

## Electronic Supplementary Information

### Specific Recognition of DNA Depurination by a Luminescent Terbium(III) Complex

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#### 1 Experimental

##### 1.1 Materials and Methods

Common reagents used in the experiments were all of analytical grade. TbL and TbL' were prepared as reported previously.<sup>1</sup> MMS was purchased from Alfa Aesar. Tris(hydroxymethyl)aminomethane (Tris), EB, CT-DNA, GMP, AMP, CMP, and TMP were purchased from Sigma. Oligonucleotides ploy(G), ploy(A), ploy(C), ploy(T), ON1, ON2, and ON3 were purchased from GenScript Co. UV-vis spectra were determined on a Perkin-Elmer Lambda 35 UV-vis spectrometer. Time-resolved luminescence spectra were recorded on a Perkin-Elmer LS 55 luminescence spectrometer with the following settings: delay time, 100  $\mu$ s; gate time, 2.00 ms; and cycle time, 20 ms. The excitation and emission slit widths were 12 nm for TbL and 5 nm for TbL', respectively. The photomultiplier voltage was 900 V. CD spectra were recorded on a Jasco J-810 spectropolarimeter. The concentrations of oligonucleotides were measured by Thermo Scientific NanoDrop 1000. The concentration of CT-DNA was determined by measuring the UV absorption at 260 nm using the known molar absorption coefficient of 6600  $\text{M}^{-1} \text{L cm}^{-1}$ . The ratio of the UV absorption at 260 and 280 nm in Tris-HCl buffer is around 1.83, indicating that DNA was sufficiently free of protein.<sup>2</sup>

##### 1.2 Reactions of TbL with nucleotides, oligonucleotides or CT-DNA

All the reactions were carried out in buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4) at 37 °C for 10 min. The time-resolved luminescence spectra of TbL (100  $\mu$ M) upon reacting with GMP, AMP, CMP, TMP, ploy(G), ploy(A), ploy(C), ploy(T), ON1, ON2, ON3, and CT-DNA, respectively, were measured at 25 °C after excitation at 260 nm. The time-resolved luminescence spectra of TbL' upon reacting with CT-DNA were measured similarly.

##### 1.3 Reactions of TbL with CT-DNA in the presence of MMS

CT-DNA (90  $\mu$ M) was incubated with MMS (0.9, 1.35, 1.8, 3.6, 7.2 mM, respectively) in buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4) at 37 °C for 24 h. TbL (100  $\mu$ M) was added to the solution and incubated at 37 °C for 10 min. The time-resolved luminescence spectra were measured at 25 °C after excitation at 260 nm.

##### 1.4 Reactions of TbL with CT-DNA in acidic conditions

The depurination of DNA induced by acid was prepared according to the literature.<sup>3</sup> CT-DNA (0.9 mM) in Tris-HCl buffer (pH 7.4) was adjusted with HCl (0.1 M) to obtain a final pH of 5 or 4.5 at 25 °C. Depurination of DNA was achieved by heating the samples for different times at 70 °C. Depurianted DNA was added to the buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4) of TbL (100  $\mu$ M) at 37 °C for 10 min (DNA final concentration: 45  $\mu$ M). The time-resolved

luminescence spectra were measured at 25 °C after excitation at 265 nm.

### 1.5 Response of TbL to CT-DNA in the presence of denaturants

CT-DNA was incubated with common DNA denaturants formamide and urea (2 mM) at 90 °C for 5 min.<sup>4</sup> The solution was then cooled with ice and added to the buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4) of TbL (100 μM) at 37 °C and reacted for 10 min ( $[DNA]_{\text{final}} = 90 \mu\text{M}$ ). The time-resolved luminescence spectra were measured at 25 °C after excitation at 265 nm.

### 1.6 Minimum detection limit and linear range of TbL for CT-DNA

The time-resolved luminescence spectra of free TbL (0.1 mM,  $\lambda_{\text{ex}} = 265 \text{ nm}$ ) in buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4) was collected for 20 times to determine the background noise  $\sigma$ .<sup>5</sup> The time-resolved luminescence spectra of TbL in the presence of CT-DNA at various concentration was measured. A linear regression curve was fitted according to the emission intensity at 545 nm in the range of 0.08 – 10 μM, and the slope of curve was obtained using Origin 8.0.

### 1.7 DNA binding mode of TbL

CT-DNA (100 μM) was incubated with TbL (10, 20, 40, 60, 80, and 100 μM) in buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4) at 37 °C for 12 h. CD spectra were measured at 25 °C in the wavelength range of 220–320 nm.

The fluorescence of the EB-DNA system was determined in buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4) at 25 °C. CT-DNA (12 μL, 0.9 mM) was added to EB buffer (1.3 μM, 3 mL). Aliquots of TbL (3 μL, 1 mM) were then added to the EB-DNA system at 25 °C in 1 min and the fluorescence spectra were measured on the Perkin-Elmer LS 55 ( $\lambda_{\text{ex}} = 495 \text{ nm}$ ,  $\lambda_{\text{em}} = 610 \text{ nm}$ ). The apparent binding constant ( $K_{\text{app}}$ ) was determined by the following equation

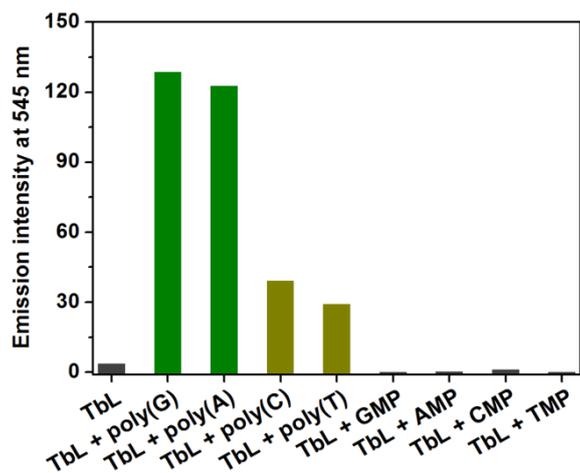
$$K_{\text{EB}}[\text{EB}] = K_{\text{app}}[\text{complex}]$$

where  $K_{\text{EB}} = 1.0 \times 10^7 \text{ M}^{-1}$ ,  $[\text{EB}] = 1.3 \mu\text{M}$ , and  $[\text{complex}]$  was the final concentration at which a 50% reduction of the fluorescence had occurred.<sup>6</sup>

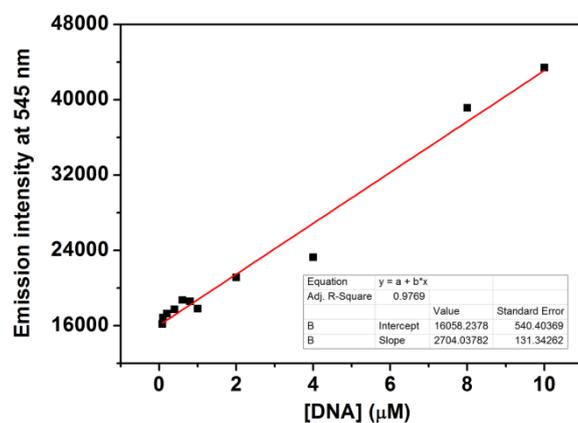
### 1.8 MD simulation

The initial coordinate of the DNA sequence was generated by using the HyperChem program.<sup>7</sup> The structure of TbL was optimized by Gaussian09 program at the density functional theory (DFT) level.<sup>8</sup> All molecular dynamics (MD) simulations were carried out using the AMBER9 package with the AMBER force fields of ff03 and gaff.<sup>9</sup> The equilibration time for each simulation was 200 ps (NPT) followed by 20 ns of data collection for analysis under the conditions of constant volume with a periodic boundary at 300 K. The ptraj program from AMBER9 simulation software was used to analyze the trajectory.

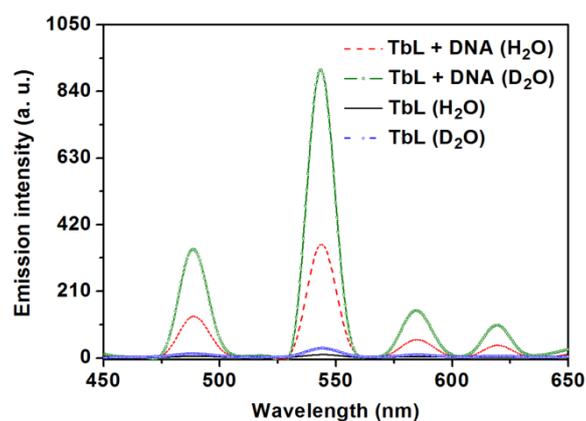
## 2 Supplementary Figures



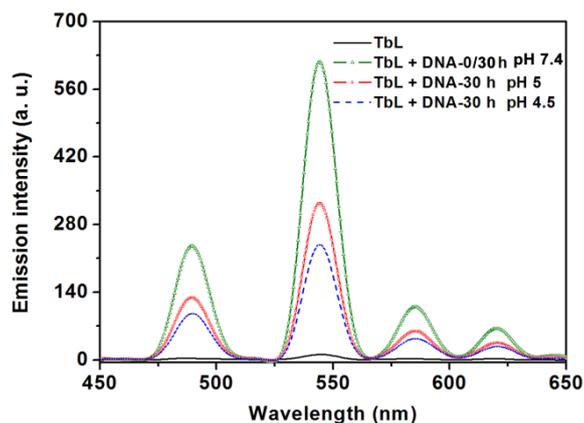
**Fig. S1** The time-resolved luminescence intensity of TbL (0.1 mM,  $\lambda_{\text{ex}} = 265$  nm) at 545 nm in the absence or presence of oligonucleotides or nucleotides (40  $\mu\text{M}$ ) in buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4).



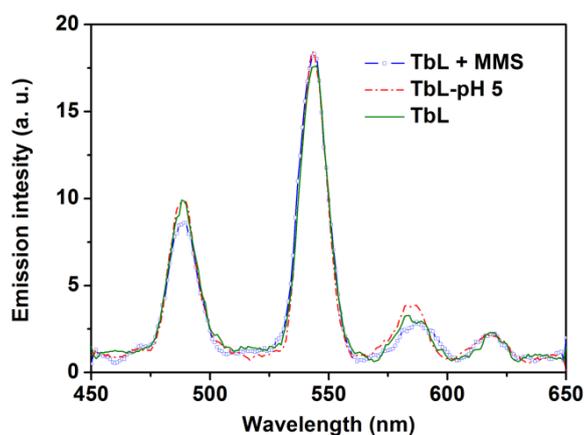
**Fig. S2** Plot of luminescence intensity of TbL (0.1 mM,  $\lambda_{\text{ex}} = 265$  nm) in buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4) at 545 nm as a function of CT-DNA concentration in the range of 0.08 – 10  $\mu\text{M}$ .



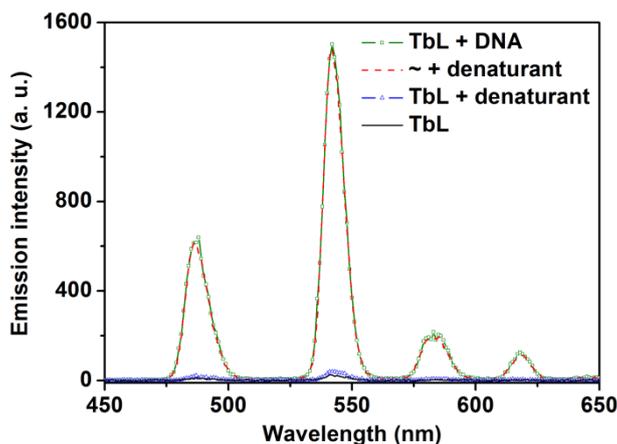
**Fig. S3** The time-resolved luminescence spectra of TbL (0.1 mM,  $\lambda_{\text{ex}} = 265$  nm) in the presence and absence of CT-DNA (45  $\mu\text{M}$ ) determined in H<sub>2</sub>O and D<sub>2</sub>O.



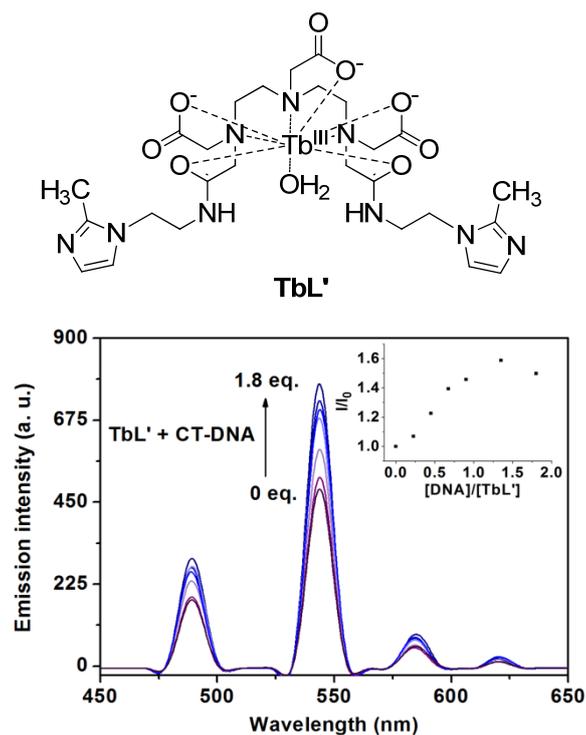
**Fig. S4** The time-resolved luminescence spectra of TbL (0.1 mM,  $\lambda_{\text{ex}} = 265$  nm) in the absence or presence of DNA after incubation at 70 °C for 0 or 30 h at different pH values.



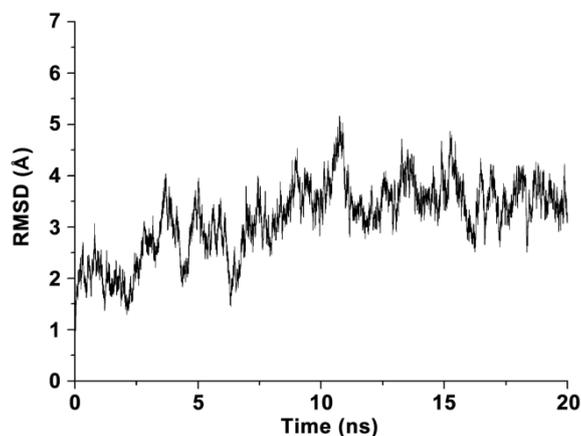
**Fig. S5** The effect of MMS (0.9 mM, pH 7.4) or acid (pH 5.0) on the time-resolved luminescence spectra of TbL (0.1 mM,  $\lambda_{\text{ex}} = 265$  nm) in the absence of DNA in buffer (5 mM Tris-HCl, 50 mM NaCl).



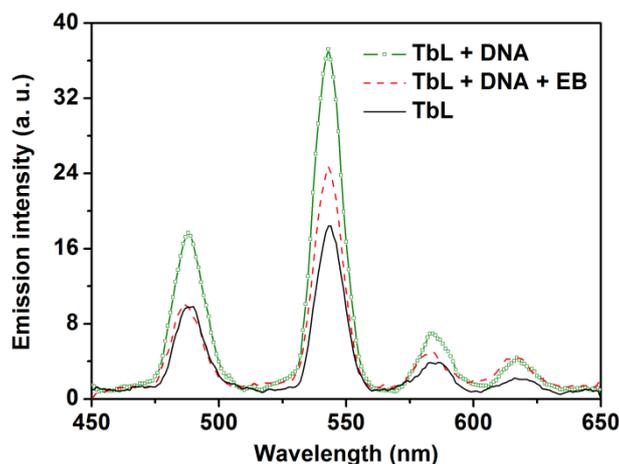
**Fig. S6** The time-resolved luminescence spectra of TbL (0.1 mM,  $\lambda_{\text{ex}} = 265$  nm) in the absence or presence of CT-DNA (90  $\mu$ M) with or without denaturants formamide (2 mM) and urea (2 mM) in buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4).



**Fig. S7** The structure of TbL' and its time-resolved luminescence spectra (0.1 mM,  $\lambda_{\text{ex}} = 265$  nm) upon addition of increasing amount of CT-DNA in buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4) after incubation at 37 °C for 10 min. Inset shows the emission intensity ratio ( $I/I_0$ ) at 545 nm versus the ratio of [DNA] to [TbL'].



**Fig. S8** RMSD values of all backbone atoms in the simulation of TbL-DNA model with respect to the starting structure.



**Fig. S9** The time-resolved luminescence spectra of TbL (0.1 mM,  $\lambda_{\text{ex}} = 265$  nm) in response to CT-DNA (3.6  $\mu\text{M}$ ) in the absence or presence of EB (1.3  $\mu\text{M}$ ) in buffer (5 mM Tris-HCl, 50 mM NaCl, pH 7.4).

**Table S1** Parameters for the  $\pi$ - $\pi$  interactions between metronidazole plane of TbL and purine bases of DNA derived from the MD simulations.

$\pi$ - $\pi$ interaction	Distance	Dihedral angle
Single-binding mode		
Metronidazole – G6	3.878 Å	9.645°
Double-binding mode		
Metronidazole – G6	3.556 Å	11.988°
Metronidazole – A16	3.773 Å	32.258°

**Table S2** Occupancies of hydrogen bonds between oxygen atoms in nitro groups of TbL and N-H groups of DNA bases.

H-bonds	Distance	Occupancy
Single-binding mode		
A16/N6 – H61 ... O86	3.0408 Å	83.33%
A16/N6 – H61 ... O87	3.9651 Å	8.54%
Double-binding mode		
T5/N3 – H3 ... O86	2.9336 Å	47.82%
T5/N3 – H3 ... O87	4.0885 Å	39.26%

## References

- 1 X. H. Wang, X. Y. Wang, Y. Q. Wang and Z. J. Guo, *Chem. Commun.*, 2011, **47**, 8127.
- 2 J. Marmur, *J. Mol. Biol.*, 1961, **3**, 208.
- 3 R. M. Schaaper and L. A. Loeb, *Proc. Natl. Acad. Sci. USA.*, 1981, **78**, 1773.
- 4 N. C. Pagratis, *Nucleic Acids Res.*, 1996, **24**, 3645.
- 5 Y. C. Chen, C. C. Zhu, Z. H. Yang, J. Li, Y. Jiao, W. J. He, J. J. Chen, Z. J. Guo, *Chem. Commun.*, 2012, **48**, 5094.
- 6 M. Lee, A. L. Rhodes, M. D. Wyatt, S. Forrow, J. A. Hartley, *Biochemistry*, 1993, **32**, 4237.
- 7 HyperChem Inc., ON, Canada, *Molecular Simulations*, Inc. San Diego, CA, USA.
- 8 M. J. Frisch, G. Trucks, H. Schlegel, G. Scuseria, M. Robb, J. Cheeseman, G. Scalmani, V.

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Barone, B. Mennucci and G. Petersson, *Gaussian 09*, Gaussian. Inc, Wallingford, CT 2009.  
9 D. A. Case, T. A. Darden, T. E. Cheatham, III, C. L. Simmerling, J. Wang, R. E. Duke, R. Luo, K. M. Merz, D. A. Pearlman, M. Crowley, R. C. Walker, W. Zhang, B. Wang, S. Hayik, A. Roitberg, G. Seabra, K. F. Wong, F. Paesani, X. Wu, S. Brozell, V. Tsui, H. Gohlke, L. Yang, C. Tan, J. Mongan, V. Hornak, G. Cui, P. Beroza, D. H. Mathews, C. Schafmeister, W. S. Ross and P. A. Kollman, *AMBER 9*, University of California, San Francisco, CA, USA, 2006.