Electronic Supplementary Material (ESI) for New Journal of Chemistry.

DNA/HSA binding and anticancer property of pendant acetate bearing mono-nuclear Ni(II) and bridging acetate bearing di-nuclear Cu(II) Schiff base complexes: An experimental and molecular docking exploration

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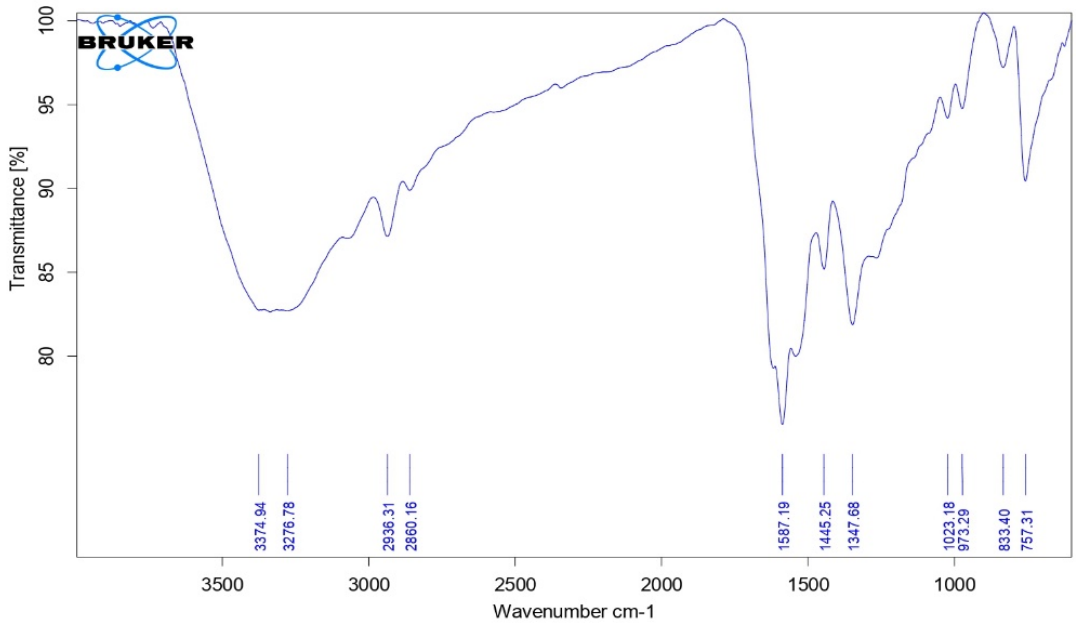


Fig. S1: FTIR spectrum of ligand **HL**

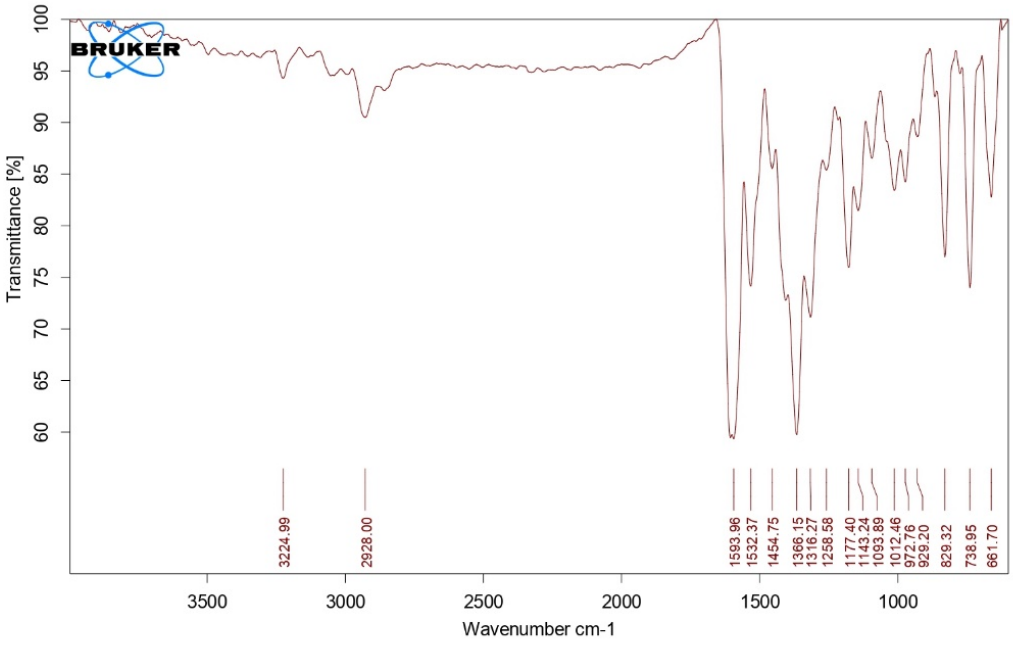


Fig. S2: FTIR spectrum of Complex **1**

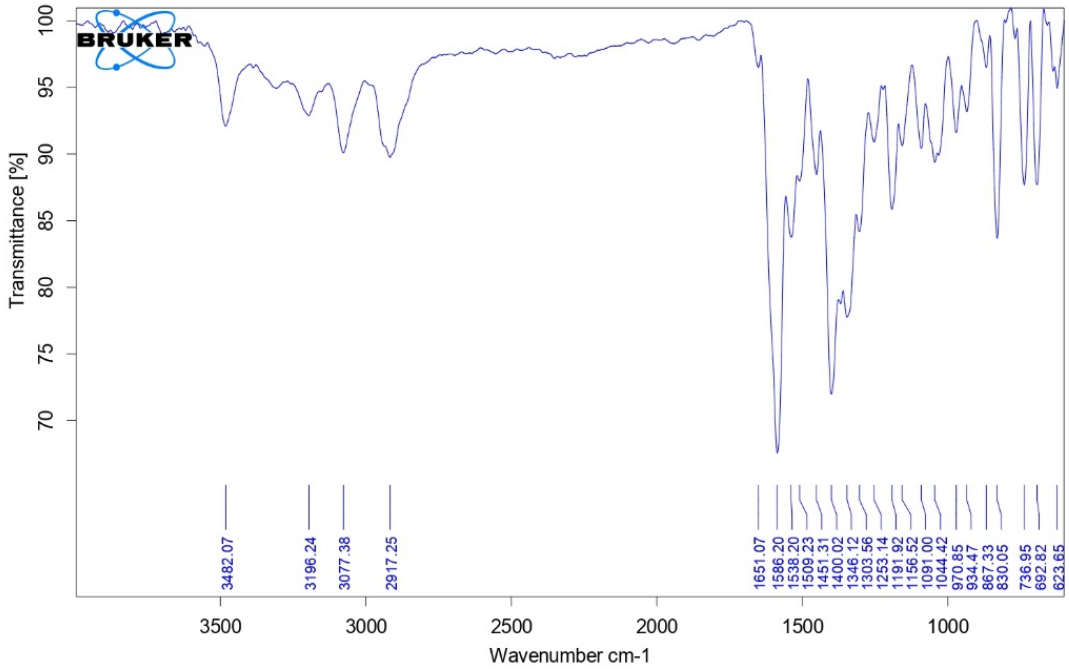


Fig. S3: FTIR spectrum of Complex **2**

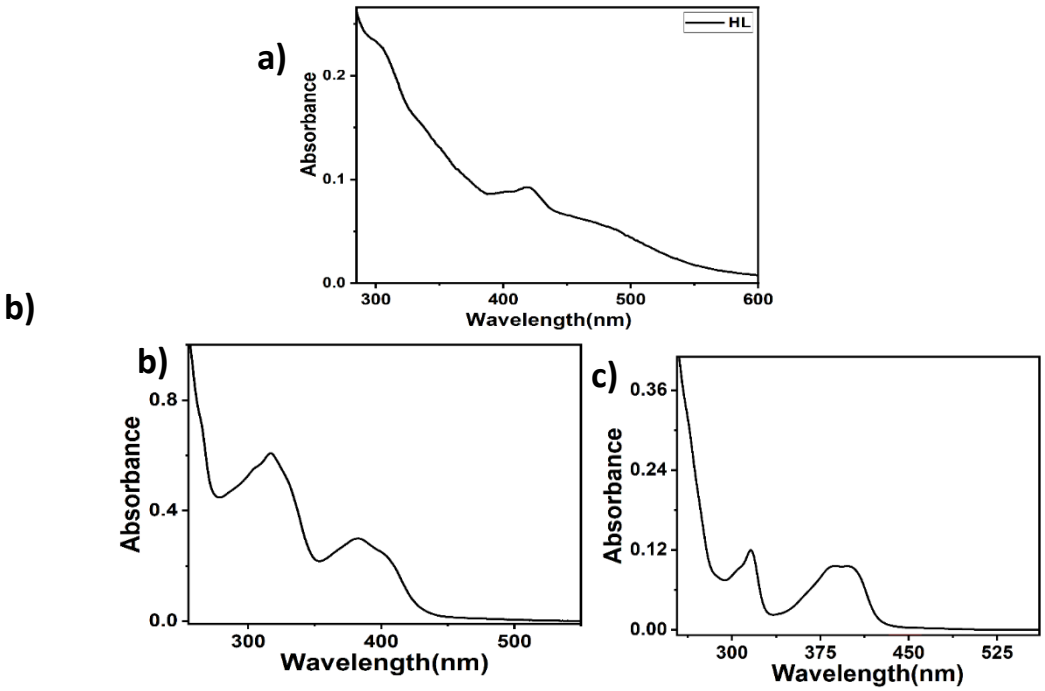


Fig. S4: UV spectra of (a) ligand **HL**, (b) complex **1** and (c) complex **2** in DMSO solvent.

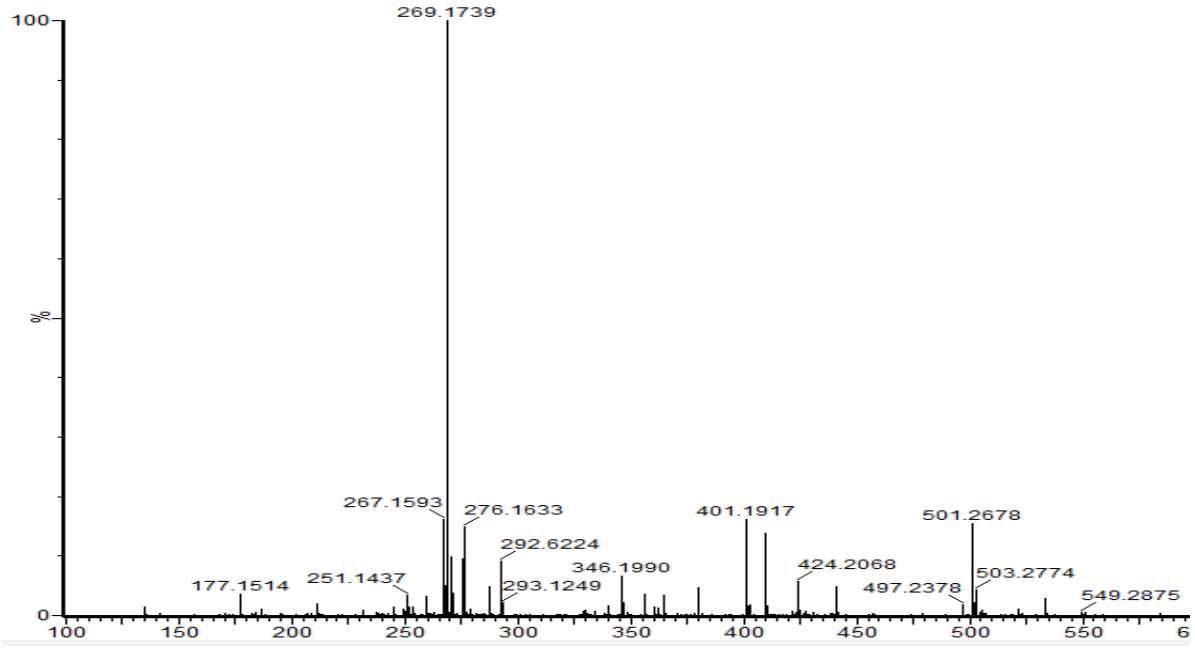


Fig. S5: Mass spectrum of ligand **HL**

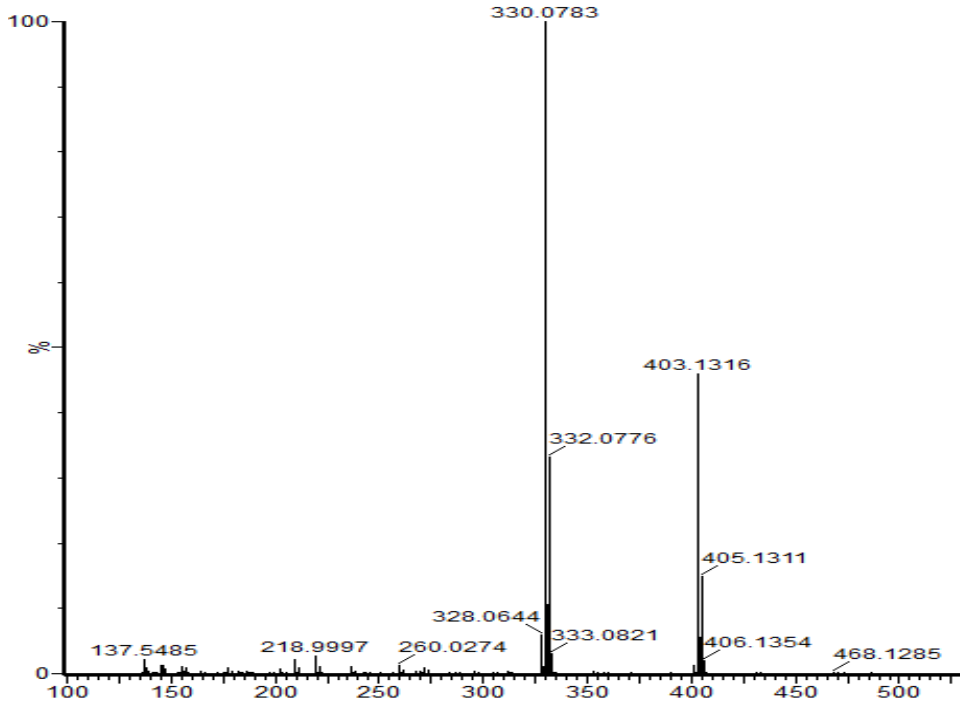


Fig. S6: Mass spectrum of Complex **1**

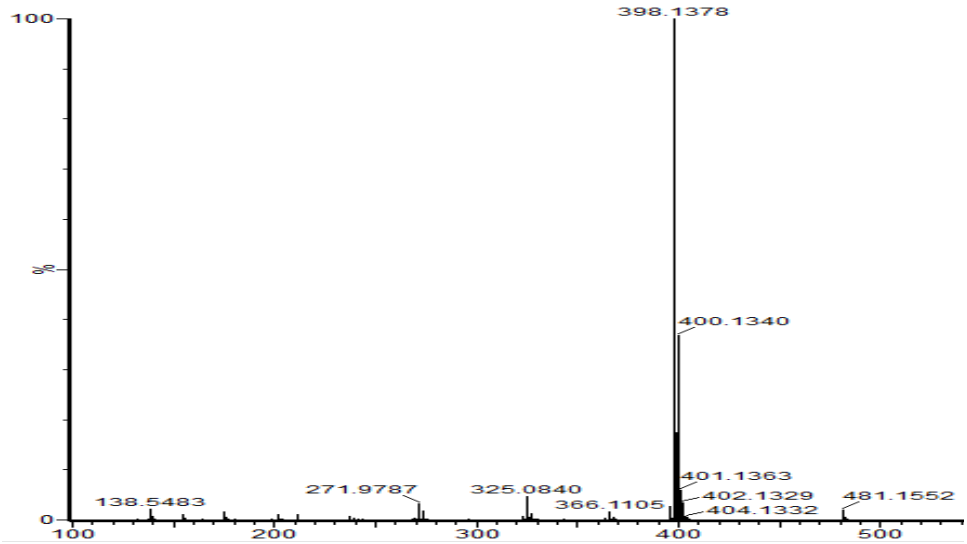


Fig. S7: Mass spectrum of Complex **2**

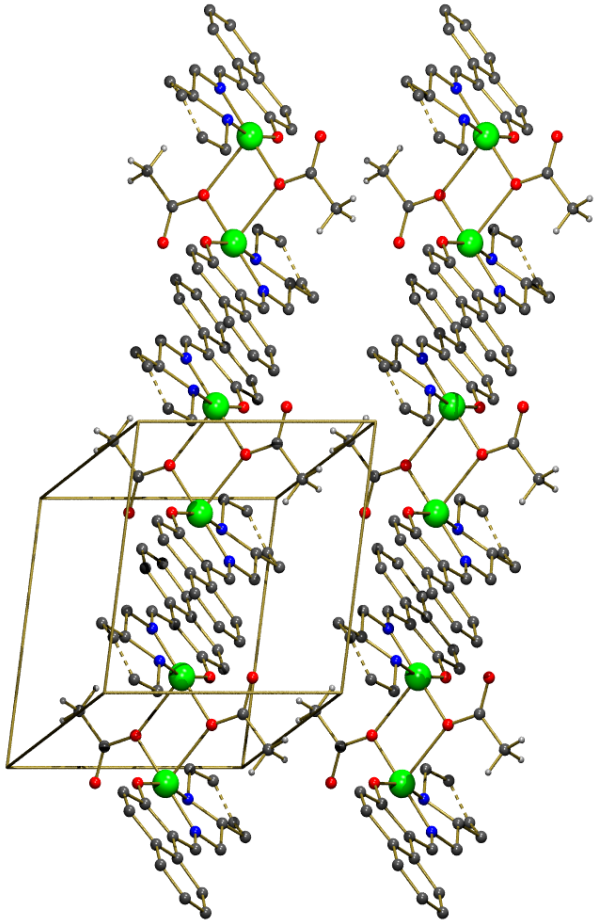


Fig. S8: The self-assembly of the Cu(II) units in the *ab*-plane in complex **2**.

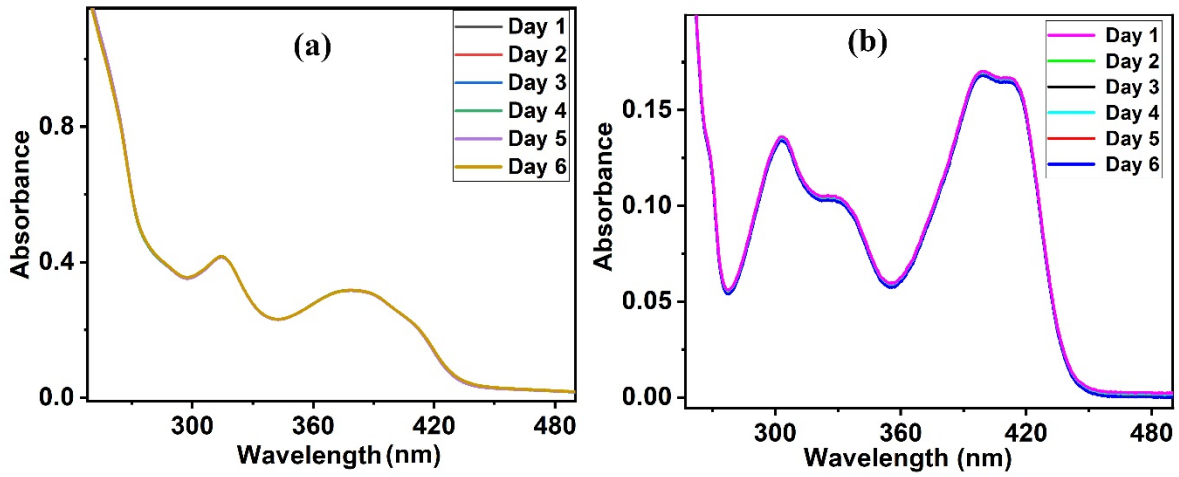


Fig. S9: (a) Change of absorbance of Complex **1** and (b) Complex **2** in buffer medium at working pH 7.4 as a function of time.

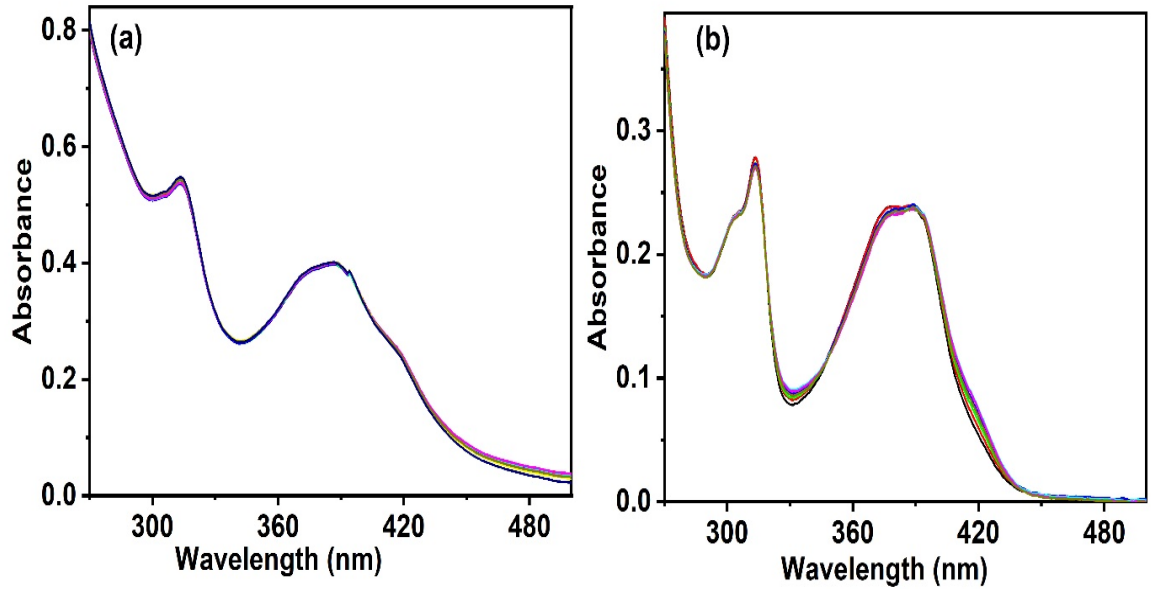


Fig. S10: Absorbance change due to dilution effect of a) complex **1** b) complex **2**

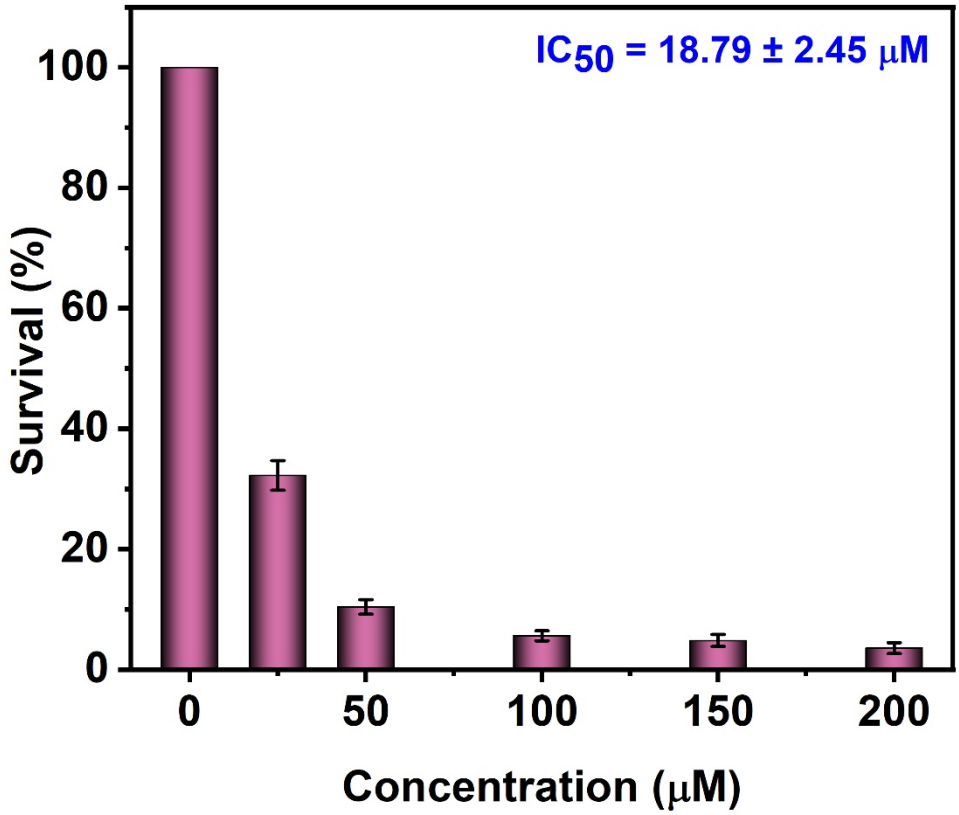


Fig. S11: Cell viability of HeLa cell line after incubation with cisplatin via dose-dependent manner for 24 hrs.

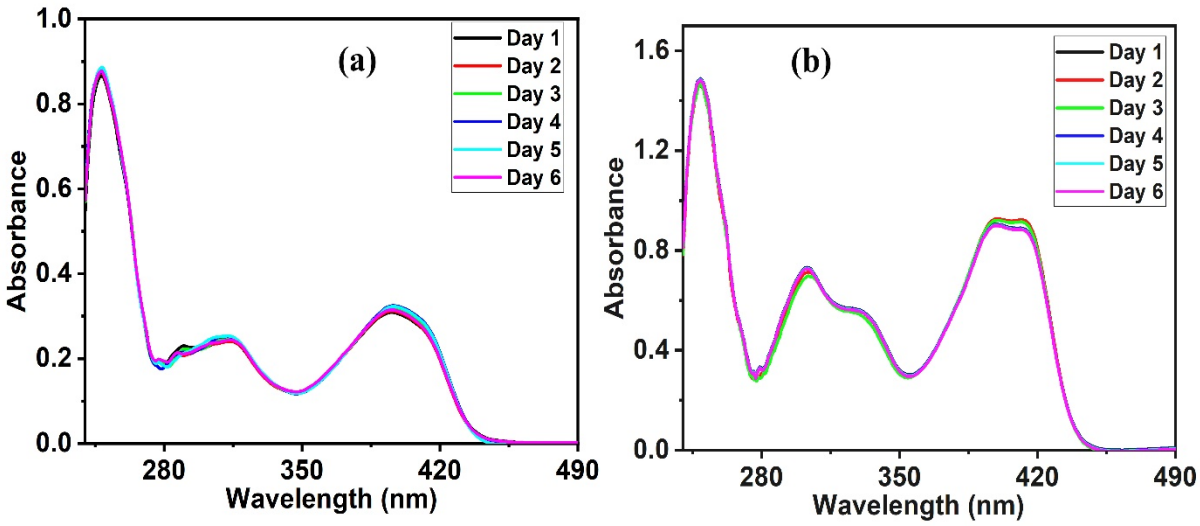


Fig. S12: (a) Change of absorbance of Complex **1** and (b) Complex **2** in cell culture solution.

Table S1: Simulated IR and Experimental FTIR spectral data of complex **1** and **2**

Complex 1							
	C=N	**C=O**	**C=C**	**Aromatic C – H**	**Aliphatic C – H**	**Aromatic ring vibration**	**Ni – O stretching**
Simulated (cm^{-1})	1629	1562	1592	3225	3031	1492	907
Experimental (cm^{-1})	1593	1532	1594	3224	3057	1457	929
Complex 2							
	C=N	**C=O**	**C=C**	**Aromatic C – H**	**Aliphatic C – H**	**Aromatic ring vibration**	**Cu – O stretching**
Simulated (cm^{-1})	1649	1564	1678	3207	3034	1489	910
Experimental (cm^{-1})	1586	1538	1651	3196	3072	1509	934

Bond Distances			
Ni1 -O1	1.8429(11)	Ni1 -N1	1.8392(11)
Ni1 -O2	1.8811(11)	Ni1 -N2	1.9223(11)
Bond Angles			
O1 -Ni1 -O2	87.68(5)	O2 -Ni1 -N1	175.36(5)
O1 -Ni1 -N1	93.94(5)	O2 -Ni1 -N2	92.69 (5)
O1 -Ni1 -N2	177.03(5)	N1 -Ni1 -N2	85.48(5)

Table S2: Bond Distances(Å) and Bond Angles (º) for complex **1**

Table S3: C-H···π and π···π interaction parameters for complex **1**

Y-X-Cg(i)	Symmetry	X-Cg(j)	gamma
C13-H13···Cg2	3/2-x,1/2-y, 1-z	2.546(14)	155.8(14)
C15-H15B···Cg4	3/2-x,1/2-y, 1-z	2.82	152
C15-H15B···Cg6	3/2-x,1/2-y, 1-z	2.89	176
Cg2: Ni1-O1-C1-C10-C11-N1 (six member chelate ring) Cg4: C1-C2-C3-C4-C9-C10 Cg6: C4-C5-C6-C7-C8-C9			

Cg(i)-Cg(j)	Symmetry	distance Cg(i)-Cg(j)	α (dihedral anlge)	β (slipanlge)	dist_perpi-j	dist_perp j-i
Cg5···Cg5	1-x, y, 3/2-z	4.4536(13)	4.68(11)	23.6	4.0816(10)	4.0815(10)
Cg5: C4-C5-C6-C7-C8-C9						

Table S4: Hydrogen Bonding parameters for complex **1**

D-H···A	D-H(Å)	H-A(Å)	D-A(Å)	<D-H···A(º)	symmetry
N2 ···H2···O100	1.0000	1.8600	2.8611(16)	175.00	x,1-y,1/2+z
O100-H10A···O1	0.76(3)	2.21(3)	2.9366(18)	163(3)	3/2-x,3/2-y,1-z
O100-H10B···O3	0.79(3)	1.93(3)	2.7234(18)	179(4)	.
C2-H2···O100	0.9500	2.5600	3.321(2)	137.00	3/2-x,3/2-y,1-z
C12-H12A···O3	0.9900	2.4100	3.3343(19)	154.00	3/2-x,1/2-y,1-z
C12-H12B···O2	0.9900	2.5200	3.3267(18)	139.00	3/2-x,-1/2+y,3/2-z
C17-H17A···O2	0.9900	2.4900	2.9193(18)	106.00	.

Table S5: Bond Distances(Å) and Bond Angles (º) for complex **2**

Bond Distances			
Cu1 -O1	1.9169(15)	Cu1 -O3	2.8205(18)
Cu1 -O2	1.9561(16)	Cu1 -N1	1.9381(18)
Cu1 -O2_a	2.5157(16)	Cu1 -N2	2.097(4)
Bond Angles			
O1 -Cu1 -O2	90.14(7)	O2 -Cu1 -N2A	95.78(16)
O1 -Cu1 -O3	90.68(6)	O2 -Cu1 -O2_a	78.13(6)
O1 -Cu1 -N1	90.84(7)	O3 -Cu1 -N1	127.74(7)
O1 -Cu1 -N2	164.76(11)	O3 -Cu1 -N2	81.78(10)
O1 -Cu1 -N2A	172.33(15)	O3 -Cu1 -N2A	96.81(15)
O1 -Cu1 -O2_a	97.89(6)	O2_a -Cu1 -O3	129.17(5)
O2 -Cu1 -O3	51.72(6)	N1 -Cu1 -N2	83.48(11)
O2 -Cu1 -N1	178.89(7)	N1 -Cu1 -N2A	83.29(16)
O2 -Cu1 -N2	95.45(11)	O2_a -Cu1 -N1	102.25(6)
O2_a -Cu1 -N2A	78.64(15)	O2_a -Cu1 -N2	97.13(10)

Symmetry code: a= 1-x,-y,1-z

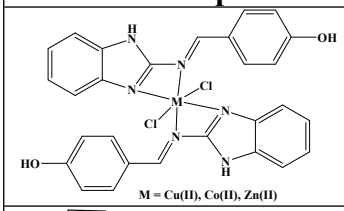
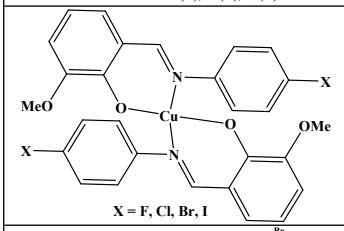
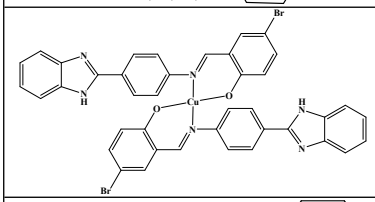
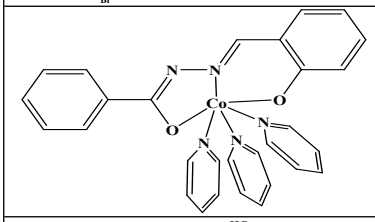
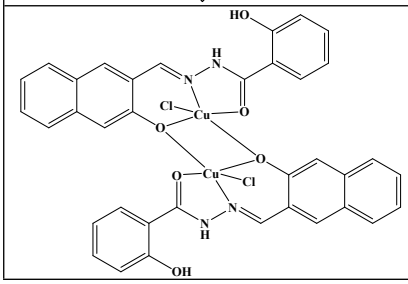
Table S6: Hydrogen Bonding parameters for complex **2**

D-H···A	D-H(Å)	H-A(Å)	D-A(Å)	<D-H···A(º)	symmetry
C11-H11···O3	0.9500	2.5100	3.311(3)	142.00	1-x,1-y,1-z
C17-H17D···O1	0.9900	2.4800	3.305(11)	140.00	1-x,-y,1-z

Table S7: π···π interaction parameters for complex **2**

Cg(i)-Cg(j)	Symmetry	distance Cg(i)-Cg(j)	α (dihedral anlge)	β (slipanlge)	dist_perpi-j	dist_perp j-i
Cg1···Cg2	1-x, 1-y, -z	3.9803(16)	3.12(12)	27.8	3.5600(10)	3.5222(11)
Cg2···Cg2	1-x, 1-y, -z	3.8024(17)	0.00(13)	22.5	3.5117(11)	3.5117(11)
Cg1: C1-C2-C3-C4-C9-C10 Cg2: C4-C5-C6-C7-C8-C9						

Table S8: Binding constant values of DNA with some complexes reported in literature

Complex	DNA Binding Constant	Reference
 M = Cu(II), Co(II), Zn(II)	7.85×10^3 (M^{-1})	01
 X = F, Cl, Br, I	$6.00 – 7.18 \times 10^3$ (M^{-1})	02
	3.1×10^4 (M^{-1})	03
	1.11×10^3 (M^{-1})	04
	1.5×10^3 (M^{-1})	05

References

1. M. Chaurasia, D. Tomar and S. Chandra, Polyhedron, 2019, **1179**, 431 – 442.
2. H. Kargar, R. B. Ardakani, V. Torabi, M. Kashani, Z. C. Natanzi, Z. Kazemi, V. Mirkhani, A. Sahraei, M. N. Tahir, M. Ashfaq and K. S. Munawar, Polyhedron, 2021, **195**, 114988.
3. K. Mahmood, W. Hashmi, H. Ismail, B. Mirza, B. Twamley, Z. Akhter, I. Rozas and R. J. Baker, Polyhedron, 2019, **157**, 326 – 334.
4. R. Fekri, M. Salehi, A. Asadi and M. Kubicki, Appl Organometal Chem. 2017, **e4019**, https://doi.org/10.1002/aoc.4019.

5. G. S. Kurdekar, S. M. Puttanagouda, N. V. Kulkarni, S. Budagumpi, V. K. Revankar, Med. Chem. Res., **2011**, **20,** 421 – 429.

Table S9: Binding score for the binding of complex **1** at DNA minor groove

Binding Score	**rmsd**	**E_conf**	**E_place**	**E_score1**
-9.5594101	10.488411	0	-29.258413	-9.5594101
-9.3701439	8.7533636	0.56503946	-47.719463	-9.3701439
-11.047505	8.308754	0	-27.411764	-11.047505
-9.3415585	8.2763529	0	-7.357955	-9.3415585
-9.8312378	8.2362041	0	-15.60262	-9.8312378
-9.8041391	8.0928917	0	-27.926329	-9.8041391
-10.428911	8.0422945	0	-31.261625	-10.428911
-9.8156738	7.9198937	0	-24.408472	-9.8156738
-9.2146139	7.8929663	0	-18.989803	-9.2146139
-9.5606594	7.8854451	0	-20.897652	-9.5606594
-9.4773407	7.8655391	0	-16.60873	-9.4773407
-10.65127	6.946672	0	-36.728935	-10.65127
-10.579386	6.9138622	0	-6.9834809	-10.579386
-9.8165855	6.7983298	0	-24.772211	-9.8165855
-9.7815619	6.7819691	0	-23.173199	-9.7815619
-10.466742	6.7427049	0	-35.744019	-10.466742
-10.014174	6.725348	0	-26.426285	-10.014174
-9.3460083	6.7120452	0.56503946	-6.9501171	-9.3460083
-9.8219976	6.7046294	0.56503946	-45.995399	-9.8219976
-9.4139929	5.9468622	0	-22.850506	-9.4139929
-10.464808	5.7475972	0	-45.201443	-10.464808
-9.1699371	5.2748322	0	-40.907139	-9.1699371
-10.239324	4.826117	0	-42.504494	-10.239324
-9.5261583	4.8025103	0.56503946	-37.755032	-9.5261583
-9.9426317	4.6285958	0	-7.988975	-9.9426317
-9.8561363	3.461	0	-33.452847	-9.8561363
-9.8886337	2.8937013	0	-31.809496	-9.8886337
-9.2372942	2.3774436	0	-10.461962	-9.2372942

Table S10: Binding score for the binding of complex **1** at DNA intercalation

Binding Score	rmsd	E_conf	E_place	E_score1
-9.1757507	6.8858218	0	-34.289497	-9.1757507
-9.0425463	6.7221174	0	-24.589159	-9.0425463
-8.6169291	6.5470996	0.32843167	-18.139566	-8.6169291
-8.7210093	6.1920862	0.32843167	-22.023687	-8.7210093
-9.3036423	6.1247444	0.32843167	-48.945301	-9.3036423
-8.9104614	6.0980945	0.97340041	-47.2509	-8.9104614
-8.6550436	6.0806723	0	-36.34576	-8.6550436
-8.413003	5.7562723	0.97340041	-56.554913	-8.413003
-9.3407478	5.7073784	0.32843167	-41.32272	-9.3407478
-9.0992947	5.4279003	0.32843167	-31.327869	-9.0992947
-8.5718279	5.402513	0.3221418	-31.888582	-8.5718279
-8.4810715	5.3780131	0.32843167	-51.250965	-8.4810715
-8.825263	5.3610024	0	-47.116901	-8.825263
-8.9347849	5.3297706	0.32843167	-22.10146	-8.9347849
-9.7532206	5.2968497	0.32843167	-27.016434	-9.7532206
-10.131186	5.2389417	0.32843167	-28.474257	-10.131186
-10.304563	5.1329727	0.3221418	-43.593754	-10.304563
-9.633791	5.0156713	0.3221418	-31.751921	-9.633791
-10.941286	4.9775343	0.3221418	-18.050821	-10.941286
-8.6640491	4.966023	0.97340041	-45.04789	-8.6640491
-8.6922283	4.9561458	0.97340041	-44.111336	-8.6922283
-9.5288811	4.9195657	0.97340041	-58.275349	-9.5288811
-9.0856762	4.7829452	0.32843167	-17.636602	-9.0856762
-9.4218464	4.7116346	0.97340041	-47.845276	-9.4218464
-8.527462	4.6860142	0	-51.589344	-8.527462
-9.2608871	4.6169739	0.3221418	-37.966972	-9.2608871
-9.0271673	4.5675316	0	-33.014801	-9.0271673
-10.6928072	3.8527055	0.97340041	-23.840168	-9.6928072
-10.3216566	2.7877915	0.3221418	-27.826639	-9.4616566

Table S11: Binding score for the binding of complex **2** at DNA minor groove

Binding Score	rmsd	E_conf	E_place	E_score1
-5.1857719	11.436229	0	97.250511	-5.1857719
-5.139678	9.0602036	0	174.02473	-5.139678
-7.2216291	9.0462446	0	66.290627	-7.2216291
-5.8535321	8.8219395	0	119.60373	-3.8535321
-4.6029191	8.7690754	0	71.073364	-4.6029191
-4.8598709	8.5990124	0	93.622353	-4.8598709
-5.4226975	8.3615885	0	106.24297	-5.4226975
-5.8418376	8.0120306	0	354.67075	-3.8418376
-4.0858569	7.8855586	0	126.70719	-4.0858569
-7.9352536	7.7861276	0	122.00208	-7.9352536
-7.4254193	7.5623584	0	70.892532	-7.4254193
-6.270031	7.3722315	0	111.62238	-6.270031
-4.0475793	7.2914929	0	314.2995	-4.0475793
-6.6081805	7.1947985	0	100.29273	-6.6081805
-5.6007333	7.1145511	0	92.111107	-5.6007333
-8.632472	7.0933418	0	60.790539	-9.632472
-8.1107388	7.0303464	0	50.607258	-9.1107388
-7.4566426	7.004076	0	90.704697	-7.4566426
-4.6959662	6.6617689	0	158.55688	-4.6959662
-4.2632871	6.3792753	0	31.003098	-4.2632871
-6.4156265	6.1319251	0	42.936256	-6.4156265
-4.0423818	6.0040855	0	105.14465	-4.0423818
-5.4528904	5.0807004	0	92.31765	-5.4528904
-6.1066651	4.8778548	0	51.703781	-6.1066651
-6.6465163	4.1891012	0	68.526207	-6.6465163
-4.751729	4.013875	0	120.81822	-4.751729
-4.6030588	3.1987524	0	68.977112	-4.6030588
-4.7474484	2.262897	0	133.01314	-4.7474484
-6.39643	1.6939558	0	96.033363	-6.39643
-8.957859	1.1584539	0	-7.1701484	-10.957859

Table S12: Binding score for the binding of complex **1** with HSA

Binding Score	rmsd	E_conf	E_place	E_score1
-10.720331	6.67345	0	-47.032963	-10.720331
-10.787185	5.811023	0	-45.286308	-10.787185
-12.026942	5.675232	0	-63.61377	-12.026942
-12.715164	5.674405	0	-65.97805	-12.715164
-12.788953	5.603033	0.5635969	-46.79921	-12.788953
-10.845725	5.505134	0	-76.004616	-10.845725
-11.580856	5.485235	0	-45.145054	-11.580856
-11.688602	5.37348	0	-55.357204	-11.688602
-13.18986	5.312163	0	-58.681335	-13.18986
-11.404141	5.203543	0	-54.618889	-11.404141
-12.929245	5.176729	0.5635969	-62.868744	-12.929245
-13.142697	5.154055	0	-47.367599	-13.142697
-11.091172	5.124368	0	-50.175652	-11.091172
-11.63429	5.092594	0.5635969	-54.403316	-11.63429
-10.69925	5.087902	0.5635969	-50.38768	-10.69925
-12.331975	5.08509	0.5635969	-50.138313	-12.331975
-11.666287	5.027835	0.5635969	-46.188126	-11.666287
-10.858206	5.020379	0	-87.362656	-10.858206
-10.844515	4.9905767	0	-46.777302	-10.844515
-10.816071	4.9540067	0	-50.11031	-10.816071
-12.291677	4.9414034	0	-46.242447	-12.291677
-10.973258	4.8814468	0	-50.420715	-10.973258
-11.396079	4.8300247	0	-61.759968	-11.396079
-10.692629	4.6763783	0	-62.886478	-10.692629
-10.756347	4.6629386	0	-52.436111	-10.756347
-10.850788	4.1815052	0	-75.747627	-10.850788
-10.673301	3.4172621	0	-95.411407	-10.673301
-10.691599	2.6416392	0	-78.054367	-10.691599
-10.661953	2.4864502	0	-57.92662	-10.661953
-10.850429	2.3283477	0	-68.022697	-10.850429

Table S13: Binding score for the binding of complex **2** with HSA

Binding Score	rmsd	E_conf	E_place	E_score1
-11.736822	9.0072575	0	-75.193123	-11.736822
-12.607366	6.877202	0	-92.89312	-12.607366
-12.460502	6.8224483	0	-40.366917	-12.460502
-12.405087	6.7066588	0	-98.615112	-12.405087
-12.249303	6.5962796	0	-38.848248	-12.249303
-11.706466	6.5779605	0	-88.803383	-11.706466
-11.963461	6.3602362	0	-90.334488	-11.963461
-12.376112	6.330719	0	-78.519203	-12.376112
-11.547637	5.9639521	0	-62.038059	-11.547637
-11.523037	5.7846317	0	-97.570129	-11.523037
-11.96915	5.5169139	0	-56.425022	-11.96915
-11.987286	5.4725761	0	-47.442356	-11.987286
-11.722466	5.4419847	0	-98.97348	-11.722466
-12.661026	5.4403319	0	-88.283401	-12.661026
-12.639564	5.3680415	0	-88.787437	-12.639564
-12.421879	5.3206921	0	-75.478432	-12.421879
-11.767261	5.0970526	0	-72.018806	-11.767261
-11.588616	5.0771875	0	-63.95927	-11.588616
-12.575379	5.0572915	0	-75.965279	-12.575379
-12.82082	4.9196701	0	-71.663315	-12.82082
-12.224266	4.7611771	0	-79.519676	-12.224266
-12.821813	4.7278781	0	-63.884499	-12.821813
-11.705542	4.6552944	0	-58.399265	-11.705542
-12.842366	4.6510158	0	-77.404785	-12.842366
-11.867752	3.6939485	0	-22.880098	-11.867752
-11.985737	3.1135659	0	-66.376793	-11.985737
-11.803231	2.2300398	0	-46.704292	-11.803231
-12.065418	1.7545201	0	-77.391121	-12.065418
-11.803637	1.6245247	0	-43.038303	-11.803637
-11.51976	1.4467862	0	-66.892357	-11.51976