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A family of mixed-ligand oxidovanadium(V) complexes with aroylhydrazone ligands: a combined experimental and computational study on the electronic effects of *para* substituents of hydrazone ligands on the electronic properties, DNA binding and nuclease activities

Debashis Patra[a], Nirmalendu Biswas[a], Bhavini Kumari[b], Prolay Das[b], Nayim Sepay[c], Shamba Chatterjee[d], Michael G. B. Drew[e] and Tapas Ghosh[a,*]

[a]*Post Graduate Department of Chemistry, Ramakrishna Mission Vivekananda Centenary College, Rahara, Kolkata-700118, India. E-mail: ictg_64@yahoo.co.in*

[b]*Department of Chemistry, Indian Institute of Technology Patna, India.*

[c]*Department of Chemistry, Jadavpur University, Kolkata-700032, India.*

[d]*Department of Organic Chemistry, Indian Association for the Cultivation of Science, Jadavpur, Kolkata-700032, India.*

[e]*Department of Chemistry, The University of Reading, P. O. Box 224, Whiteknights, Reading RG6 6AD, UK.*

SUPPLEMENTARY DATA

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Fig. S2: Overlay of the electronic spectra of **1-4** complexes in CH_2Cl_2 solution.

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Fig. S4: Cyclic voltammogram of the complexes **1-4** in CH_2Cl_2 solution.

Fig. S5: Cyclic voltammogram of **1-4** complexes in CH_2Cl_2 solution at different scan rate. Concentration of the complexes: ~ 1×10^{-3} mol dm^{-3}; supporting electrolyte: tetrabutylammonium perchlorate.

Fig. S6: Plot of λ_{max} versus $E_{1/2}$ for the complexes **1-4**.

Fig. S7: Absorption spectra of the complexes **1-4** in the presence of increasing amounts of CT DNA. A fixed concentration of complex (10^{-5} M) was treated with increasing amounts of DNA over a range of (1-10) × 10^{-6} M. (**inset:** The linear fit of [DNA]/(ε_a-ε_f) *versus* [DNA]).

Fig. S8: Fluorescence spectra of (a) EB + 10^{-4} M DNA control and (b)-(k) EB + DNA + (1-10) × 10^{-5} M ligands H_3L^1, H_3L^2, H_3L^3 and H_3L^4. The arrow shows that the intensity decreases with increasing concentration of ligands H_3L^1, H_3L^2, H_3L^3 and H_3L^4. (Inset: Stern-Volmer plot for the quenching of fluorescence of the ethidium bromide (EB) DNA complex caused by ligands H_3L^1, H_3L^2, H_3L^3 and H_3L^4 respectively).

Fig. S9: Nuclease activity of complexes **1-4**:

pUC19 incubated with 0.25 mM of complex **1**, **2**, **3** and **4**. Lane 1 contains pUC19 as control and lane 2, 3, 4 and 5 contain pUC19 incubated with complex **1**, **2**, **3** and **4** respectively. The upper bands correspond to the OC form and the lower bands for SC form of the Plasmid.

Fig. S10: Nuclease activity of ligands H_3L^{1-4}:

pUC19 incubated with 0.5 mM of ligand H_3L^1, H_3L^2, H_3L^3 and H_3L^4. Lane 1 contains pUC19 as control and lane 2, 3, 4 and 5 contain pUC19 incubated with ligand H_3L^1, H_3L^2, H_3L^3 and H_3L^4 respectively. The upper bands correspond to the OC form, the middle band for LC and the lower bands for SC form of the Plasmid.

Fig. S11: Docked pose of ligands H_3L^1 (top left), H_3L^2 (top right), H_3L^3 (bottom left) and H_3L^4 (bottom right) showing interaction with DNA base pairs.

Table S1: Crystal data and structure determination summary of **H_3L^3**, **1**, **2**, **3** and **4**

	H_3L^3	**1**	**2**	**3**	**4**
Emperical formula	$C_{17.5}H_{19}N_2O_{4.5}$	$C_{24}H_{18}N_3O_5V$	$C_{25}H_{20}N_3O_5V$	$C_{25}H_{20}N_3O_6V$	$C_{24}H_{17}ClN_3O_5V$
Formula weight	329.35	479.35	493.38	509.38	513.80
Crystal colour	white	black	black	black	black
Temperature (K)	150(2)	150(2)	150(2)	293(2)	150(2)
Crystal system	triclinic	monoclinic	triclinic	monoclinic	triclinic
Space group	*P-1*	$P2_1/c$	*P-1*	$P2_1/c$	*P-1*
a/Å	12.1814(14)	13.5975(17)	8.7713(6)	7.668(3)	8.3143(6)
b/Å	12.8382(18)	11.4633(19)	10.1477(8)	14.153(6)	11.3015(7)
c/Å	13.3641(15)	14.148(2)	13.3468(9)	21.853(10)	12.1012(8)
α/°	112.58(12)	90	74.541(7)	90	72.559(6)
β/°	96.537(10)	105.616(16)	84.262(6)	96.860(6)	84.859(6)
γ/°	117.044(13)	90	73.896(7)	90	76.042(6)
V /Å^3	1609.5(3)	2123.9(6)	1099.63(14)	2354.5(18)	1052.60(12)
Z	4	4	2	4	2
D_x (g cm^{-3})	1.359	1.499	1.490	1.437	1.621
μ (mm^{-1})	0.099	0.510	0.495	0.468	0.643
F(000)	696	984	508	1048	524
Data/restraints/parameters	8976/0/441	5923/1/300	6167/0/310	4134/0/319	5889/0/309
Goodness-of-fit on F^2	1.038	0.939	1.003	0.964	0.810
R indices,[I>2σ(I)] R1,wR2	0.0940, 0.1706	0.0706, 0.1202	0.0572, 0.1095	0.0662, 0.1503	0.0506, 0.1275
R indices(all data) R1,wR2	0.1663, 0.2107	0.1775, 0.1676	0.0871, 0.1239	0.1241, 0.1767	0.0751,0.1513
$\Delta\rho_{max}$, min (e Å^{-3})	0.403, -0.353	0.293, -0.339	0.402, -0.418	0.342, -0.595	0.486, -0.586

Table S2: Selected bond lengths (Å) of the H_3L^3 ligand in molecules **A** and **B**

	A	**B**
C(7)-N(1)	1.292(4)	1.284(4)
N(1)-N(2)	1.370(3)	1.370(3)
C(8)-N(2)	1.351(3)	1.343(4)
C(8)-O(3)	1.243(4)	1.249(3)

Table S3: Hydrogen bond parameters in the structure of H_3L^3 ligand

D-H…A	d(D-H)	d(H…A)	d(D…A)	<(DHA)
N(2A)-H(2A)…O(5A)	0.86	1.92	2.600(3)	135.2
O(2A)-H(2A)…N(1A)	0.82	1.82	2.533(3)	144.9
O(5B)-H(5B)…O(3A)$^{(ii)}$	0.82	1.78	2.597(3)	176.4
N(2B)-H(2B)…O(5B)	0.86	1.91	2.588(3)	135.3
O(2B)-H(2B)…N(1B)	0.82	1.82	2.533(3)	144.3
O(5A)-H(5A)…O(3B)$^{(i)}$	0.82	1.80	2.597(3)	163.5

Symmetry elements: (i) 1+x,-1+y,z; (ii) -1+x,y,z

Table S4: Hydrogen bond parameters [bond lengths (Å) and angles (°)] of the complexes **1**-**4**

Complex	D-H…A	d(D-H)	d(H…A)	d(D…A)	<(DHA)
1	O(5)-H(5)…N(2)	0.82	1.88	2.599 (4)	145.6
2	O(5)-H(5)…N(2)	0.82	1.87	2.585 (2)	145.3
3	O(5)-H(5)…N(2)	0.82	1.91	2.633 (3)	145.9
4	O(5)-H(5)…N(2)	0.82	1.87	2.598 (2)	145.5

Table S5: Selected bond lengths (Å) and angles (º) in complexes **1-4** obtained by DFT method

	6-311++G**				6-31G			
	1	**2**	**3**	**4**	**1**	**2**	**3**	**4**
V-O1	1.571	1.572	1.572	1.571	1.593	1.593	1.594	1.593
V-O2	1.842	1.840	1.834	1.846	1.832	1.830	1.826	1.837
V-O3	1.945	1.947	1.951	1.944	1.929	1.931	1.933	1.927
V-O4	1.840	1.841	1.842	1.838	1.825	1.826	1.826	1.822
V-N1	2.123	2.124	2.129	2.127	2.126	2.126	2.131	2.130
V-N3	2.521	2.522	2.521	2.518	2.543	2.544	2.542	2.536
O1-V-O2	101.36	101.39	101.58	101.23	100.82	100.82	100.95	100.59
O1-V-O3	101.72	101.77	101.69	101.81	101.26	101.13	101.01	101.21
O1-V-O4	103.67	103.67	103.64	103.66	103.80	103.86	103.86	103.85
O2-V-O3	148.97	148.88	148.61	148.89	149.68	149.82	149.67	149.83
O2-V-O4	102.25	101.44	102.64	102.10	102.24	102.26	102.38	101.91
O3-V-O4	92.11	91.94	91.99	92.44	92.36	92.27	92.34	92.82
O1-V-N1	96.09	95.94	95.67	95.82	95.80	95.90	95.68	95.72
O2-V-N1	82.28	82.31	82.27	82.27	81.77	81.80	81.79	81.76
O3-V-N1	74.91	74.88	74.73	74.86	75.56	75.58	75.46	75.55
O4-V-N1	158.28	158.32	158.52	158.65	158.73	158.55	158.70	158.93
O1-V-N3	176.80	176.73	176.65	176.90	176.57	176.50	176.42	176.80
O2-V-N3	80.40	80.52	80.58	80.42	81.47	81.68	81.77	81.54
O3-V-N3	77.62	77.42	77.26	77.62	77.54	77.42	77.31	77.68
O4-V-N3	73.28	73.25	73.29	73.37	73.13	73.11	73.16	73.28
N1-V-N3	86.77	86.92	87.14	86.99	87.02	86.85	86.98	86.93

Table S6: Vertical excitation energies (E_{cal}), oscillator strengths (f_{cal}), and type of excitations of the lowest three excited singlets obtained from TD-DFT calculations of **1**-**4**

Complex	State	$E_{cal/\ nm}$	f_{cal}	Excitation
1	S_1	642.77	0.0033	HOMO-2 → LUMO (0.16154)
				HOMO-1 → LUMO (0.17784)
	S_2	508.05	0.0028	HOMO-3 → LUMO (0.17631)
				HOMO-2 → LUMO (0.60430)
				HOMO → LUMO (-0.30393)
	S_3	487.08	0.2004	HOMO-3 → LUMO (0.12808)
				HOMO-1 → LUMO (0.67793)
2	S_1	665.26	0.0038	HOMO-2 → LUMO (0.16154)
				HOMO-1→ LUMO (0.17784)
				HOMO → LUMO (0.65819)
	S_2	511.35	0.0024	HOMO-3 → LUMO (-0.19657)
				HOMO-2 → LUMO (0.44163)
				HOMO-1 → LUMO (0.45607)
				HOMO → LUMO (-0.23424)
	S_3	486.36	0.2027	HOMO-3 → LUMO (0.15100)
				HOMO-2 → LUMO (-0.45876)
				HOMO-1 → LUMO (0.49482)
3	S_1	709.80	0.0017	HOMO → LUMO (0.69400)
	S_2	527.55	0.0052	HOMO-3 → LUMO (-0.23432)
				HOMO-1 → LUMO (0.65961)
	S_3	485.80	0.1898	HOMO-3 → LUMO (-0.19267)
				HOMO-2 → LUMO (0.64869)
				HOMO-1 → LUMO (-0.10117)
4	S_1	653.55	0.0037	HOMO-2 → LUMO (0.13330)
				HOMO-1 → LUMO (0.25045)
				HOMO → LUMO (0.63972)
	S_2	518.91	0.0028	HOMO-3 → LUMO (-0.12311)
				HOMO-2 → LUMO (0.30141)
				HOMO-1 → LUMO (0.55649)
				HOMO → LUMO (-0.28431)
	S_3	489.47	0.2111	HOMO-3 → LUMO (-0.11321)
				HOMO-2 → LUMO (0.59391)
				HOMO-1→ LUMO (-0.33682)

Table S7: Extent of DNA SC pUC19 (500ng) cleavage by 0.25 mM **1-4** complexes

Complex	pUC form I (% Super Coil)	pUC form II (% Open Circular)	pUC form III (% linear Coil)
1	58.3	33.5	0.0
2	56.8	34.9	0.0
3	52.6	38.8	0.0
4	53.1	38.4	0.0

Table S8: Extent of DNA SC pUC19 (500 ng) cleavage by 0.5 mM ligands H_3L^{1-4}.

Ligand	pUC form I (% Super Coil)	pUC form II (% Open Circular)	pUC form III (% linear Coil)
H_3L^1	68.8	24.2	0.0
H_3L^2	78.6	16.1	0.0
H_3L^3	69.2	19.3	5.0
H_3L^4	70.4	22.9	0.0

Table S9: Different type of interactions between the CT-DNA and the each of the complexes obtained from molecular docking study

Complex	Hydrogen bonds					π- interactions			
	No.of hydrogen bonds	DNA End	Complex End	Distances Å	D--H—A angle	No. of ionic interact-ions	DNA End	Complex End	Bond Distances Å
1	1	Chain A, O atom of phosphate of Thimin 8	Free OH	1.98	124.89	3	Chain B, O atom of phosphate of C21	Phenyl ring	3.60
							Chain B, H atom of Suger of T20	O18	1.88
							Chain B, H atom of Suger of T20	O18	2.93
2	3	Chain A, H atom of NH_2 group of G4	V=O	2.10	135.3	2	Chain B, aromatic ring of C23	Phenyl ring	5.70
		Chain A, H atom of NH group of G4	V=O	1.72	144.4		Chain A, H atom of Suger of A5	V=O	2.91
		Chain A, H atom of NH_2 group of G4	O of V-O-aromatic moiety	3.15	114.9				
3	3	Chain A, H atom of NH_2 group of G4	V=O	1.85	136.9	2	Chain A, H atom of Suger of A5	V=O	2.53
		Chain A, H atom of NH group of G4	V=O	2.02	127.7		Chain A, H atom of Suger of A5	V=O	2.86
		Chain A, H atom of NH_2 group of G4	O of V-O-aromatic moiety	2.63	113.5				
4	1	O of phosphate of T8 of Chain A	Free OH	2.17	148.55	3	Chain B, O of phosphate of C21	Phenyl ring	3.18
							Chain B,H of sugar of T20	O of V-O-aromatic ring	1.97
							Chain B,H of sugar of T20	O of V-O-aromatic ring	2.67

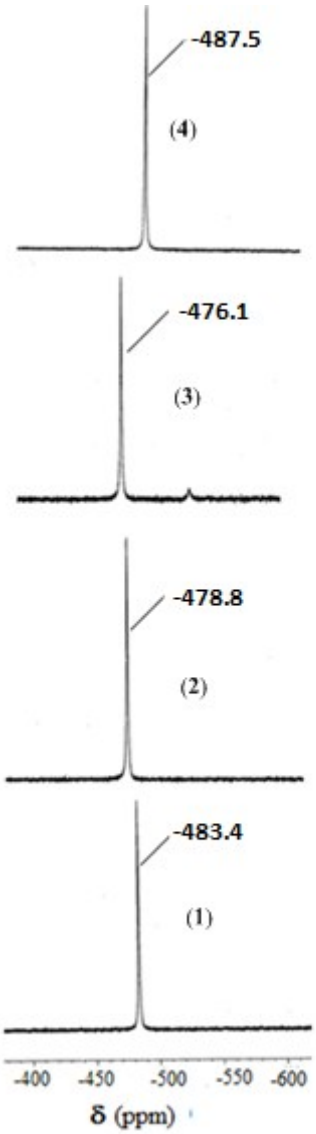
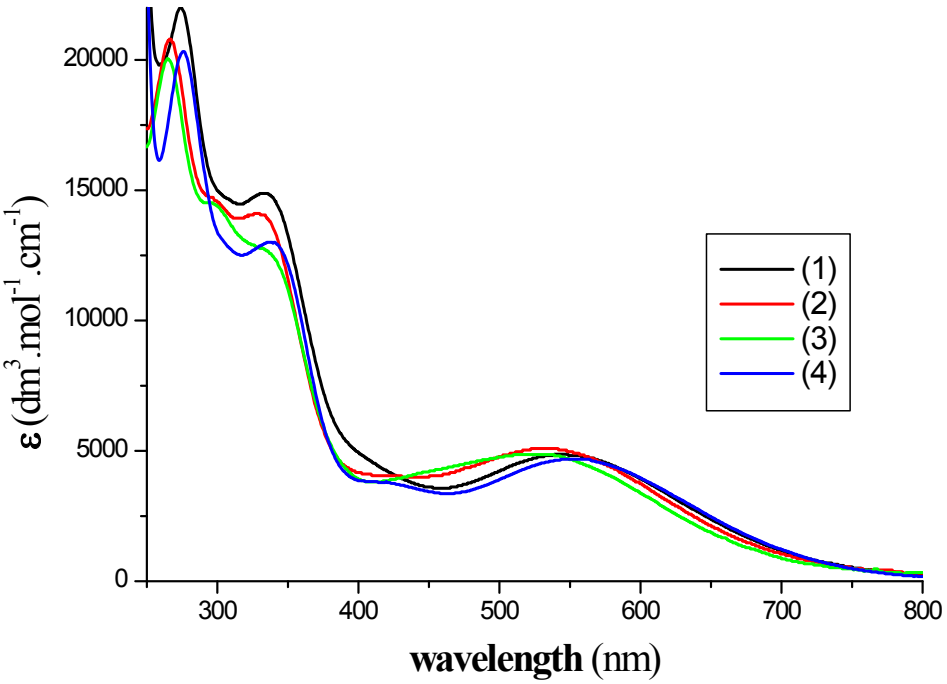


Fig. S1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400
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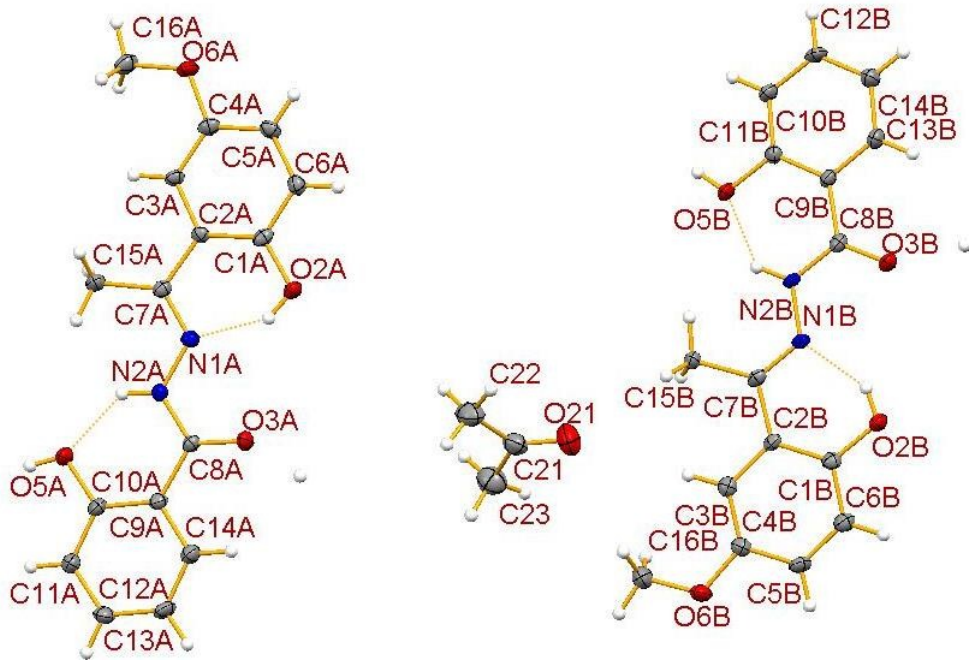
wavelength (nm)
(1)
(2)
(3)
(4)

Fig. S2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O6A
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O3A
O5A
C10A
C8A
C9A
C14A
C11A
C12A
C13A
C22
O21
C21
C23
C12B
C14B
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N1B
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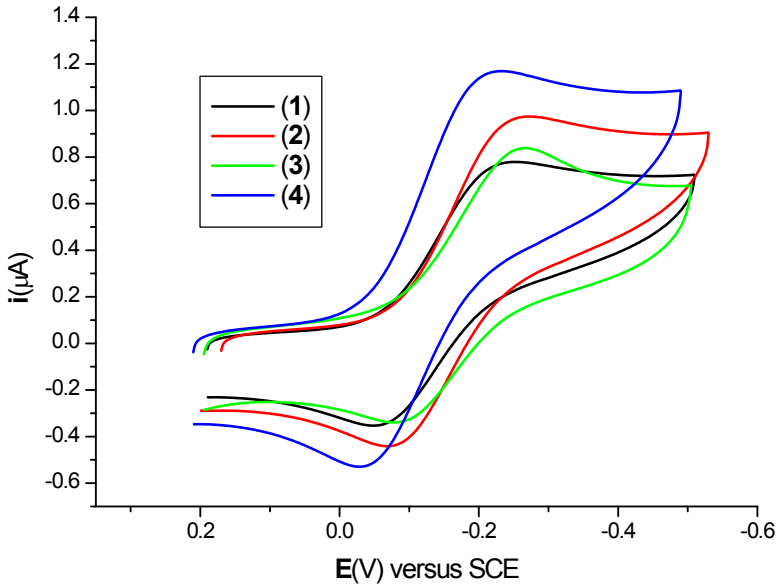
O6B

Fig. S3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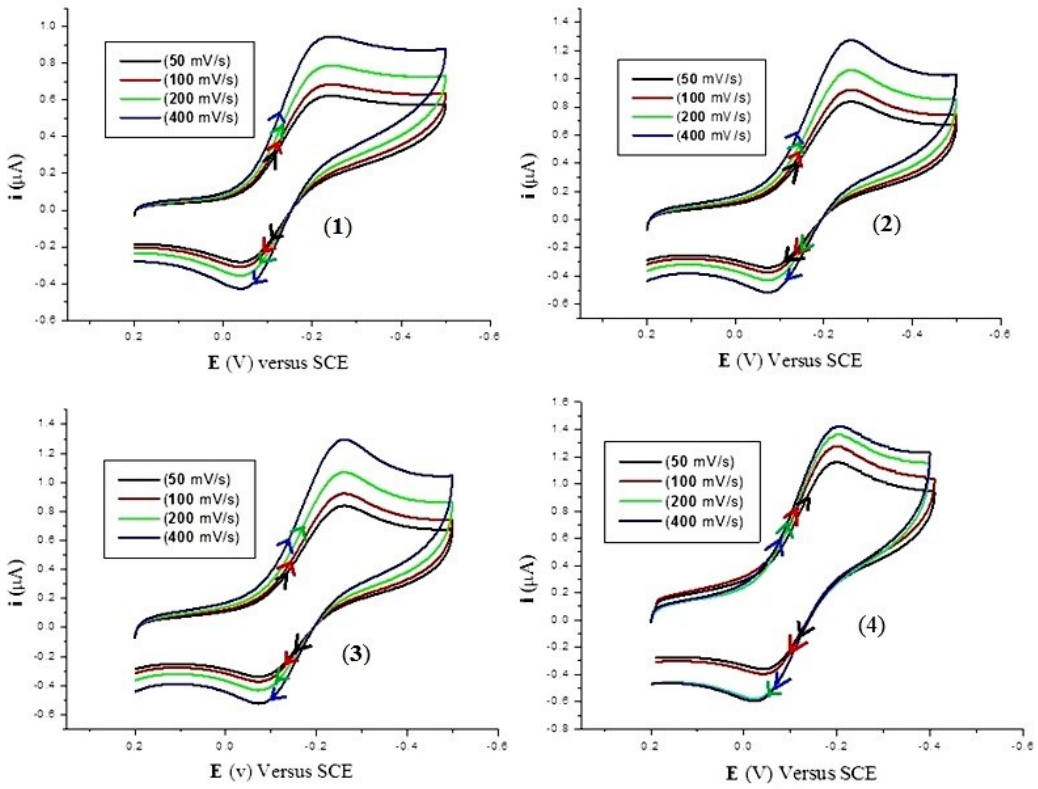
(2)
(3)
(4)
i(μA)
E(V) versus SCE

Fig. S4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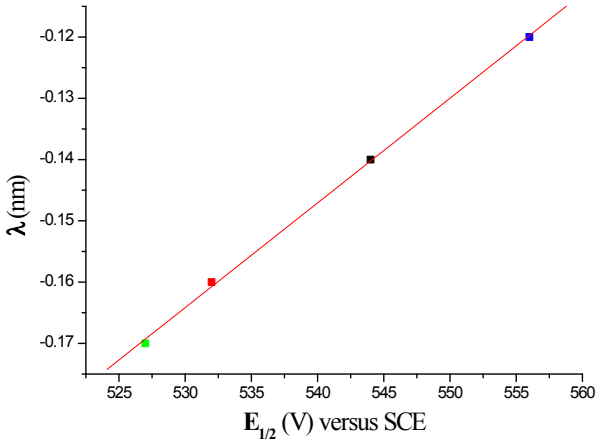
(100 mV/s)
(200 mV/s)
(400 mV/s)
(1)
E (V) versus SCE
(2)
E (V) Versus SCE
(3)
E (v) Versus SCE
(4)
I (μA)

Fig. S5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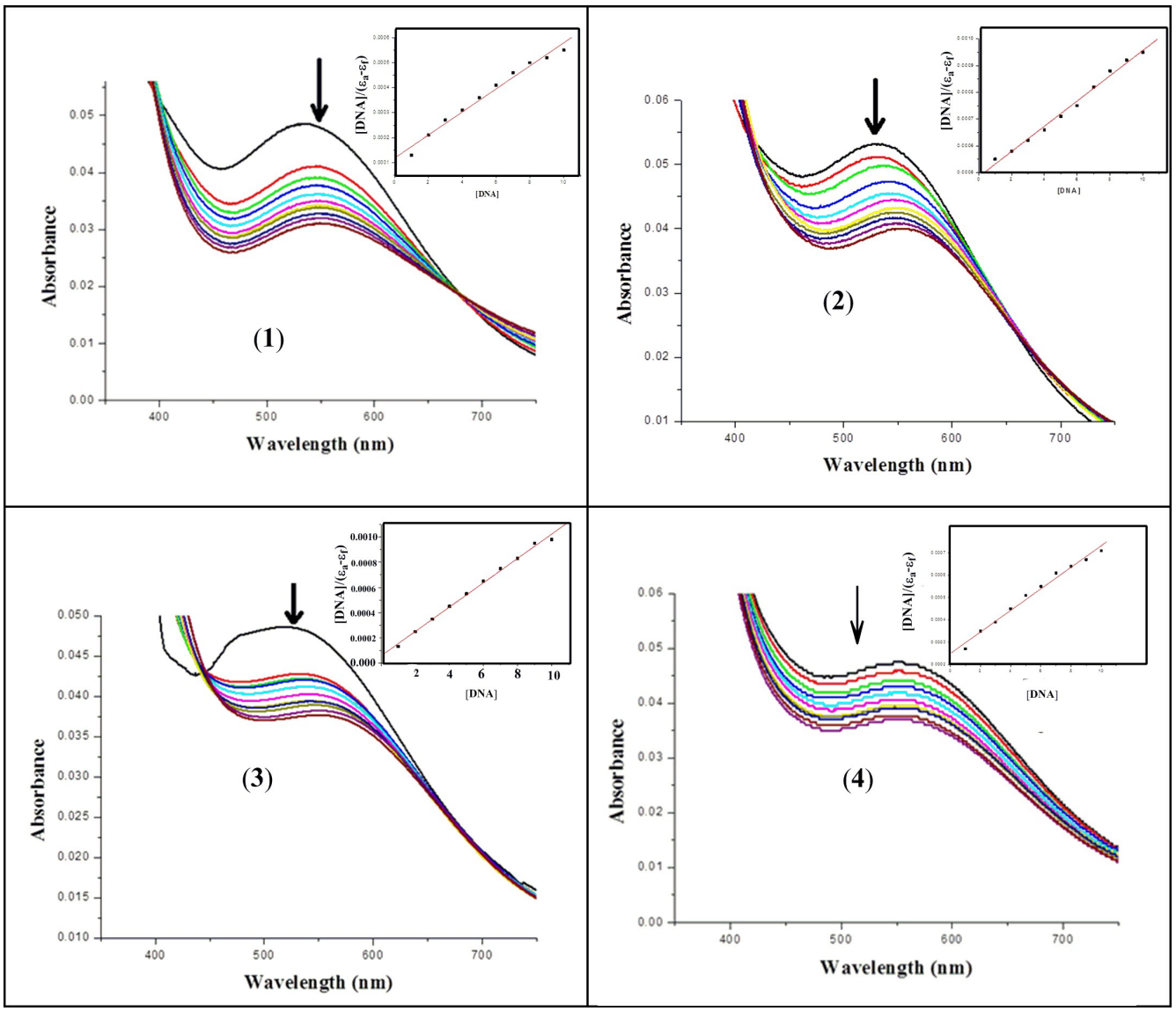
530
535
540
545
550
555
560
E1/2 (V) versus SCE

Fig. S6


Absorbance
Wavelength (nm)
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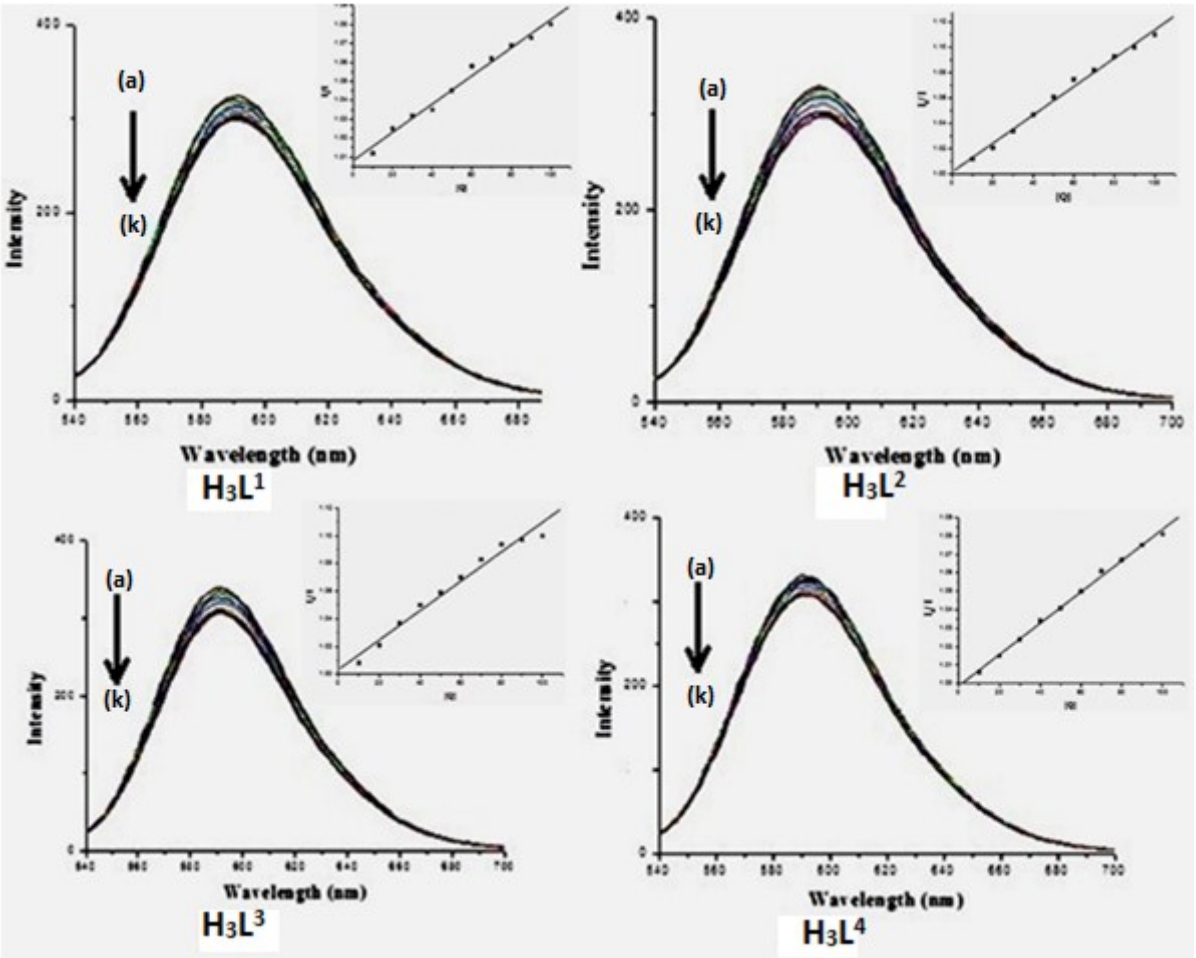
(2)
(3)
(4)
[DNA]/(εa-εf)
[DNA]

Fig. S7


(a)
(k)
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Wavelength (nm)
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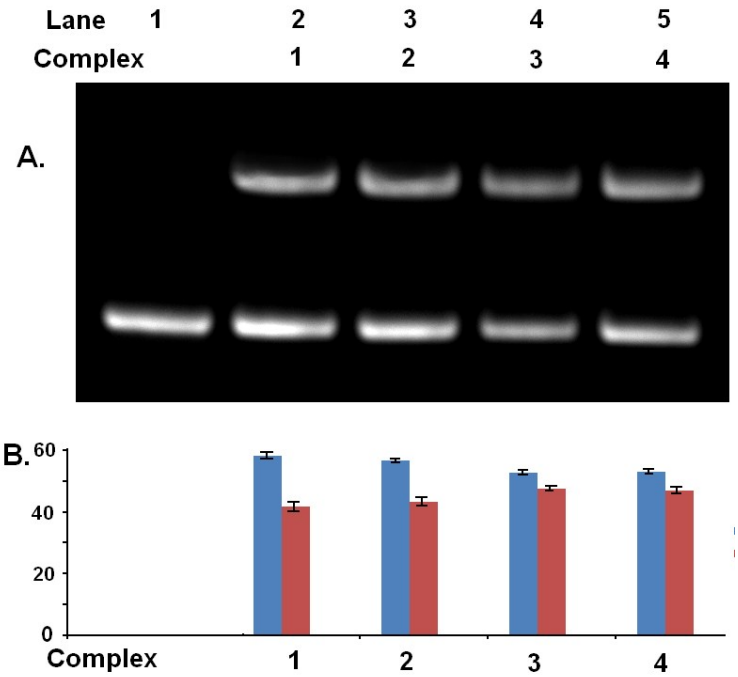
H3L2
H3L3
H3L4

Fig. S8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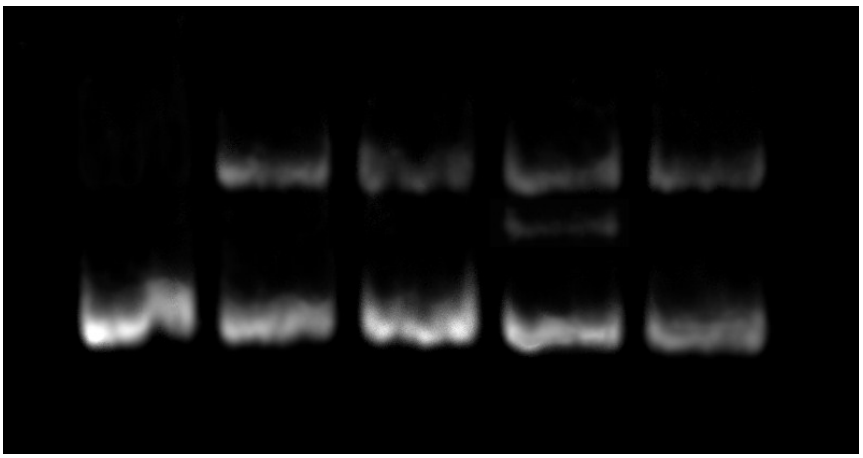
Complex 1 2 3 4
A.
B.
60
40
20
0
Complex 1 2 3 4

Fig. S9

Lane	1	2	3	4	5
Ligand		H_3L^1	H_3L^2	H_3L^3	H_3L^4



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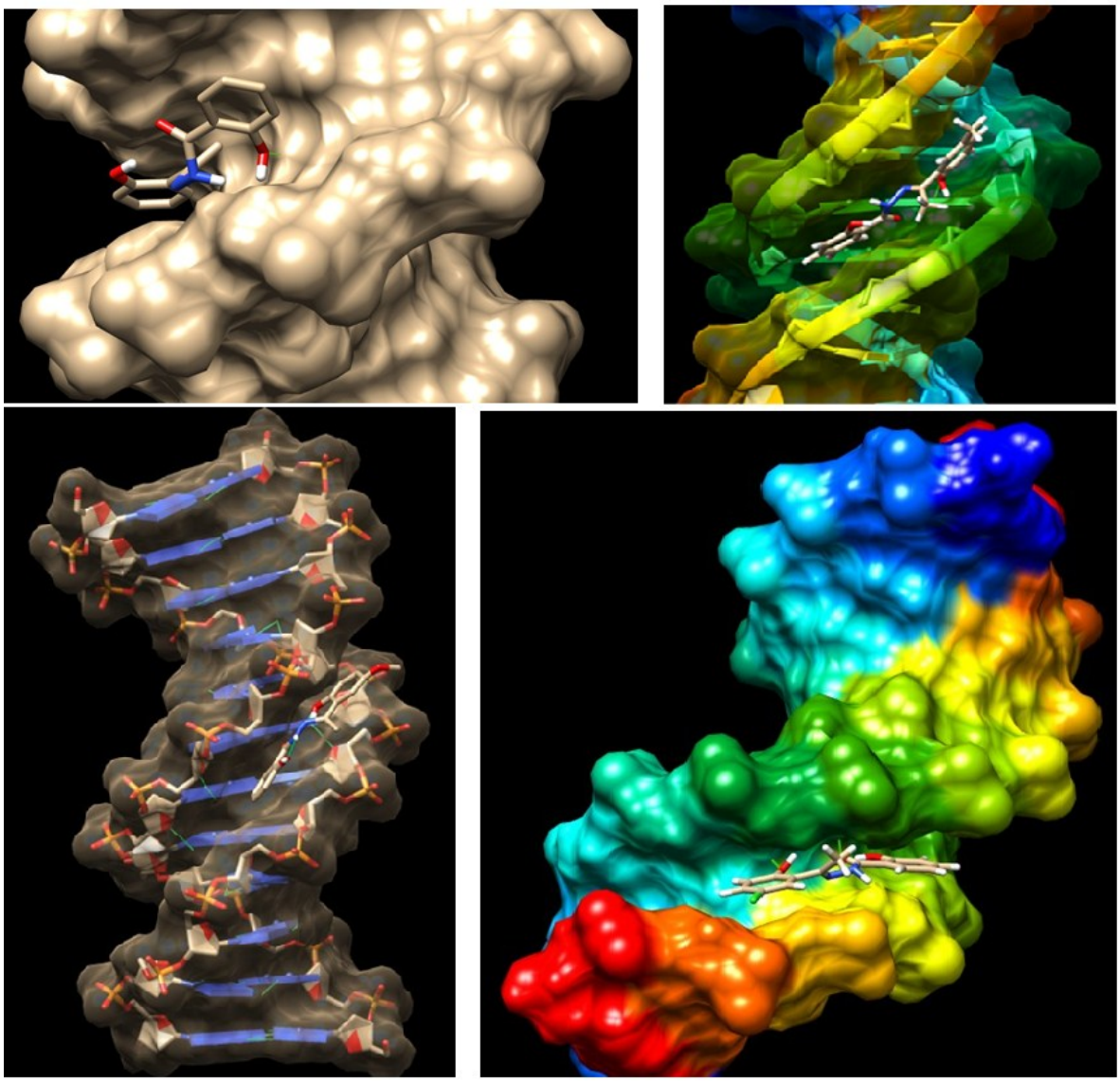

Fig. S11