Formation of Adenine-N3/Guanine-N7 Cross-Link in the Reaction of *trans*-Oriented Platinum Substrates with Dinucleotides.

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Supporting Information

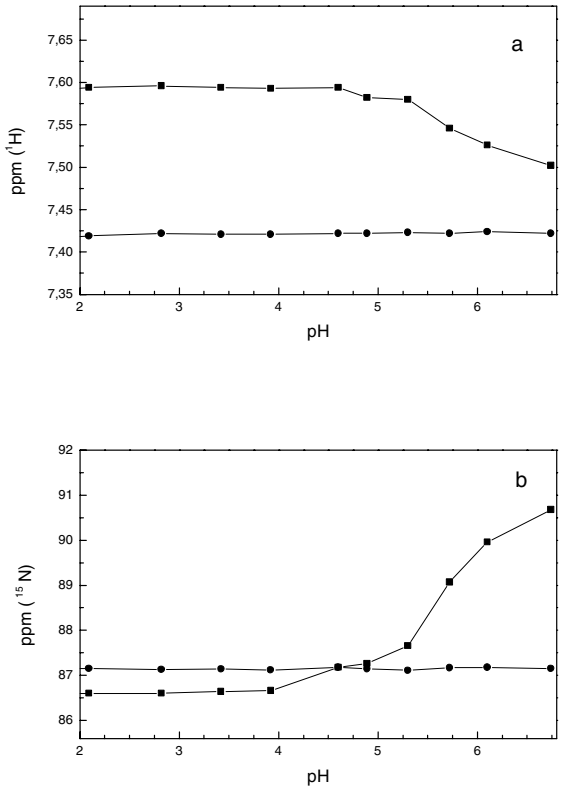
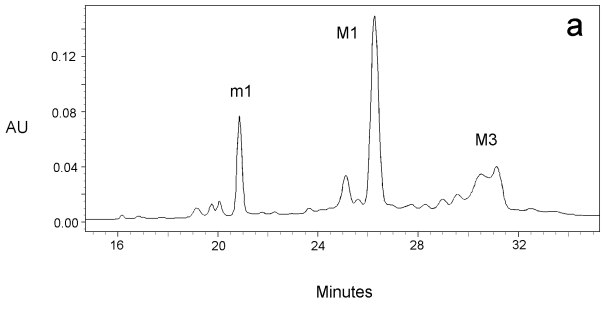


Figure S1. 1H (a) and 15N (b) chemical shifts *versus* pH for the iminic group (=N-H) of 15N labelled *trans-EE* measured by HMQC. (●) dichloro species; (•) solvated species.



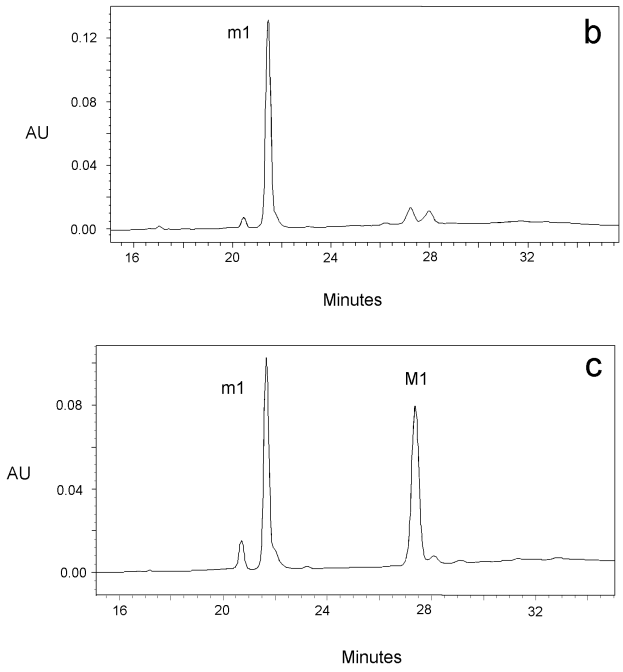


Figure S2. HPLC profiles for the reaction between d(GpA) and *trans-EE.* (a) species distribution after 14 days; (b) purified m1 species; (c) conversion of m1 to M1 by addion of 1 M NaCl. No formation of M2 chelate has been detected.

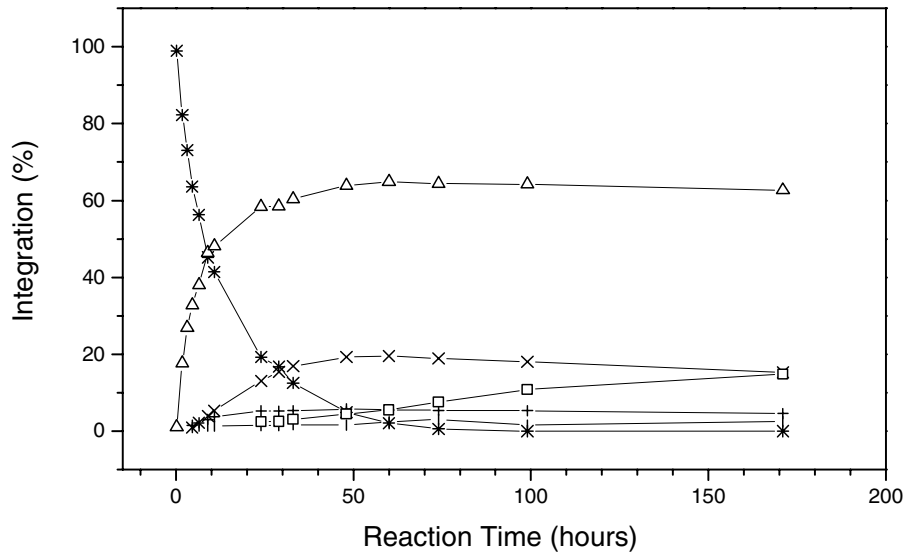


Figure S3. Species distribution in the reaction of *trans-EE* with d(GpA) at pH 4.0 monitored by HPLC.

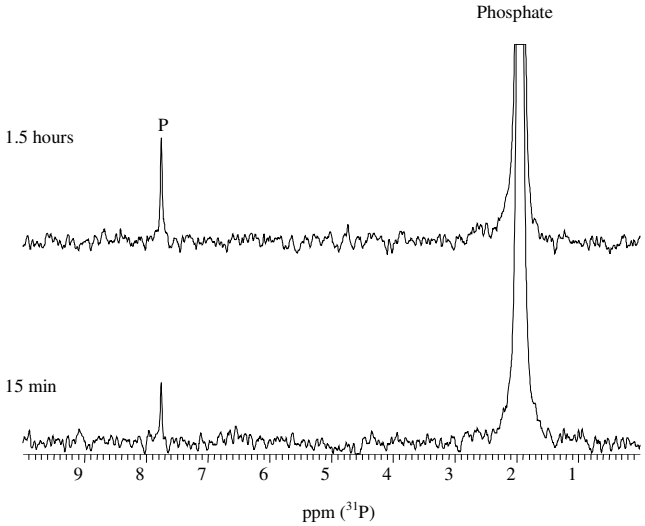


Figure S4. 31P NMR spectra of *trans-EE* in 20 mM phosphate buffer at 298 K. The reaction time is labeled in the figure. The appearance of peak P indicates formation of a phosphate adduct of *trans-EE*.

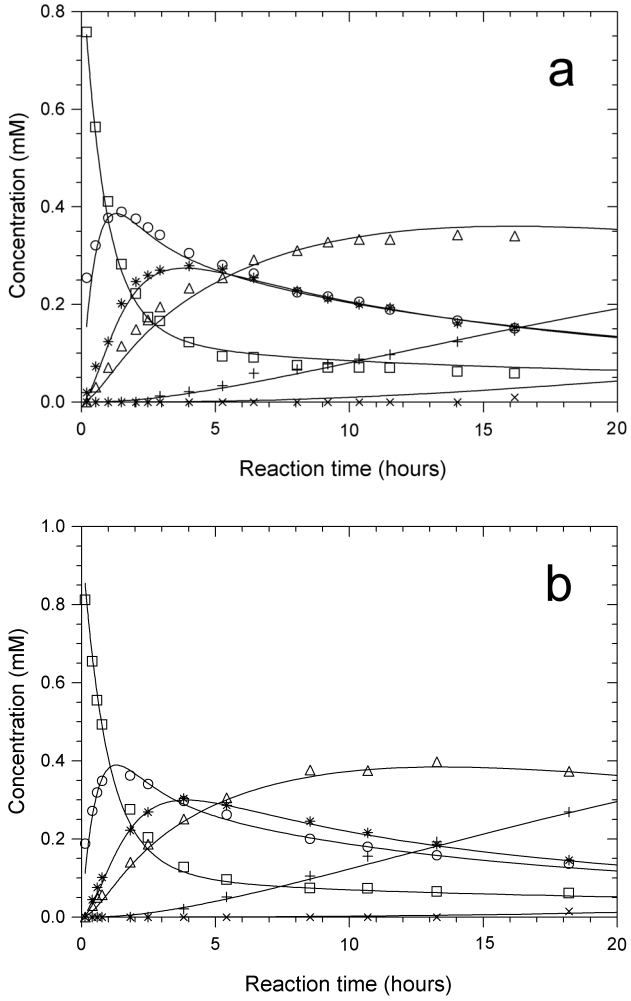


Figure S5. Species distribution (NMR data) and theoretically fitted curves for the reaction of *trans-EE* with d(ApG) (a) and d(GpA) (b) in 20 mM phosphate buffer. Symbols: (•) *trans-EE*; (o) *trans-EE* monochloro/monoaqua; (Δ) M1; (+) m1; (*) *trans-EE* monochloro/monophosphate; (×) *trans-EE* G-N7/monophosphate or A-N7/monophosphate.

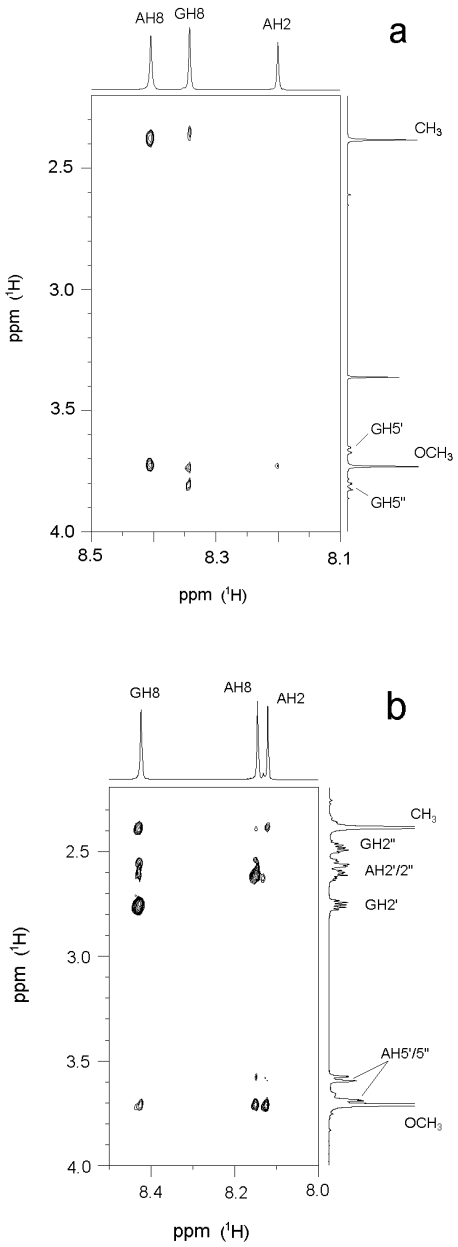


Figure S6. 1H ROESY NMR spectra of M1. (a) *trans-EE*/r(ApG) M1 adduct, (b) *trans-EE*/d(ApG) M1 adduct.

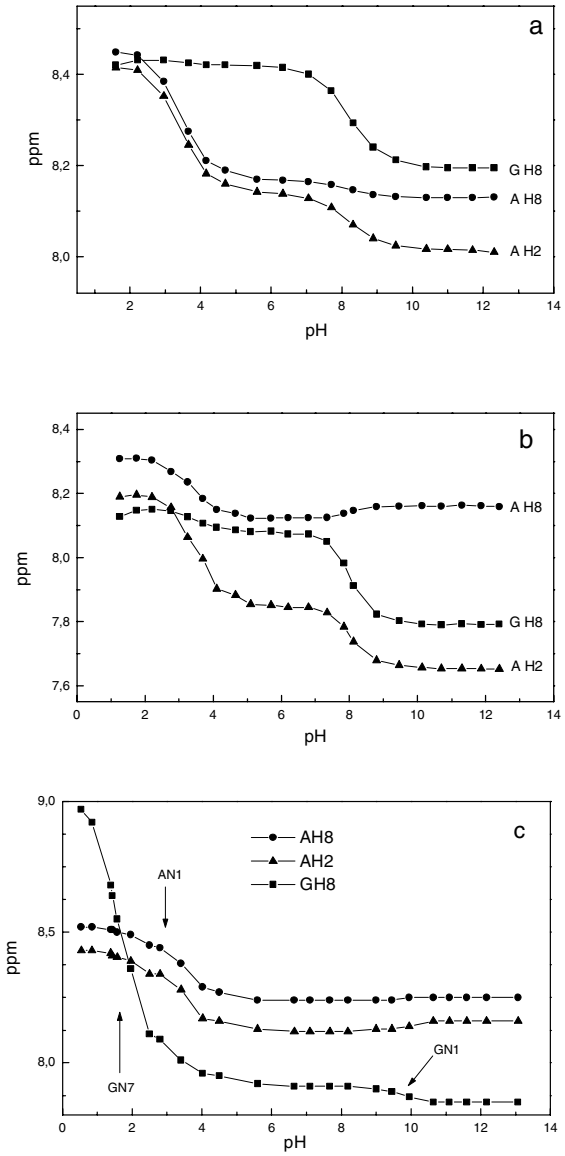


Figure S7. 1H NMR chemical shifts versus pH for A-H8, G-H8 and A-H2. (a) d(ApG) adduct M1; (b) d(GpA) adduct M1; (c) free r(ApG). In Figure (c) the (de)protonation sites are labelled with the corresponding N atom.

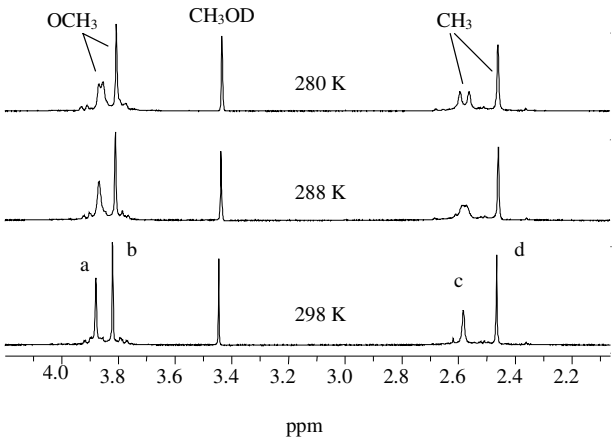


Figure S8. Selected region of 1D NMR spectra of the HPLC M3 fraction of r(ApG) at various temperatures. The resonances marked (a, c) and (b, d) are assigned to the adenine and guanine residues, respectively. (the ppm scale is correct for T = 298 K). 1M NaCl was added to the fraction in order to simplify the spectra by reducing the amount of aqua species.

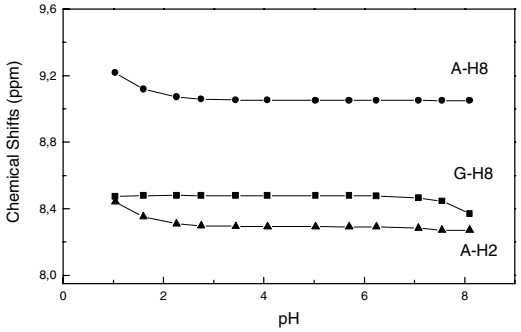


Figure S9. 1H NMR chemical shifts versus pH for A-H8, G-H8, and A-H2 in the r(ApG) adduct M3. This adduct is extremely unstable in basic condition and decomposes at pH > 8.

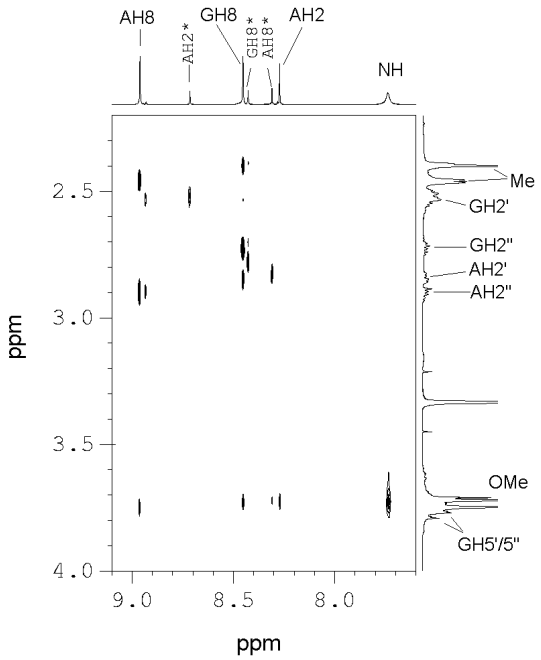


Figure S10. 1H ROESY NMR spectra of d(ApG) adducts M3 and M3'. The major species M3 has G-N7/A-N7 binding while the minor species M3'has G-N7/A-N1 binding. Peaks from the latter species are marked (∗) in the 1D spectrum.

Table S1. Chemical shifts of *trans-EE*/dinucleotide monofunctional adducts M1 at pH 4. The difference in chemical shift with respect to the free nucleotides is reported in parenthesis

	r(ApG) M1 298 K	d(ApG) M1 280 K	d(GpA) M1 298 K
AH8	8.34(0.05)	8.15(0.09)	8.45(0.11)
AH2	8.20(0.02)	8.12(0.02)	8.24(0.04)
GH8	8.40(0.48)	8.43(0.48)	8.33(0.60)
AH1'	6.03(0.10)	6.30(0.14)	6.50(0.13)
GH1'	5.91(0.12)	6.20(0.19)	6.15(0.18)
AH2'	4.96(0.27)	2.63(0.07)	2.85(0.01)
AH2"	-	2.55(0.28)	2.64(0.09)
GH2'	4.69(0.06)	2.76(0.08)	2.51(0.17)
GH2"	-	2.49(0.11)	2.51(0.40)
AH3'	4.81(0.15)	4.87(0.09)	4.74(-0.06
GH3'	4.45(-0.02)	4.69(-0.03	4.74(-0.01
AH4'	4.41(0.09)	4.21(0.01)	4.29(0.04)
GH4'	4.35(0.05)	4.21(0.06)	4.19(0.04)
AH5'	3.81(0.0)	3.69(0.02)	4.13(0.02)
AH5"	3.67(-0.1)	3.59(-0.08	4.12(0.01)
GH5'	4.35(-0.07)	4.18(0.05)	3.74(0.06)
GH5"	4.28(0.13)	4.18(0.11)	3.70(0.02)
OCH3	3.73	3.71	3.80
CH3	2.38	2.39	2.50

Table S2. Chemical shifts of binuclear adducts M3 (pH = 4, 280 K)

	r(ApG) M3	d(ApG) M3 (AN7/GN7)	d(ApG) M3* (AN1/GN7)
AH8	9.06(0.82)	8.96(0.90)	8.31(0.25)
AH2	8.29(0.22)	8.27(0.17)	8.71(0.61)
GH8	8.46(0.60)	8.45(0.50)	8.43(0.49)
AH1’	6.18(0.31)	6.53(0.37)	6.41(0.25)
GH1’	5.94(0.21)	6.27(0.26)	6.25(0.23)
AH2’	5.01(0.37)	2.91(0.35)	2.82(0.26)
AH2”	—	2.83(0.56)	2.70(0.43)
GH2'	4.65(0.07)	2.73(0.05)	ND
GH2'	—	2.54(0.16)	ND
AH3'	4.91(0.30)	5.05(0.27)	5.00(0.22)
GH3'	4.46(0.02)	4.65(-0.07)	ND
AH4'	4.49(0.23)	4.34(0.14)	4.27(0.07)
GH4'	4.33(0.07)	4.23(0.08)	ND
AH5'	3.89(0.10)	3.77(0.10)	3.74(0.05)
AH5"	3.84(0.10)	3.78(0.11)	3.64(-0.03)
GH5'	4.31(0.05)	4.20(0.07)	ND
GH5"	4.22(0.12)	4.17(0.10)	ND
NH	7.70	7.74	ND
OCH3	3.75 3.72	3.74 3.73	ND
CH3	2.46 2.40	2.46 2.40	ND

ND: not determined because of overlapping or too weak signals.