Electronic Supplementary Material (ESI) for Dalton Transactions.

Deciphering of Interactions between Platinated DNA and HMGB1 by Hydrogen/Deuterium Exchange Mass Spectrometry

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Electronic Supplementary Information

Table S1
Figures S1 – S9

Table S1 Deuterium incorporation (%) of peptides produced from peptic digestion of non-ligated HMGB1a and ligated HMGB1a with 1,2-CDDP-**III** or 1-*trans*-PtTz-**VI** after incubated in 90% D_2O at 298 K for different time.

Peptic Peptides	sequences	HMGB1a		1,2-*cis*-Pt-**III**-HMGB1a		HMGB1a		1-*trans*-PtTz-**VI**-HMGB1a	
		1 min	10 min	1 min	10 min	1 min	10 min	1 min	10 min
T1	S5 – F17	53.5	66.9	36.5	55.0	59.2	68.4	46.4	52.4
T2	S14 – P31	65.2	74.8	33.3	70.8	65.7	71.1	32.7	50.8
T3	Q20 – D61	33.0	45.6	15.7	42.9	34.9	38.9	24.1	35.3
T4	H26 – C44	54.3	63.4	28.8	55.9	60.5	66.3	33.7	51.6
T5	S41 – T50	46.4	61.5	11.0	45.8	41.9	52.0	28.1	40.1

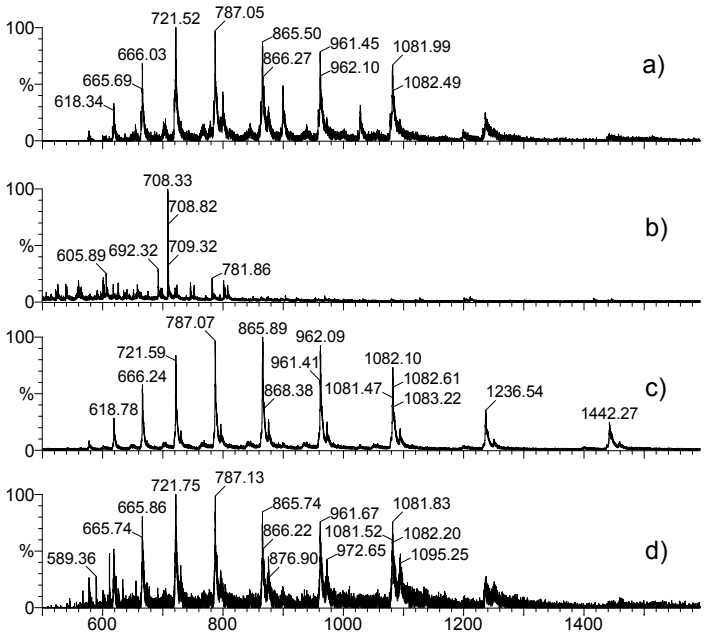

Fig. S1 (a, b) ESI-MS spectra of HMGB1a in the mixture of HMGB1a with (a) equimolar or (b) 10-fold excess of cisplatin-crosslinked dsDNA **III** in the absence of protamine sulfate; (c, d) ESI-MS spectra of HMGB1a in the mixture of HMGB1a with (c) equimolar or (d) 10-fold excess of cisplatin-crosslinked dsDNA **III** in the presence of protamine sulfate.

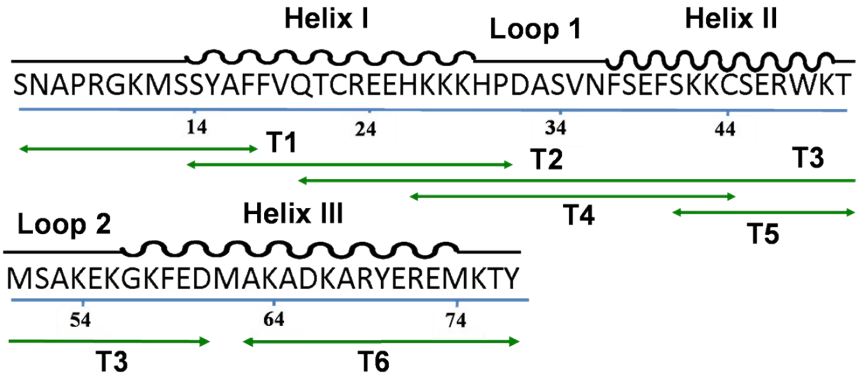

Fig. S2 Sequence coverage map of peptic peptides of HMGB1a identified by HPLC-ESI-MS. The sequence position follows the X-ray crystal structure reported previously (PDB code: 1CKT).

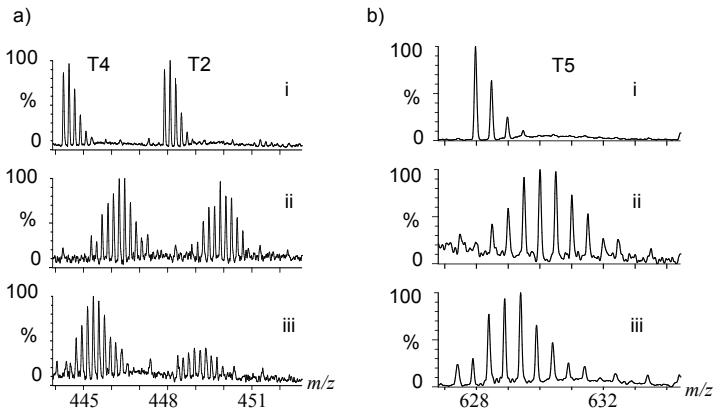

Fig. S3 Mass spectra of peptic peptides T2 (S14 – P31), T4 (H26 – C44) and T5 (S41 – T50). i: non-deuterated peptides; ii: deuterated peptides of non-ligated HMGB1a; and iii: deuterated peptides of ligated HMGB1a with 1,2-cis-Pt-**III** after incubated in 90% D_2O buffer for 1 min at 298 K.

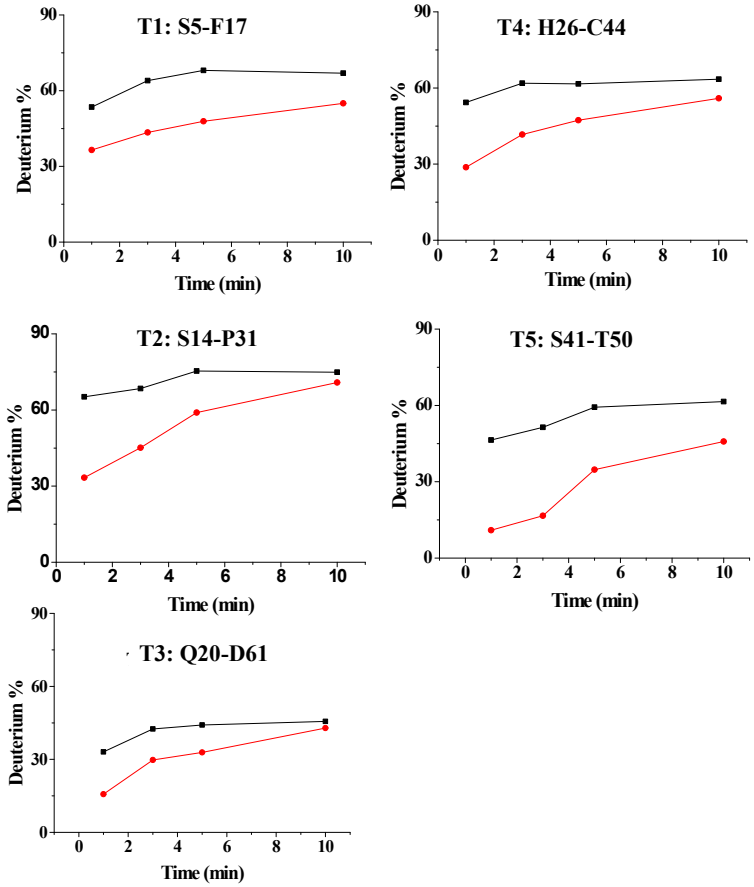

Fig. S4 Kinetic plots of deuterium incorporation (%) for peptides T1 – T5 derived from peptic digestion of HMGB1a (squares) and the ligated HMGB1a with 1,2-*cis*-Pt-**III** (circles).

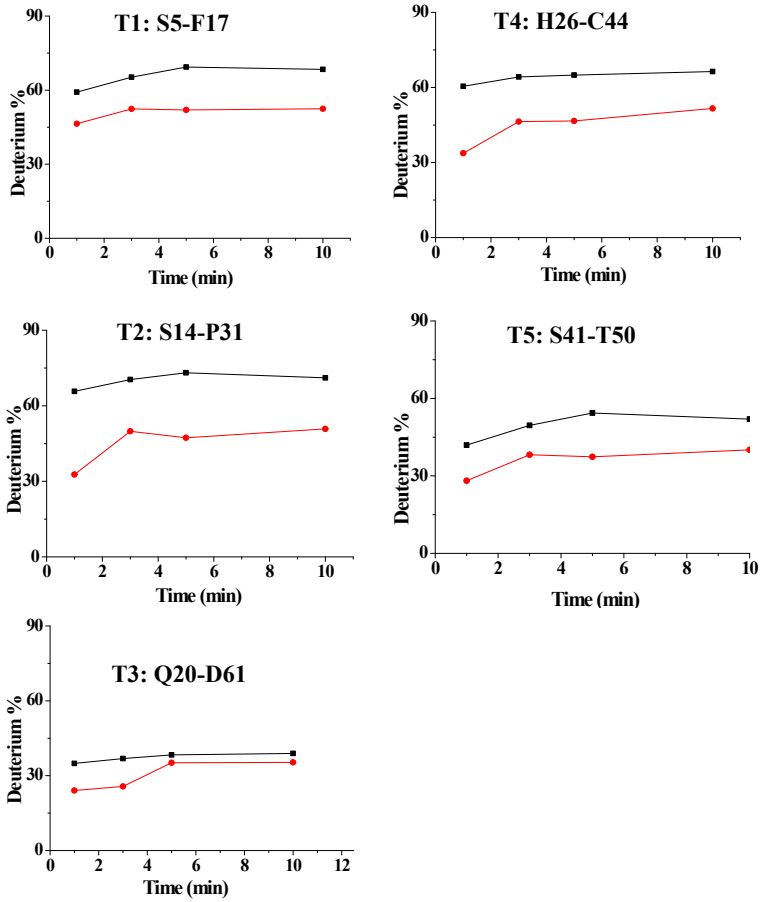

Fig. S5 Kinetic plots of deuterium incorporation (%) for peptides T1 – T5 derived from peptic digestion of HMGB1a (squares) and the ligated HMGB1a with 1-*trans*-PtTz-**VI** (circles).

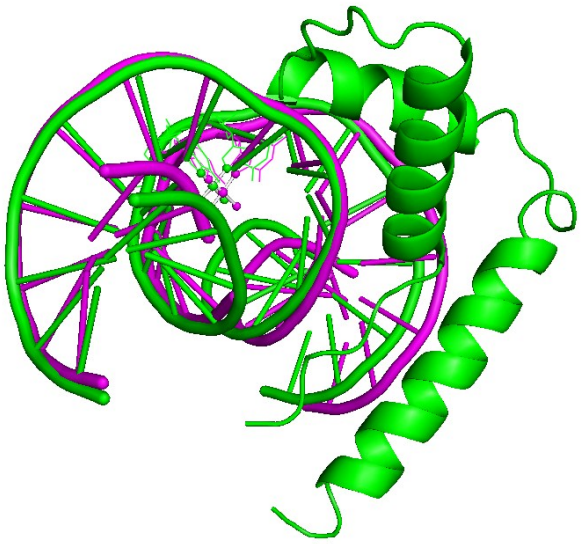

Fig. S6 Superimposition of conformation of the 1,2-GG cisplatin crosslinked dsDNA binding to HMGB1a in the crystal stucture (code: 1CKT, green) and in an energy-minimized model generated by docking simulation (purple).

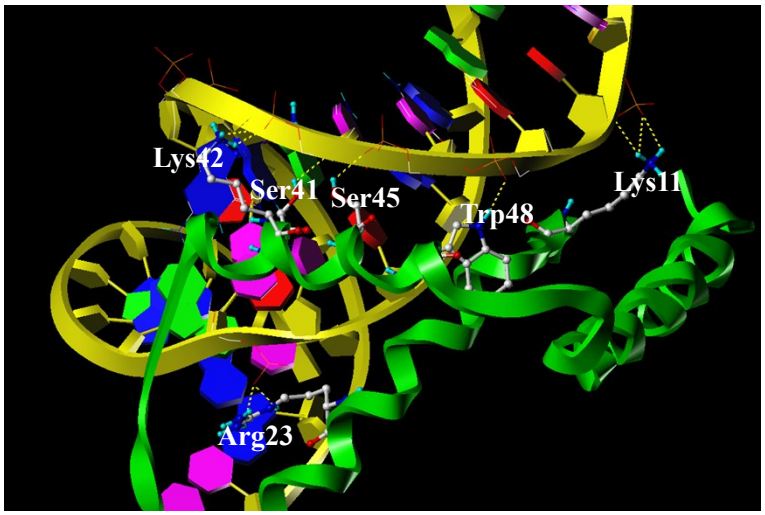

Fig. S7 The conformation of HMGB1a ligated with 1,2-GG-intrastranded crosslinked dsDNA by cisplatin regenerated by SYBYL 1.1 program based on the X-ray crystal structure available in Protein Data Bank (code: 1CKT). The dotted yellow lines illustrate the positions of H-bonding interactions between HMGB1a and cisplatin crosslinked DNA.

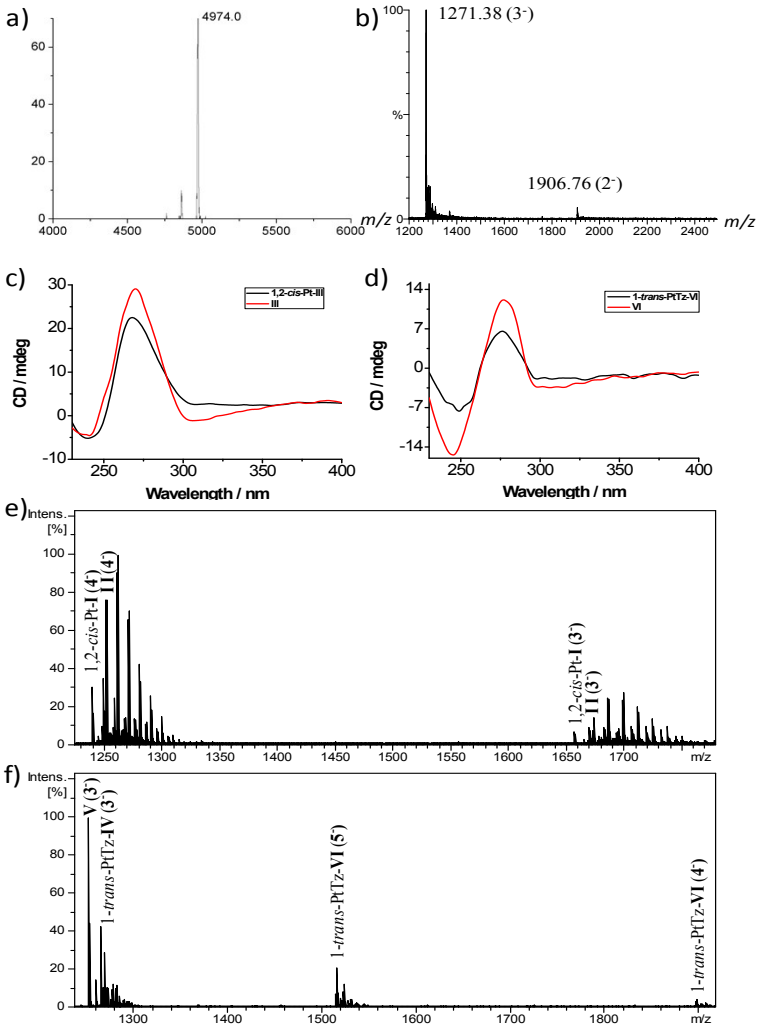

Fig. S8 (a, b) MALDI-TOF-MS spectra of 1,2-intrastand crosslinked single-stranded oligonucleotide (ONT) **I** by cisplatin (a) and monofunctional single-stranded ONT **IV** modified by *trans*-PtTz (b). (c, d) Circular dichroism (CD) spectra of non-modified **III** (= **I** + **II**) and 1,2-intrastand crosslinked double stranded ONT **III** by cisplatin (c), and non-modified **IV** (**IV** + **V**) and monofunctional platinated double stranded ONT **VI** by *trans*-PtTz (d). (e, f) FT-ICR-MS spectra of 1,2-intrastand crosslinked double stranded DNA **III** by cisplatin (e) and monofunctional platinated double stranded ONT **VI** by *trans*-PtTz (f).