

# Recognition and discrimination of DNA quadruplexes by acridine-peptide conjugates

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Page 2 – **Table S1.** Amino acid analysis and mass spectrometry of peptides **7 – 21**.

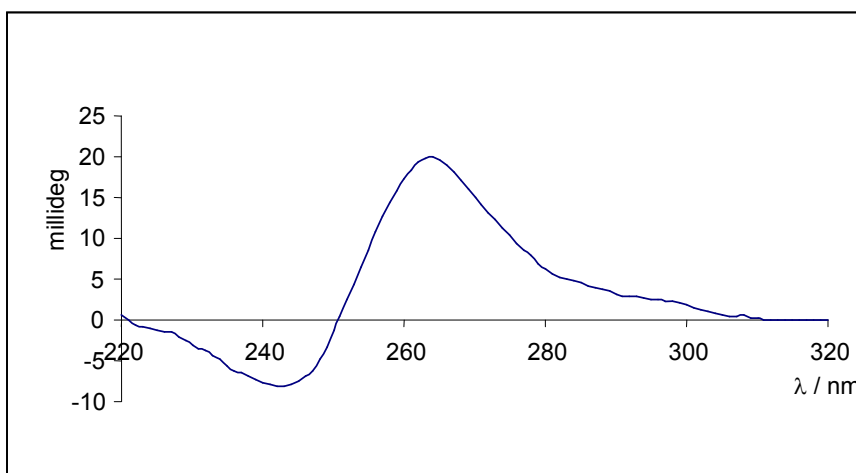
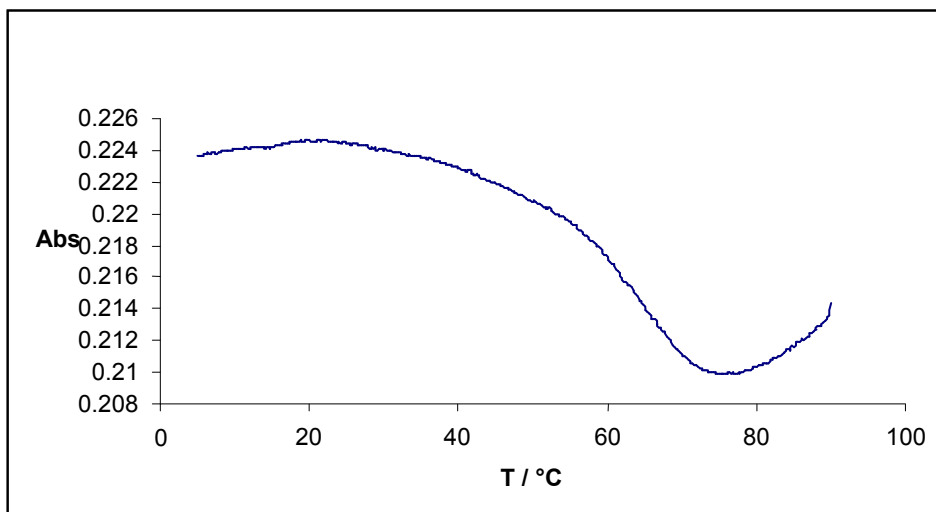
Page 3 – **Figure S1.** CD spectrum and UV thermal melt of *N-ras* DNA quadruplex.

Page 4 – **Table S2.**  $T_m$  of *N-ras* as a function of cation type and  $K^+$  concentration.

Compound	Observed $m/z$	r.t./min	Amino acid analysis mol.mol <sup>-1</sup> (std devn)
7	912.4 [M+2H] <sup>2+</sup> 608.7 [M+3H] <sup>3+</sup>	22.7 <sup>a</sup>	F 2.04 (0.02), H 2.06 (0.00), R 3.90 (0.02)
8	843.0 [M+2H] <sup>2+</sup> 562.3 [M+3H] <sup>3+</sup>	17.7 <sup>a</sup>	S 1.92 (0.02), K 2.16 (0.00), R 3.94 (0.02)
9	827.0 [M+2H] <sup>2+</sup> 552.0 [M+3H] <sup>3+</sup>	19.2 <sup>a</sup>	V 1.98, K 4.00 (0.02), R 2.02 (0.02)
10	1190.6 [M+H] <sup>+</sup> 596.2 [M+2H] <sup>2+</sup>	19.6 <sup>b</sup>	F 1.03 (0.01), H 1.02 (0.01), R 1.94 (0.02)
11	1190.6 [M+H] <sup>+</sup> 596.0 [M+2H] <sup>2+</sup>	19.0 <sup>b</sup>	F 1.05 (0.00), H 1.04 (0.00), R 1.91 (0.00)
12	1190.7 [M+H] <sup>+</sup> 596.2 [M+2H] <sup>2+</sup>	19.5 <sup>b</sup>	F 1.00 (0.00), H 0.98 (0.01), R 2.02 (0.02)
13	562.0 [M+2H] <sup>2+</sup> 375.3 [M+3H] <sup>3+</sup>	16.4 <sup>b</sup>	S 0.96 (0.12), K 0.98 (0.09), R 2.07 (0.21)
14	1121.6 [M+H] <sup>+</sup> 561.5 [M+2H] <sup>2+</sup>	15.3 <sup>b</sup>	S 1.06 (0.00), K 1.05 (0.00), R 1.89 (0.00)
15	1122.1 [M+H] <sup>+</sup> 562.0 [M+2H] <sup>2+</sup>	12.3 <sup>b</sup>	S 0.98 (0.00), K 1.05 (0.01), R 1.97 (0.01)
16	596.7 [M+2H] <sup>2+</sup>	20.2 <sup>b</sup>	F 1.04 (0.03), H 0.98 (0.03), R 1.97 (0.06)
17	1192.6 [M+H] <sup>+</sup> 596.6 [M+2H] <sup>2+</sup>	19.2 <sup>b</sup>	F 1.05 (0.00), H 1.03 (0.01), R 1.92 (0.01)
18	1191.6 [M+H] <sup>+</sup> 596.7 [M+2H] <sup>2+</sup>	19.5 <sup>b</sup>	F 1.00 (0.01), H 1.02 (0.01), R 1.98 (0.02)
19	562.1 [M+2H] <sup>2+</sup>	16.5 <sup>b</sup>	S 0.89 (0.01), K 1.19 (0.03), R 1.93 (0.02)
20	1122.7 [M+H] <sup>+</sup> 562.0 [M+2H] <sup>2+</sup>	15.6 <sup>b</sup>	S 1.01 (0.00), K 1.06 (0.00), R 1.93 (0.00)
21	1123.1 [M+H] <sup>+</sup> 562.4 [M+2H] <sup>2+</sup>	14.2 <sup>b</sup>	S 0.98 (0.00), K 1.04 (0.00), R 1.98 (0.00)

HPLC methods: Solvent A = H<sub>2</sub>O, 0.1% TFA, solvent B = MeCN, 0.1% TFA. Phenomenex C18 Luna 5  $\mu$ M, 250  $\times$  4.6 mm column, flow rate 1 mL min<sup>-1</sup>. UV detection at 220 nm. Gradient <sup>a</sup>0 – 2.5 min 5% B, 32.5 min 40% B. <sup>b</sup>0 – 2.5 min 10% B, 32.5 min 40% B.

**Table S1.** Amino acid analysis and mass spectrometry of peptides 7 – 21.



**Figure S1.** UV thermal melt and circular dichroism spectrum of *N-ras*. a) UV thermal melt at 295 nm of the *N-ras* (4  $\mu$ M unbiotinylated oligonucleotide) in 100 mM KCl, 10 mM Tris-HCl, pH 7.4. Melting temperature,  $T_m = 61$   $^{\circ}$ C, calculated as the point where the second derivative of the curve is zero.  $T_m$  was found to be independent of oligonucleotide concentration over the range 2 – 10  $\mu$ M. b) Circular dichroism spectrum of *N-ras* (4  $\mu$ M unbiotinylated oligonucleotide in 10 mM Tris-HCl, 100 mM KCl, pH 7.4, 4  $^{\circ}$ C).

a)

[K <sup>+</sup> ] mM	$T_m$ °C
0	<sup>a</sup>
10	43
50	60
100	65
200	72

<sup>a</sup> No melting transition observed.

b)

Cation	$T_m$ °C
K <sup>+</sup>	66
Na <sup>+</sup>	34.2
Li <sup>+</sup>	<sup>a</sup>
NH <sub>4</sub> <sup>+</sup>	<sup>a</sup>

<sup>a</sup> No melting transition observed.

**Table S2.** a)  $T_m$  of *N-ras* (4 μM in 10 mM Tris-HCl, pH 7.4) as a function of KCl concentration. b)  $T_m$  of *N-ras* (4 μM in 10 mM Tris-HCl, pH 7.4) as a function of monovalent cation, supplied as 100 mM chloride salt.