Synthesis and photophysical evaluation of a pyridinium 4-amino-1,8-naphthalimide derivative that upon intercalation displays preference for AT-rich double stranded DNA

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The association constant, K for the binding of mononucleotide 5'-monophosphate with $\mathbf{1}$ was determined from the slope of Scatchard plot using the equation 1.¹

$$\frac{\Delta A}{[NI][XMP]} = K\Delta\epsilon - K\frac{\Delta A}{[NI]}$$
(1)

 ΔA is the change in absorbance of **1** at 435 nm in the presence of mononucleotide XMP, $\Delta \epsilon = (\epsilon_f - \epsilon_b)$. ϵ_f and ϵ_b are the molar extinction coefficients of free and bound naphthalimide, respectively. [NI], [XMP] refer to the total concentration of naphthalimide and mononucleotide respectively.

The binding constant for the association of 1 with GMP was also determined assuming 1:1 complex formation using equation 2.²

$$\frac{\Delta A}{[NI]} = \frac{K\Delta\varepsilon[GMP]}{1 + K[GMP]}$$
(2)

The binding constant for the association of 1 with AMP was estimated from equation 3 assuming both 1:1 and 1:2 complex formations.³

$$\frac{\Delta A}{[NI]} = \frac{K_1 \,\Delta \epsilon_1 [AMP] + K_1 K_2 \Delta \epsilon_2 [AMP]^2}{1 + K_1 [AMP] + K_1 K_2 [AMP]^2} \tag{3}$$

The absorbance change at 435 nm was analysed and fitted to the noncooperative model of McGhee and von Hippel described in equation 4 using the non-linear curve fitting algorithm in OriginPro 8 softwareto determine the binding constant, K, where *r* is the binding density and given by $r = C_b/\text{total DNA}$ concentration and *n* is the average no of occupied sites, C_f and C_b are the concentrations of free and bound ligand, respectively.⁴

$$= K(1) - nr) \left[\frac{1 - nr}{1 - (n - 1)r} \right]^{n - 1}$$
(4)

 C_b and C_f were calculated from the absorbance data using the equations 5 and 6, respectively.

(5)

$$C_b = \frac{\mathrm{Af} - \mathrm{A}}{\mathrm{Af} - \mathrm{Ab}} \tag{6}$$

 $C_f = C - C_b$

 A_f and A_b are the absorbance values corresponding to free and fully bound ligand. A is the absorbance of the mixture at any point during titration and C is the total ligand concentration.



Figure ESI 1B: ¹³C-NMR of 3 in DMSO-d6 (400 MHz)



Figure ESI 1C: ¹H-NMR of 4 in DMSO-d6 (400 MHz)





Figure ESI 1E: ¹H-NMR of 1 in DMSO-d6 (600 MHz)



Figure ESI 1D: ¹³C-NMR of 4 in DMSO-d6 (400 MHz)



Figure ESI 1F:13-C NMR of 1 in DMSO-d6 (150 MHz)

Figure ESI 2: (a) UV/vis absorption and (b) emission of **1** in water containing 10 mM NaCl as a function of pH. Insets: Normalised absorbance or fluorescence intensity as a function of pH



(b) Plot of chemical shift (δ) *vs.* log(naphthalimide concentration) (Assuming no aggregation at 0.001 M, chemical shift for each proton has been normalized using the equation (δ - δ at 0.001 M)/ δ at 0.001 mM)

Н	δin 10 mM	δ in 1 mM	δ in 0.1 mM	δ in 0.01 mM	δ in 0.001 mM
2	7.56	7.88	8.05	8.18	8.18
3	6.46	6.72	6.85	6.93	6.93
5	7.91	8.23	8.37	8.42	8.43
6	7.26	7.50	7.61	7.68	7.68
7	7.84	8.14	8.31	8.42	8.42
9	4.43	4.59	-	-	-
10	4.80	4.88	-	-	-
11	8.74	8.76	8.79	8.82	8.82
12	7.89	7.88	7.90	7.92	7.92
13	8.46	8.46	8.48	8.47	8.48

Table 1: Summary of chemical shifts at various concentration of 1

Identification code	sb07		
Empirical formula	$C_{19}H_{16}F_6N_3O_2P$		
Formula weight	463.32		
Temperature	112(2) K		
Wavelength	0.71073 Å		
Crystal system	Monoclinic		
Space group	P2(1)/c		
Unit cell dimensions	$a = 9.4536(19) \text{ Å} \qquad \alpha = 90^{\circ}.$		
	b = 9.3865(19) Å	$\beta = 100.03(3)^{\circ}$.	
	c = 21.293(4) Å	$\gamma = 90^{\circ}$.	
Volume	1860.6(7) Å ³	•	
Z	4		
Density (calculated)	1.654 Mg/m^3		
Absorption coefficient	0.230 mm ⁻¹		
F(000)	944		
Crystal size	0.63 x 0.44 x 0.43 mm ³		
Theta range for data collection	2.19 to 25.00°.		
Index ranges	-11<=h<=10, -7<=k<=11, -16<=l<=25		
Reflections collected	6793		
Independent reflections	3184 [R(int) = 0.0428]		
Completeness to theta = 25.00°	97.2 %		
Absorption correction	Semi-empirical from equivalents		
Max. and min. transmission	1.0000 and 0.5575		
Refinement method	Full-matrix least-squares on F ²		
Data / restraints / parameters	3184 / 0 / 282		
Goodness-of-fit on F ²	1.085		
Final R indices [I>2sigma(I)]	R1 = 0.0548, wR2 = 0.1447		
R indices (all data)	R1 = 0.0600, wR2 = 0.1512		
Largest diff. peak and hole	0.721 and -0.408 e.Å ⁻³		

Table 2. Crystal data and structure refinement for **1**.

References

- 1. G. Scatchard, Proc. New York Acad. Sci., 1949,51, 660
- 2. D. A. Deranleau, J.Am. Chem. Soc. 1969,91, 4044.
- 3. D. A. Deranleau, J.Am. Chem. Soc. 1969,91, 4050.
- 4. J. D. McGhee and P.H. von Hippel, J.Mol.Biol. 1974, 86, 469.