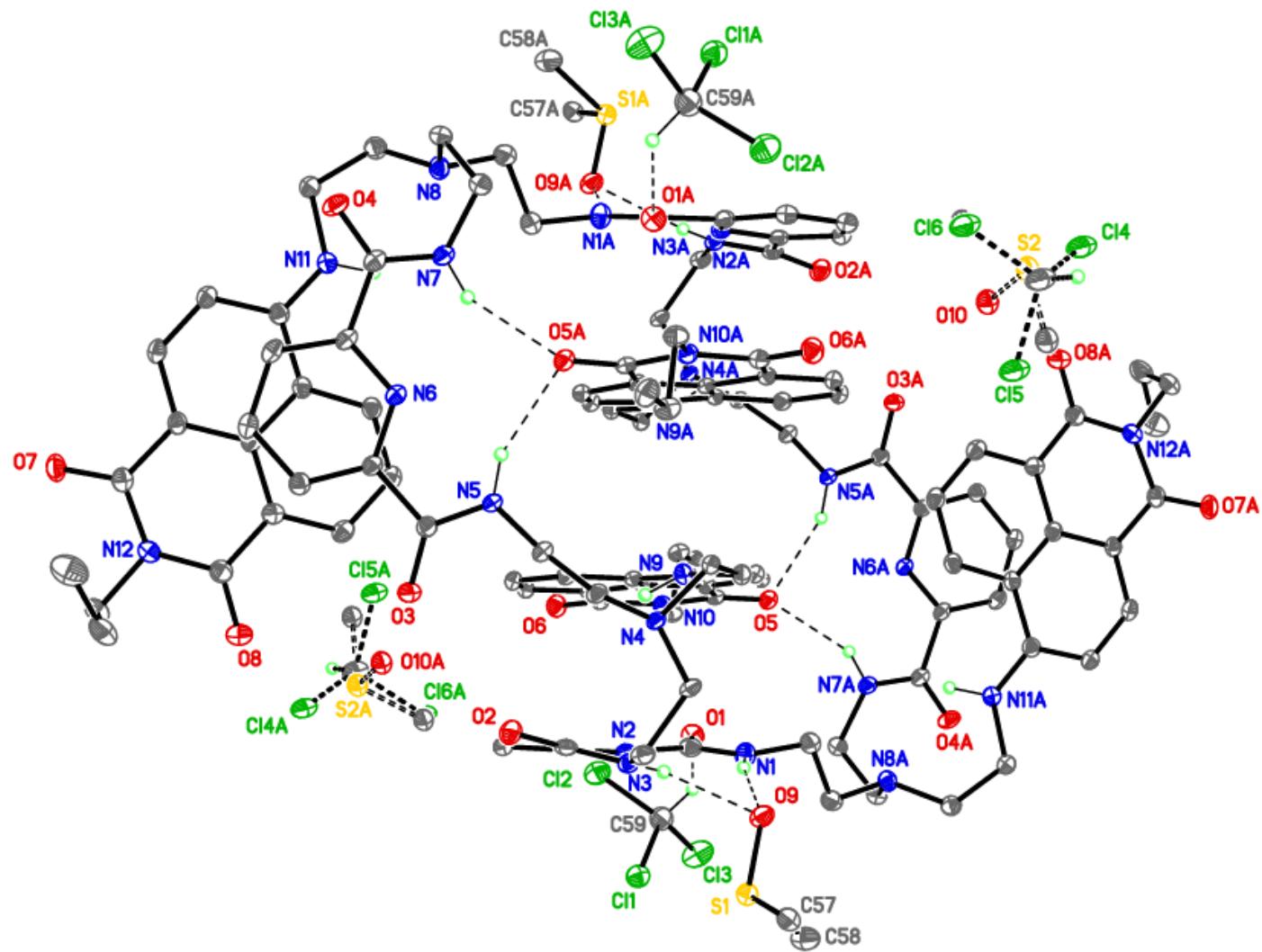
Reflections collected	15837	61869	45525	78233
Independent reflections, R_{int}	6030, 0.107	12004, 0.085	13089, 0.112	24936, 0.095
Reflections with $I > 2\sigma(I)$	3561	9231	9305	13670
Data / restraints / parameters	6030 / 12 / 404	12004 / 0 / 795	13089 / 12 / 800	24936 / 6 / 1559
R_1 [$I > 2\sigma(I)$]	0.065	0.070	0.073	0.091
wR_2 [all data]	0.172	0.180	0.189	0.204
Goodness-of-fit on F^2	1.003	1.045	1.032	1.023
Extinction coefficient	0.017(3)	0.00251(15)	0.0016(3)	0.00306(14)
T_{\min} / T_{\max}	0.920 / 0.980	0.970 / 0.980	0.860 / 0.930	0.950 / 0.980
$\Delta\rho_{\max} / \Delta\rho_{\min}$, e·Å ⁻³	0.377 / -0.437	0.765 / -0.551	0.653 / -0.983	0.461 / -0.530
Crystallization conditions	crystallized from DMSO concentrated solution over 5 days	crystallized from DMSO-water solution 1:5 in the presence of 3 equiv. of sulfuric acid	crystallized from DMSO concentrated solution over 5 days	crystallized from MeOH concentrated solution over 5 days

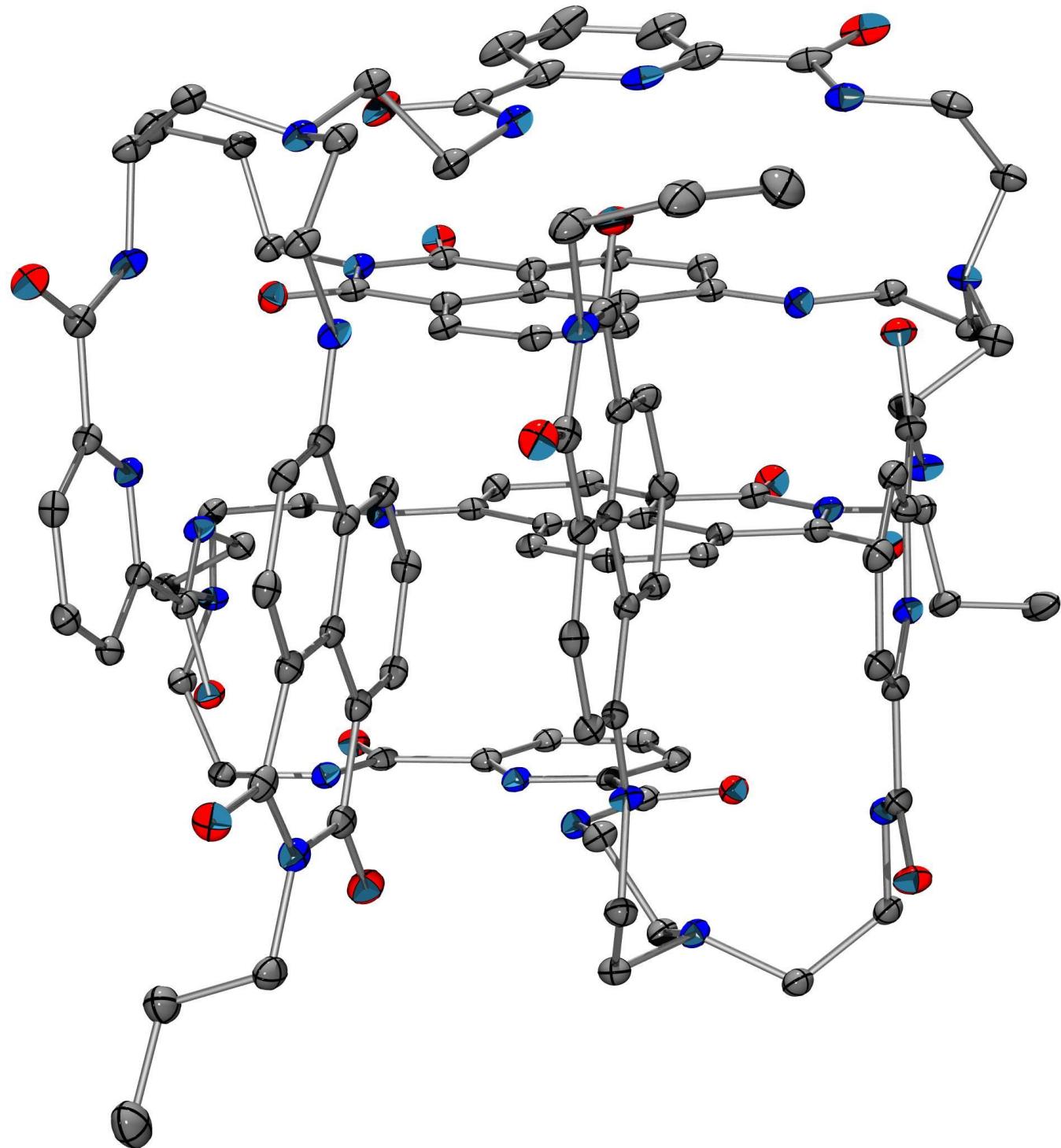


Thermal ellipsoid plot (ORTEP) diagrams for compound 3. Most hydrogen atoms are omitted for clarity.
Thermal ellipsoids are shown at the 50% probability level.



Thermal ellipsoid plot (ORTEP) diagrams for compound **3**·H₂SO₄. Thermal ellipsoids are shown at the 50% probability level.





Thermal ellipsoid plot (ORTEP) diagrams for compound **4** crystallized from MeOH. Most hydrogen atoms and solvent molecules are omitted for clarity. Thermal ellipsoids are shown at the 50% probability level.

6. References

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- (4) Evans, P. Scaling and assessment of data quality. *Acta Crystallographica Section D-Structural Biology* **2006**, *62*, 72.
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