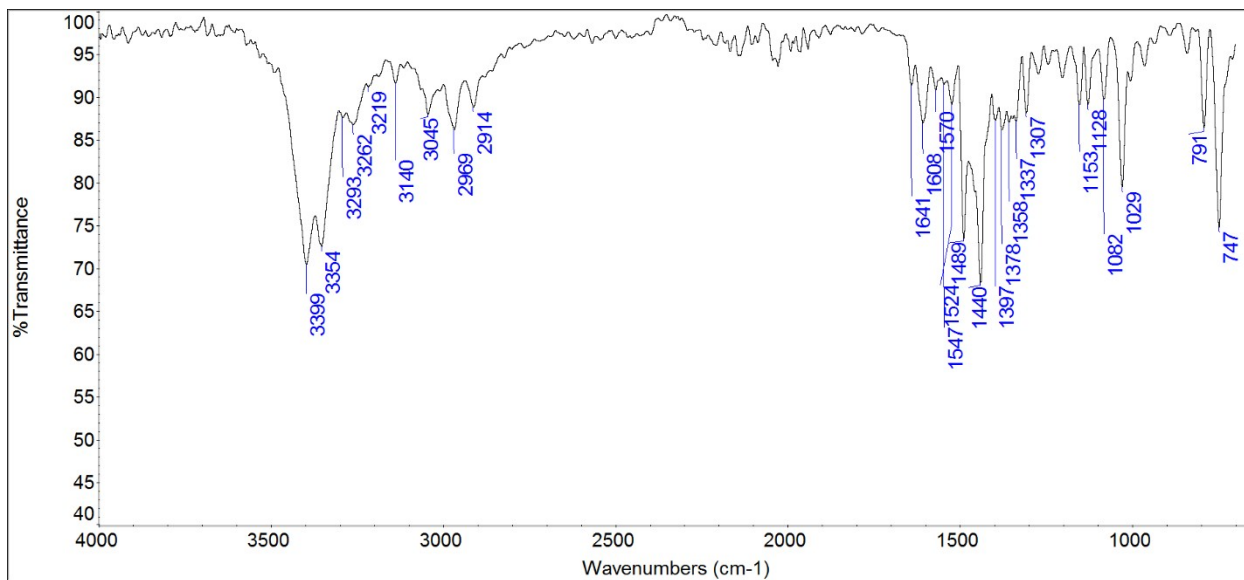
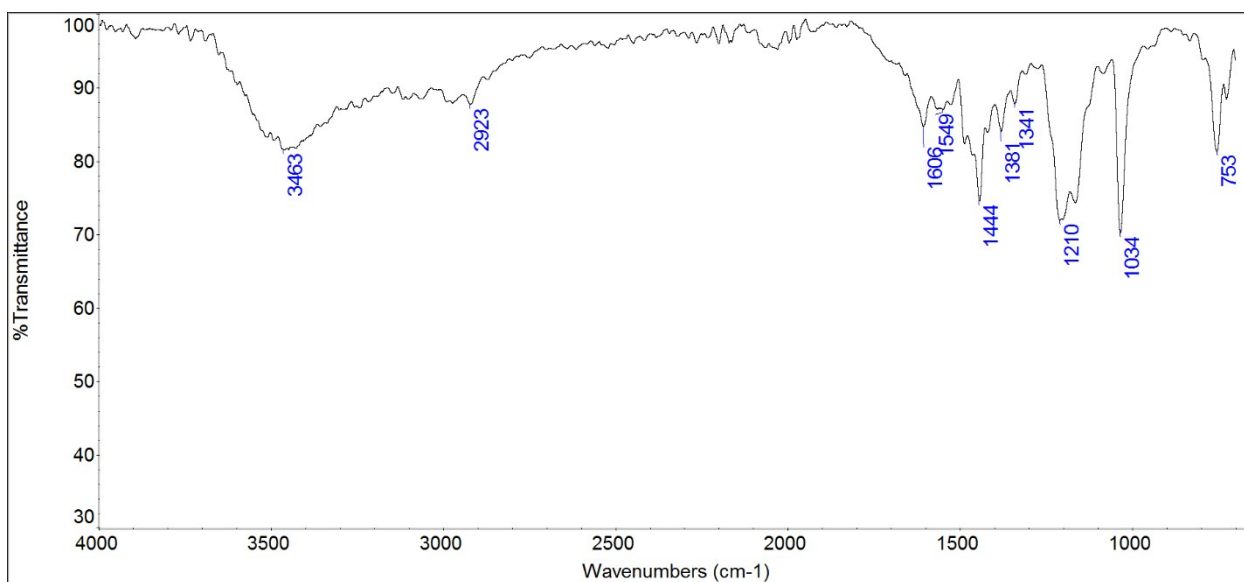


Supporting Information

Figure S1	AT IR spectra of half-sandwich Ir(III) compounds a) 1 , b) 2 and c) 3 .
Figure S2	NMR analysis of $[\{\eta^5\text{-C}_5\text{Me}_5\}\text{IrCl}]_2(\mu\text{-Cl})_2$ in CDCl_3 , a) ^1H and b) ^{13}C .
Figure S3	NMR analysis of 1 in $[\text{D}_6]$ DMSO, a) ^1H , b) ^{13}C , c) $\{^1\text{H}, ^1\text{H}\}$ COS90 and d) $\{^{13}\text{C}, ^1\text{H}\}$ HSQC.
Figure S4	NMR analysis of 2 in $[\text{D}_6]$ DMSO, a) ^{13}C , and b) $\{^{13}\text{C}, ^1\text{H}\}$ HSQC.
Figure S5	NMR analysis of 3 in CD_3CN , a) ^1H , b) ^{13}C , and c) $\{^{13}\text{C}, ^1\text{H}\}$ HSQC.
Table S1	Atomic coordinates of the optimized structure of 1 .
Table S2	Atomic coordinates of the optimized structure of 2 .
Table S3	Atomic coordinates of the optimized structure of 3 .
Figure S6	Absorption spectra of complex a) 1 and b) 2 in Tris-buffer (in 20% (v/v) DMSO/tris-buffer (NaCl 50 mM, Tris-HCl 5 mM, pH = 7.4)), in absence ($R = 0.0$) and presence ($R > 0.0$) of increasing amounts of calf-thymus DNA ($R = [\text{DNA}]/[\text{complex}]$, $[\text{complex}] = 3.22 \times 10^{-5}$ M (1) and 2.80×10^{-5} M (2)).
Table S4	Computed excitation energies (eV), electronic transition configurations and oscillator strengths (f) of the studied complexes (selected).
Figure S7	Selected Frontiers molecular orbitals of 2 calculated at B3LYP/LANL2DZ level of theory.
Figure S8	Stability of a) 1 and b) 2 (aromatic region) in $[\text{D}_6]$ DMSO followed by ^1H NMR at different time interval [a (10 min), b (1 h), c (6 h) and d (24 h)].
Figure S9	^{13}C NMR spectra of complex 1 ($[\text{D}_6]$ DMSO) in presence and absence of imidazole.
	Biological studies



a)



b)

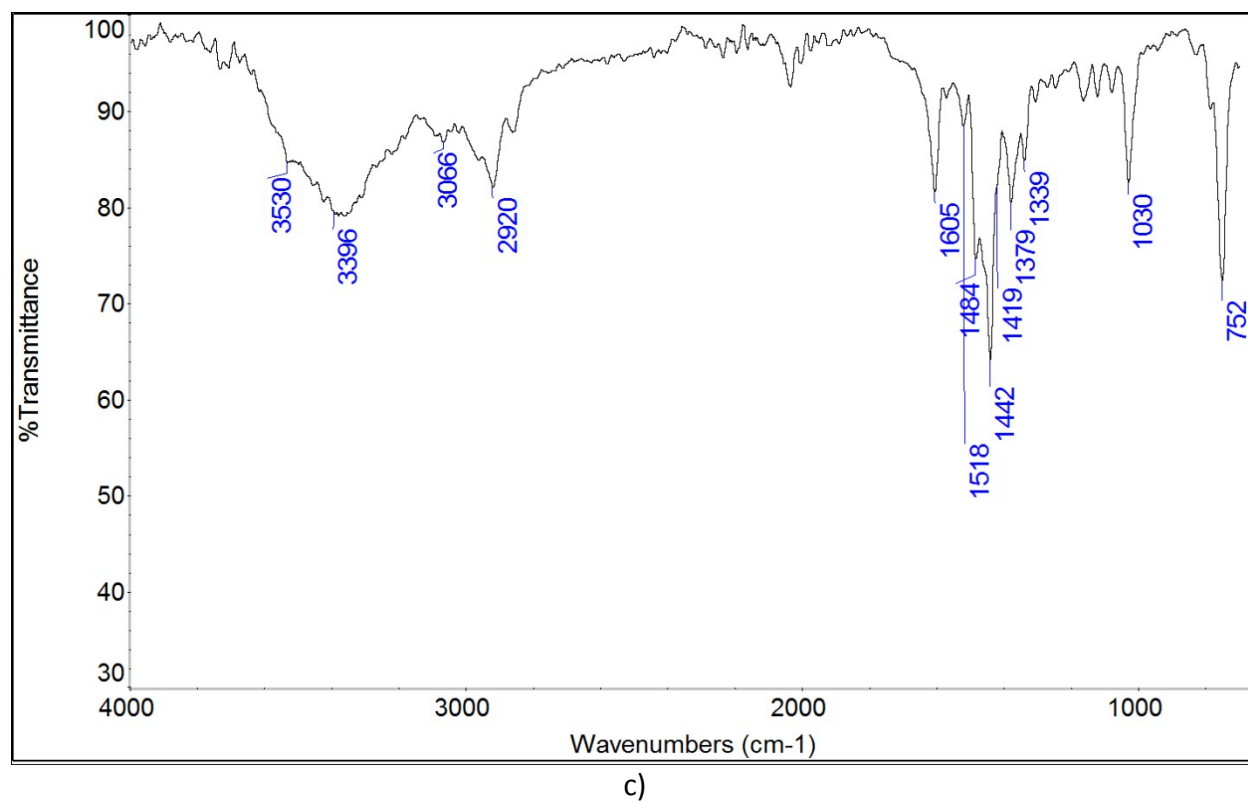
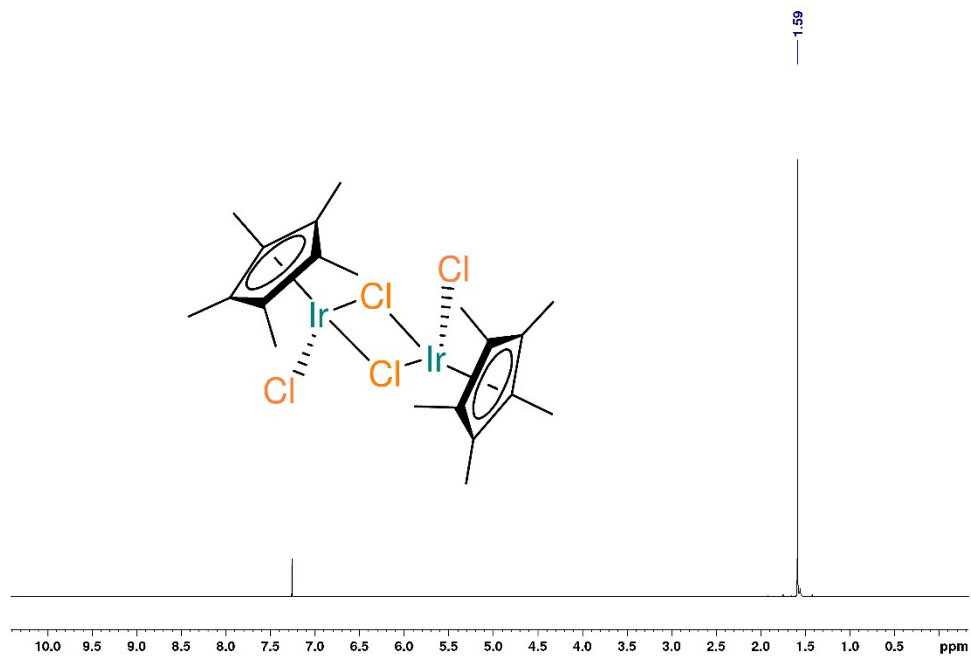
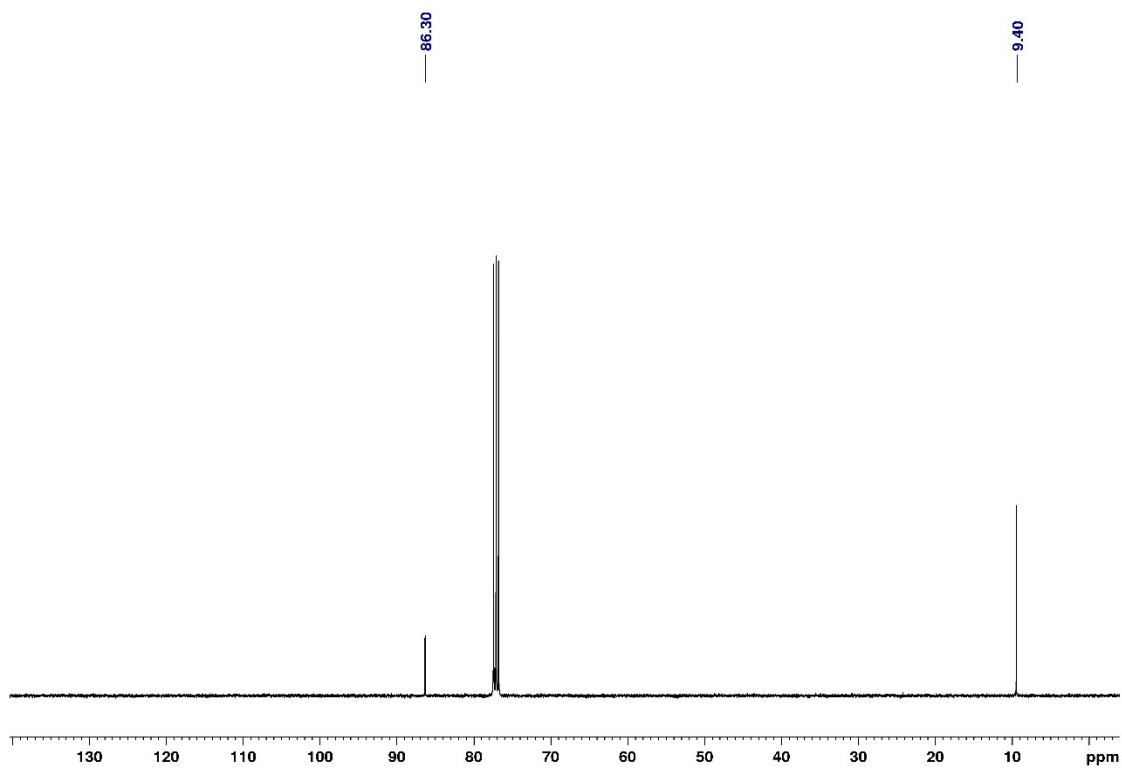


Figure S1 AT IR spectra of half-sandwich Ir(III) compounds a) **1**, b) **2** and c) **3**.

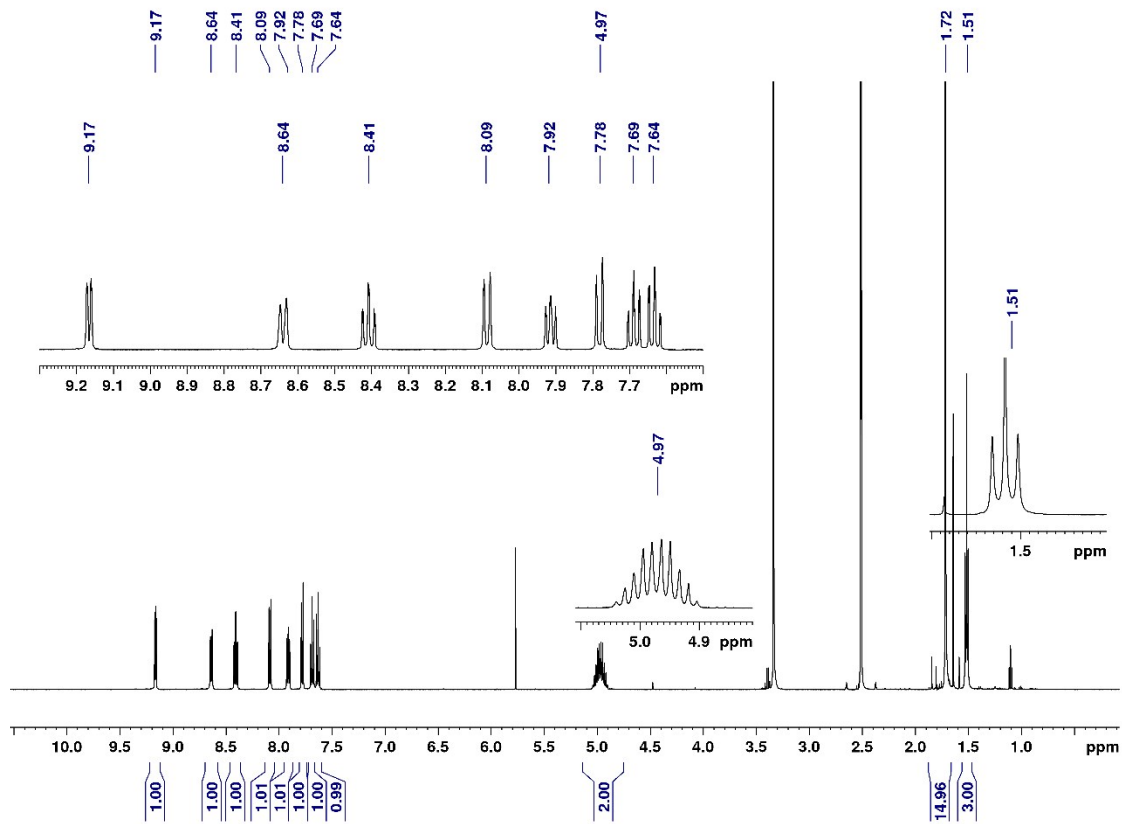


a)

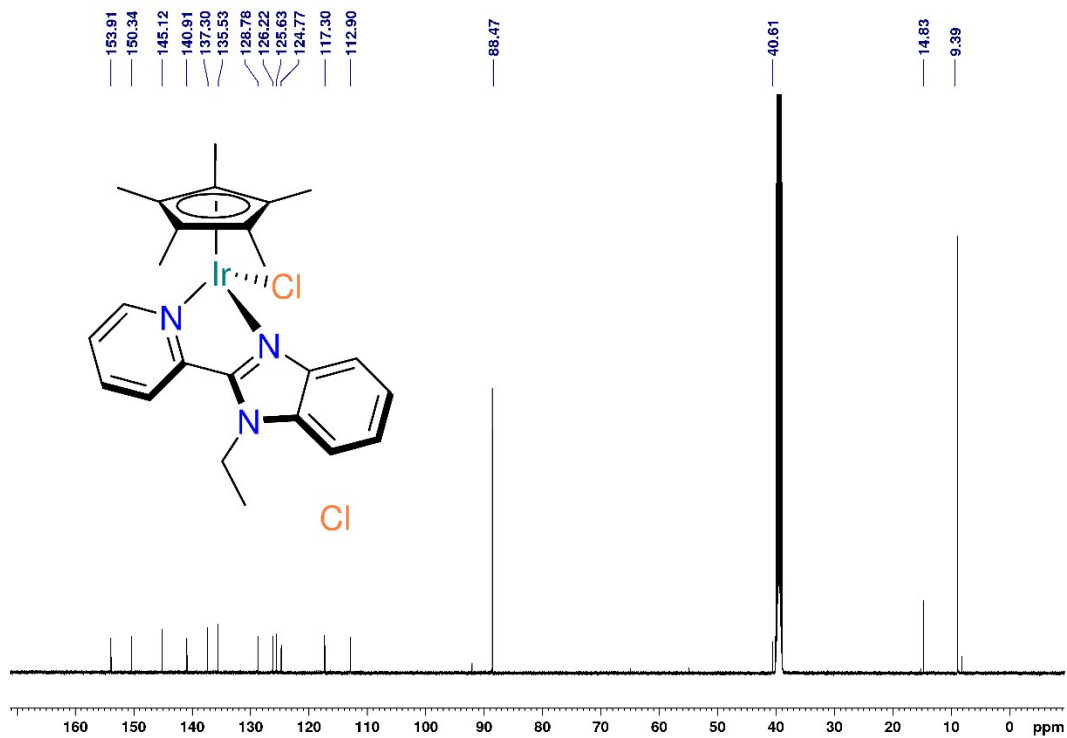


b)

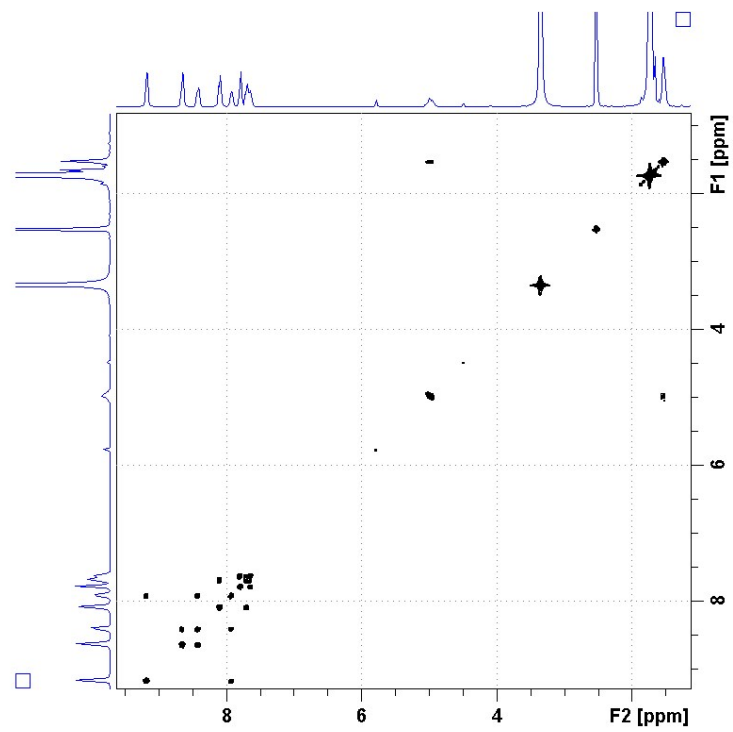
Figure S2 NMR analysis of $[\{\eta^5\text{-C}_5\text{Me}_5\}\text{IrCl}_2(\mu\text{-Cl})_2]$ in CDCl_3 , a) ^1H and b) ^{13}C .



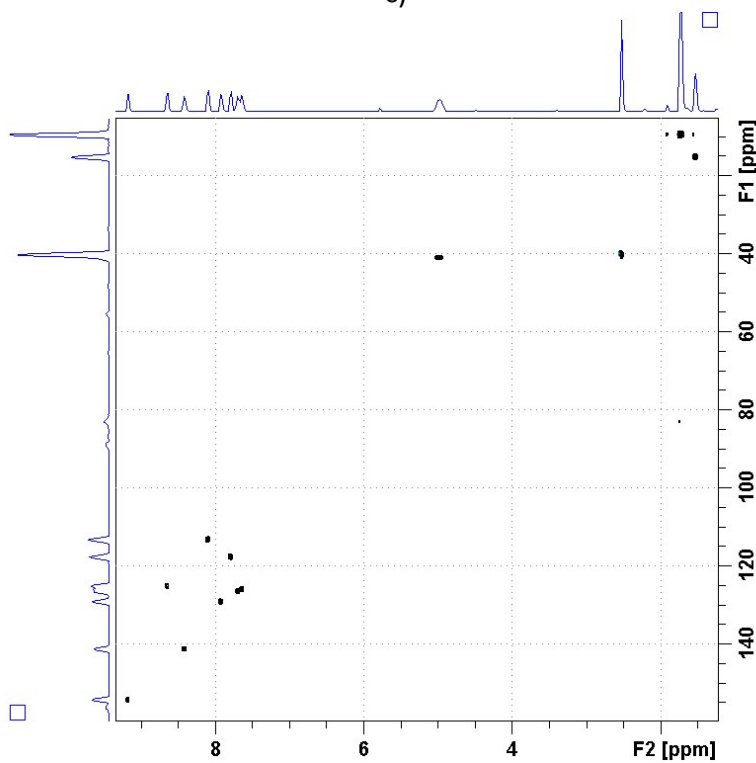
a)



b)

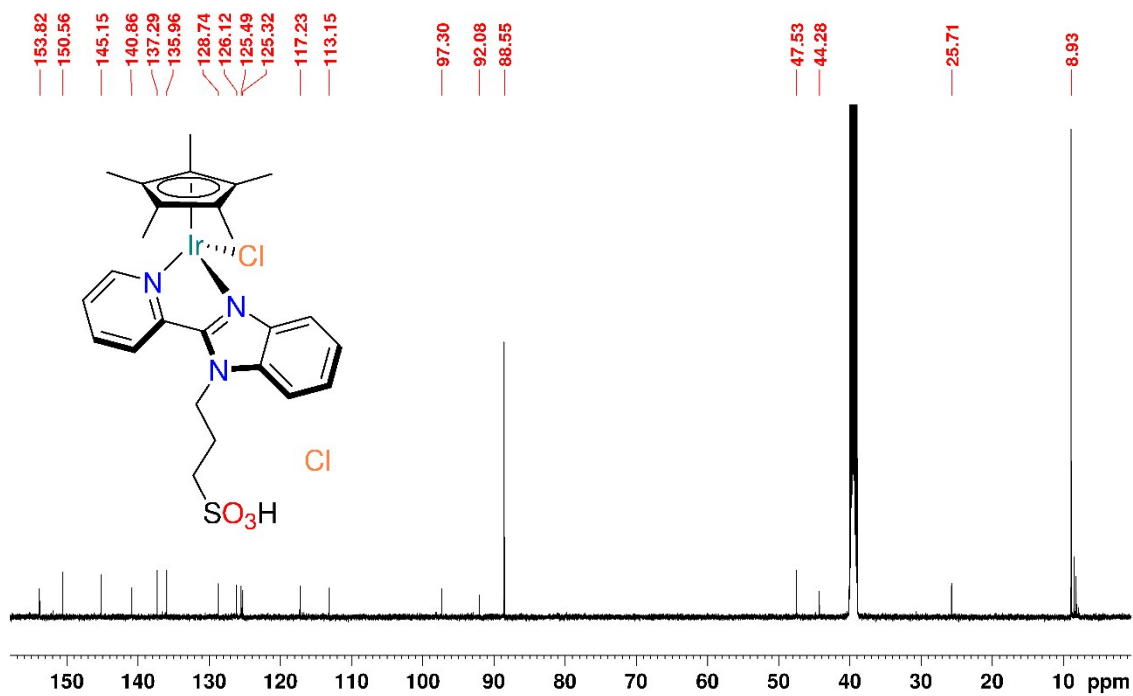


c)

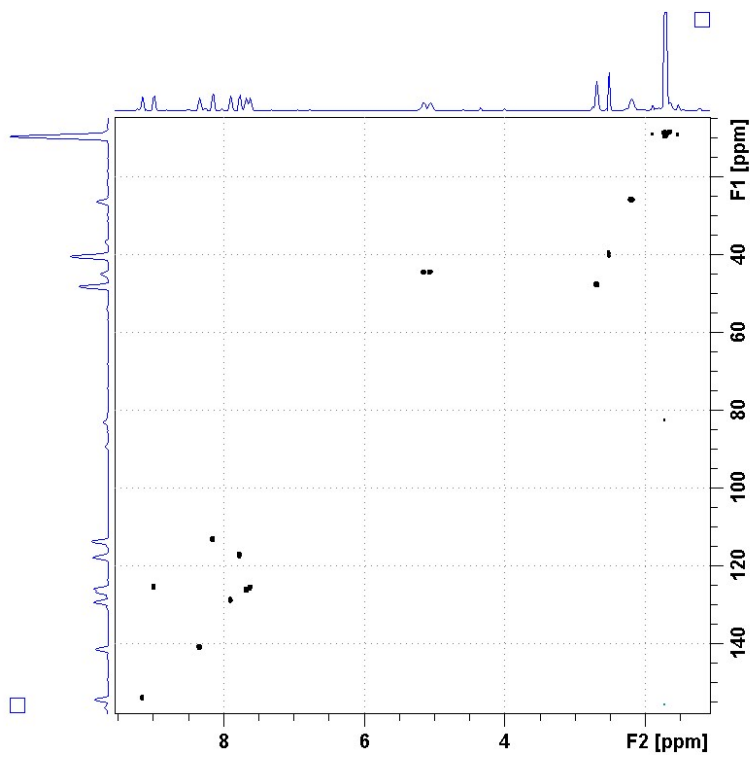


d)

Figure S3 NMR analysis of **1** in $[D_6]$ DMSO, a) 1H , b) ^{13}C , c) $\{^1H, ^1H\}$ COSY and d) $\{^{13}C, ^1H\}$ HSQC.

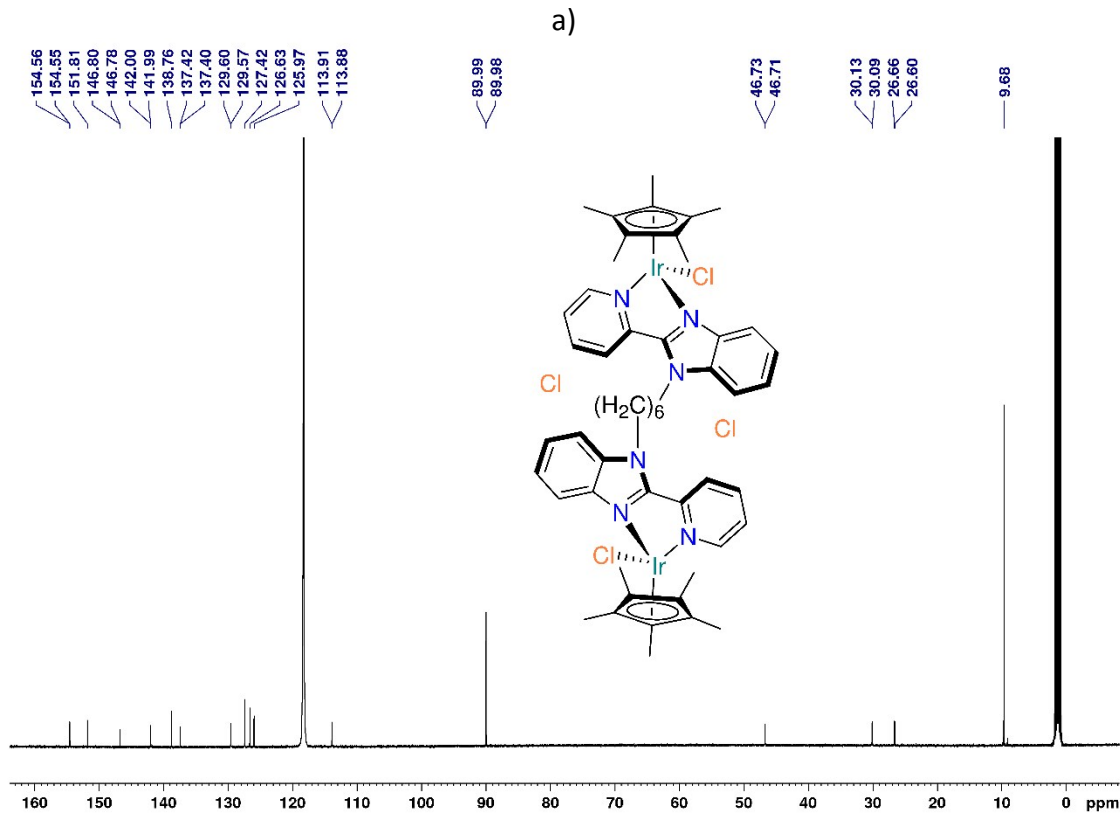
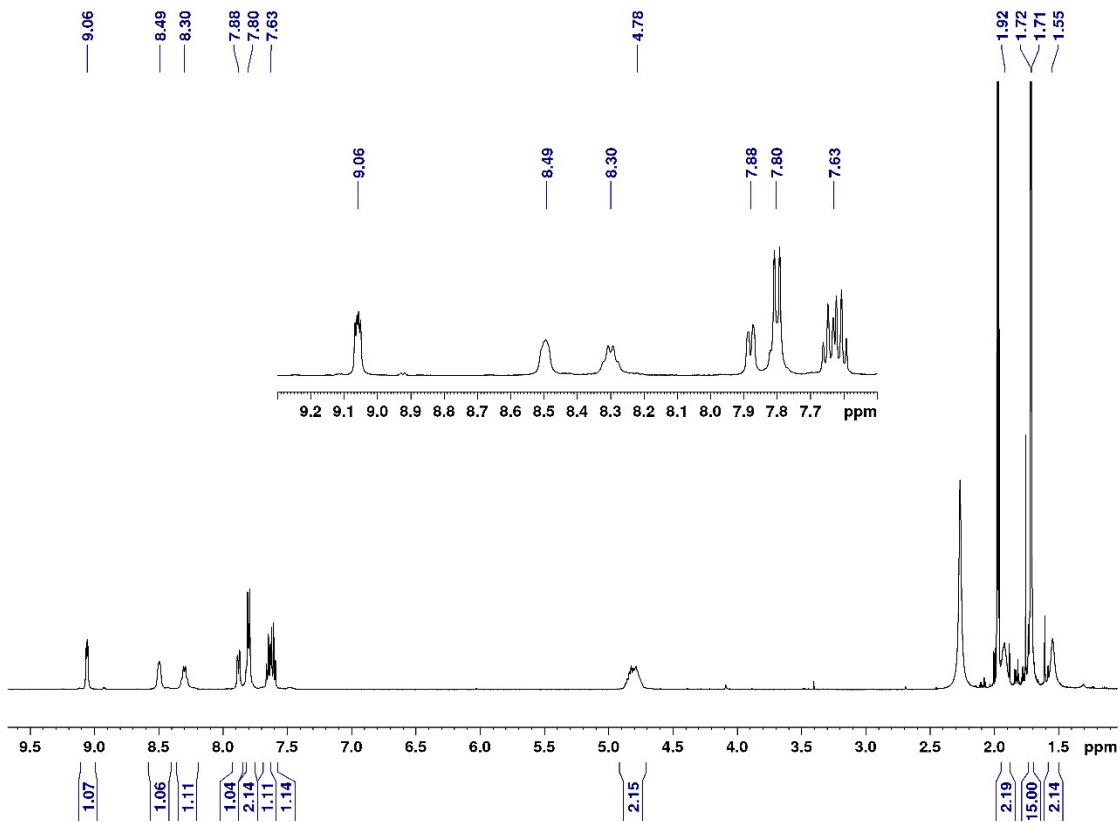


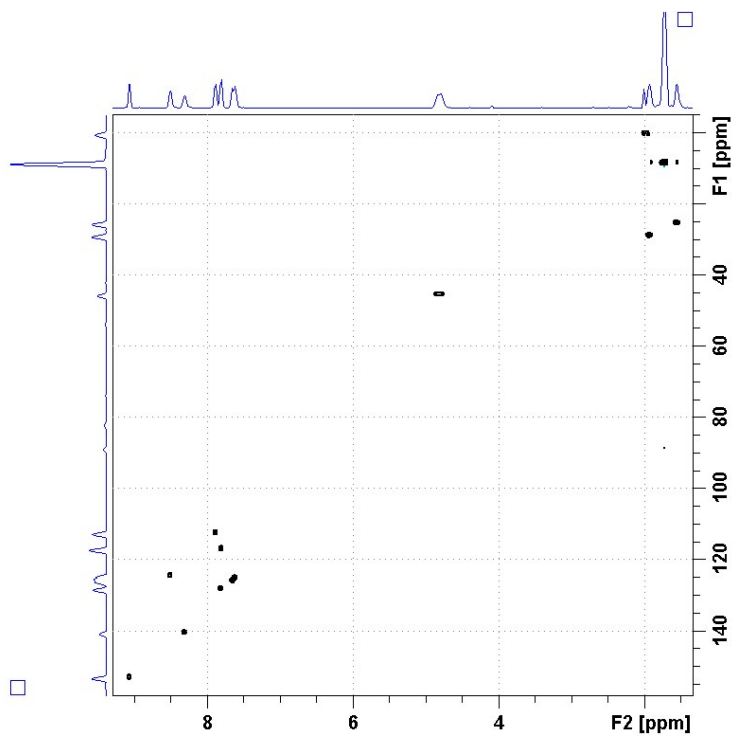
a)



b)

Figure S4 NMR analysis of **2** in $[\text{D}_6]$ DMSO, a) ^{13}C , and b) $\{^{13}\text{C}, ^1\text{H}\}$ HSQC.





c)
Figure S5 NMR analysis of **3** in CD₃CN, a) ¹H, b) ¹³C, and c) {¹³C, ¹H} HSQC.

Table S1 Atomic coordinates of the optimized structure of 1 .					
Center Number	Atomic Number	Atomic Type	Coordinates (Angstroms)		
			X	Y	Z
1	17	0	0.615087	-0.087319	-2.545769
2	6	0	2.964318	0.296407	0.734634
3	6	0	-1.98671	-1.442099	-0.119132
4	6	0	2.05691	-0.161041	1.782839
5	6	0	3.056907	-0.724586	-0.258571
6	6	0	2.200854	-1.833735	0.149034
7	6	0	1.636333	-1.494402	1.436505
8	6	0	1.793135	0.541291	3.082281
9	1	0	1.747091	1.626724	2.955219
10	1	0	2.594655	0.327371	3.801724
11	1	0	0.851098	0.215388	3.53094
12	6	0	3.770258	1.55953	0.784073
13	1	0	4.705195	1.373959	1.328581
14	1	0	3.24569	2.361661	1.310505
15	1	0	4.041842	1.913908	-0.214029
16	6	0	3.912232	-0.720027	-1.487119
17	1	0	4.295738	0.277121	-1.714138
18	1	0	3.350186	-1.068506	-2.357203
19	1	0	4.771359	-1.386987	-1.338204
20	6	0	2.149823	-3.155727	-0.559365
21	1	0	3.114233	-3.671056	-0.464606
22	1	0	1.939474	-3.026191	-1.624837
23	1	0	1.388621	-3.816264	-0.137275
24	6	0	0.802017	-2.380227	2.310986
25	1	0	1.438774	-2.823358	3.087632
26	1	0	0.342899	-3.197302	1.753409
27	1	0	0.006491	-1.822524	2.812277
28	7	0	0.097144	1.912554	-0.230712
29	6	0	-1.254903	2.03971	-0.092306
30	6	0	-1.853789	3.304064	-0.071811
31	1	0	-2.917263	3.410188	0.085537
32	6	0	-1.068827	4.439692	-0.251908
33	1	0	-1.526467	5.423669	-0.239775
34	6	0	0.299928	4.290728	-0.46167
35	1	0	0.945866	5.14425	-0.634797
36	6	0	0.840612	3.009218	-0.442061
37	1	0	1.896734	2.841662	-0.603684
38	7	0	-1.14924	-0.346336	-0.053438
39	6	0	-1.92079	0.745327	-0.025435
40	7	0	-3.250073	0.415586	-0.036971
41	6	0	-3.317618	-0.972232	-0.081829
42	6	0	-4.411591	-1.845238	-0.117443

43	1	0	-5.436129	-1.491713	-0.073141
44	6	0	-4.128786	-3.20065	-0.220327
45	1	0	-4.948659	-3.911024	-0.255374
46	6	0	-2.800822	-3.676363	-0.298311
47	1	0	-2.628317	-4.742306	-0.408286
48	6	0	-1.718252	-2.811306	-0.251583
49	1	0	-0.701874	-3.168918	-0.350655
50	6	0	-4.434507	1.286859	-0.030579
51	1	0	-5.238051	0.711289	-0.495159
52	1	0	-4.245756	2.129485	-0.699208
53	6	0	-4.841492	1.739343	1.373179
54	1	0	-5.746583	2.352484	1.31529
55	1	0	-4.057191	2.332887	1.854825
56	1	0	-5.053571	0.876826	2.012352
57	77	0	0.922223	-0.059586	-0.130084
Rotational constants (GHz)			0.2040899	0.1439974	0.1070289
E (a.u.)			-1660.48906147		

Center Number	Atomic Number	Atomic Type	Coordinates (Angstroms)		
			X	Y	Z
1	17	0	-2.282501	0.189419	-2.438590

2	6	0	-3.61108	-1.336083	1.01914
3	6	0	0.178277	2.170519	-0.328056
4	6	0	-2.676715	-0.77704	1.993164
5	6	0	-4.219607	-0.25541	0.311888
6	6	0	-3.663606	0.992026	0.816089
7	6	0	-2.749821	0.656196	1.890154
8	6	0	-1.933756	-1.555871	3.038166
9	1	0	-1.601003	-2.527129	2.660983
10	1	0	-2.581971	-1.743978	3.904207
11	1	0	-1.053586	-1.014892	3.394896
12	6	0	-3.990775	-2.782811	0.910266
13	1	0	-4.847968	-2.985767	1.565315
14	1	0	-3.181985	-3.445779	1.228993
15	1	0	-4.288592	-3.054572	-0.106386
16	6	0	-5.280231	-0.350294	-0.7393
17	1	0	-5.354224	-1.357664	-1.154203
18	1	0	-5.0781	0.336435	-1.564583
19	1	0	-6.252729	-0.090669	-0.300508
20	6	0	-4.18227	2.350362	0.44214
21	1	0	-5.217671	2.464082	0.787929
22	1	0	-4.172784	2.498148	-0.64156
23	1	0	-3.600961	3.151008	0.905398
24	6	0	-2.044515	1.620223	2.795264
25	1	0	-2.634414	1.755481	3.711191
26	1	0	-1.916733	2.601986	2.336208
27	1	0	-1.057409	1.253108	3.0881
28	7	0	-0.611219	-1.693685	-0.636179
29	6	0	0.689249	-1.31943	-0.811794
30	6	0	1.667444	-2.267583	-1.131248
31	1	0	2.705718	-1.983379	-1.220872
32	6	0	1.300995	-3.596292	-1.325615
33	1	0	2.053914	-4.337132	-1.574498
34	6	0	-0.040255	-3.952117	-1.207029
35	1	0	-0.376578	-4.969358	-1.373861
36	6	0	-0.961365	-2.969496	-0.859741
37	1	0	-2.013645	-3.196909	-0.759055
38	7	0	-0.197035	0.841131	-0.302771
39	6	0	0.870017	0.117767	-0.654939
40	7	0	1.957433	0.918593	-0.891896
41	6	0	1.545142	2.229341	-0.674342
42	6	0	2.233923	3.443719	-0.772166
43	1	0	3.288436	3.494279	-1.021504
44	6	0	1.501796	4.599905	-0.536609
45	1	0	1.99724	5.5631	-0.605082
46	6	0	0.125275	4.552786	-0.224339
47	1	0	-0.413288	5.483031	-0.074056

48	6	0	-0.552361	3.347579	-0.118078
49	1	0	-1.613813	3.3118	0.086411
50	6	0	3.311856	0.562767	-1.325886
51	1	0	3.703465	1.433569	-1.858111
52	1	0	3.244628	-0.237741	-2.066303
53	6	0	4.228732	0.194352	-0.149315
54	1	0	3.843903	-0.692139	0.366804
55	1	0	4.23113	1.011337	0.578945
56	6	0	5.661496	-0.062729	-0.622077
57	1	0	6.103586	0.824089	-1.089509
58	1	0	5.7459	-0.898634	-1.322354
59	16	0	6.77348	-0.438592	0.757212
60	8	0	6.534621	0.529647	1.818693
61	8	0	6.108241	-1.887736	1.189355
62	8	0	8.114846	-0.705511	0.251202
63	1	0	6.847255	-2.469366	1.456917
64	77	0	-2.008232	-0.181906	-0.047684
Rotational constants (GHz)			0.1716053	0.0588426	0.0516041
E (a.u.)			-2323.58027462		

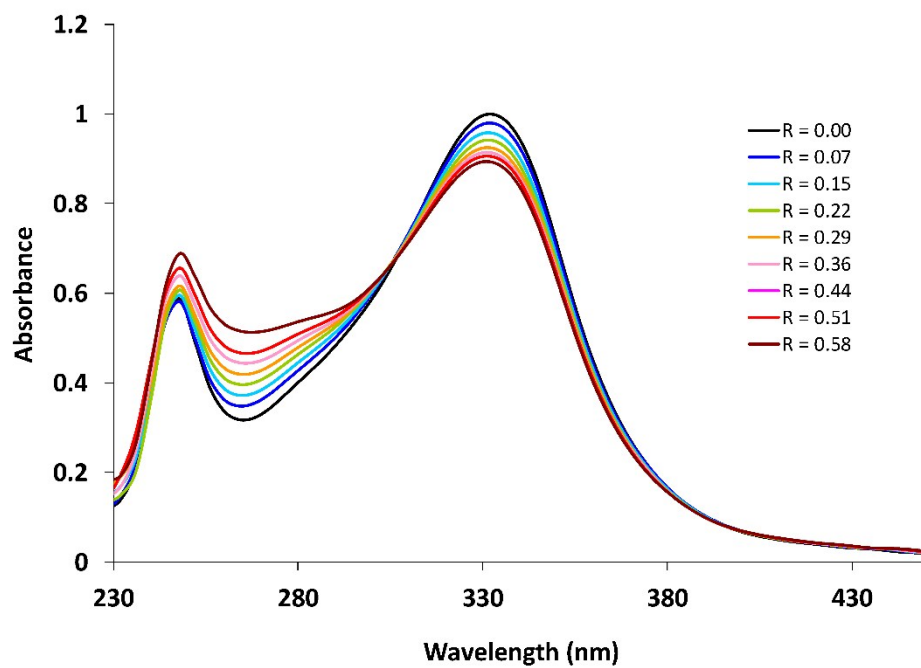
Table S3 Atomic coordinates of the optimized structure of **3**.

Center Number	Atomic Number	Atomic Type	Coordinates (Angstroms)		
			X	Y	Z
1	17	0	-8.091166	-1.278954	-2.090816
2	6	0	-10.05705	-0.64948	1.32461
3	6	0	-5.976971	1.711341	-1.215734
4	6	0	-9.281679	0.41424	1.959323
5	6	0	-10.492059	-0.182744	0.046464
6	6	0	-9.97745	1.163174	-0.14907
7	6	0	-9.272918	1.538895	1.062808
8	6	0	-8.755956	0.391802	3.363886
9	1	0	-8.419298	-0.607231	3.655617

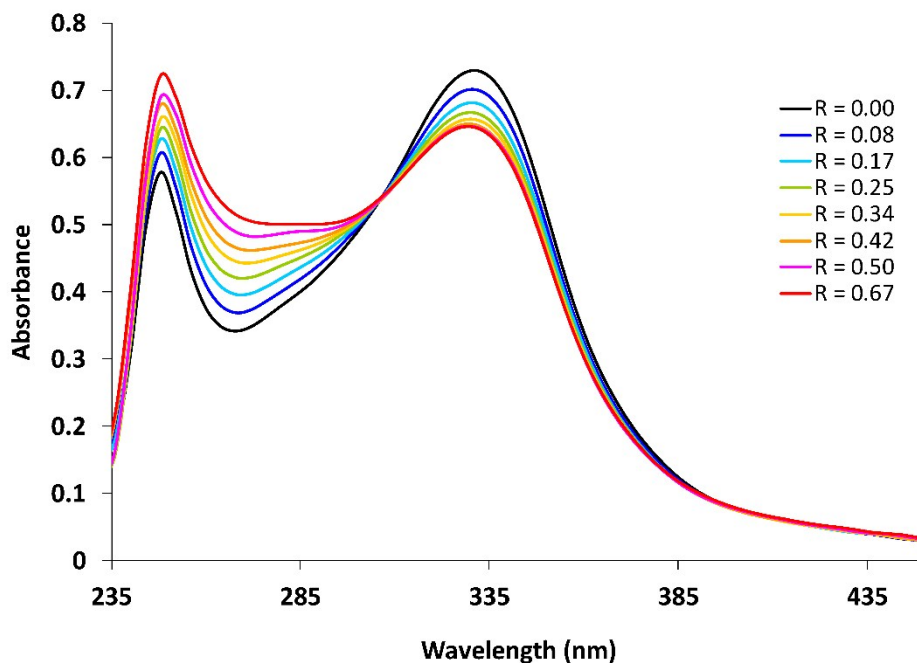
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11	1	0	-7.91573	1.07926	3.490723
12	6	0	-10.478787	-1.931826	1.97786
13	1	0	-11.462266	-1.796796	2.446285
14	1	0	-9.789097	-2.236817	2.769219
15	1	0	-10.57274	-2.749372	1.257424
16	6	0	-11.363954	-0.910532	-0.927407
17	1	0	-11.425006	-1.977387	-0.703527
18	1	0	-10.990335	-0.803463	-1.948463
19	1	0	-12.379831	-0.496095	-0.88404
20	6	0	-10.377942	2.05475	-1.28863
21	1	0	-11.448908	2.285205	-1.222084
22	1	0	-10.19876	1.577159	-2.256011
23	1	0	-9.845371	3.008499	-1.268433
24	6	0	-8.692342	2.885886	1.369398
25	1	0	-9.444088	3.496944	1.885771
26	1	0	-8.394539	3.422112	0.466522
27	1	0	-7.819112	2.811513	2.022428
28	7	0	-6.811414	-1.654126	0.699149
29	6	0	-5.491836	-1.363828	0.510529
30	6	0	-4.495773	-2.234412	0.966473
31	1	0	-3.451164	-1.972513	0.874475
32	6	0	-4.855893	-3.441487	1.558878
33	1	0	-4.09108	-4.124494	1.914396
34	6	0	-6.206723	-3.759695	1.676989
35	1	0	-6.535094	-4.699667	2.106391
36	6	0	-7.149512	-2.835865	1.237695
37	1	0	-8.208836	-3.039778	1.309223
38	7	0	-6.3847	0.633946	-0.452062
39	6	0	-5.302337	-0.107245	-0.200617
40	7	0	-4.175459	0.447267	-0.753454
41	6	0	-4.580744	1.613962	-1.394538
42	6	0	-3.859851	2.559866	-2.131698
43	1	0	-2.785346	2.492108	-2.265162
44	6	0	-4.585696	3.599287	-2.699504
45	1	0	-4.065893	4.352925	-3.282509
46	6	0	-5.986657	3.689872	-2.549089
47	1	0	-6.517325	4.505009	-3.030556
48	6	0	-6.697817	2.753051	-1.813846
49	1	0	-7.775046	2.799872	-1.731407
50	6	0	-2.814774	-0.092443	-0.864529
51	1	0	-2.438631	0.228979	-1.84043
52	1	0	-2.877169	-1.182023	-0.910614
53	6	0	-1.865878	0.378314	0.248098
54	1	0	-2.246305	0.052613	1.225573
55	1	0	-1.863404	1.475512	0.269813

56	6	0	-0.435162	-0.145873	0.040807
57	1	0	-0.443792	-1.245952	0.039362
58	1	0	-0.086761	0.159688	-0.955785
59	6	0	0.540388	0.349553	1.122611
60	6	0	1.964646	-0.229693	1.026114
61	1	0	0.585231	1.448064	1.096676
62	1	0	0.137765	0.08772	2.109256
63	6	0	2.74581	0.256873	-0.204796
64	1	0	2.522262	0.03774	1.932688
65	1	0	1.922362	-1.326275	1.007835
66	7	0	4.092551	-0.319371	-0.305495
67	1	0	2.230867	-0.020966	-1.127874
68	1	0	2.833133	1.34568	-0.223655
69	6	0	5.29933	0.173972	0.122316
70	6	0	4.369599	-1.474308	-1.029336
71	6	0	5.623327	1.388921	0.857285
72	7	0	6.312957	-0.593397	-0.287334
73	6	0	5.772316	-1.626254	-1.029583
74	6	0	3.526697	-2.369544	-1.696975
75	7	0	6.96699	1.620855	0.901389
76	6	0	4.724643	2.269816	1.469306
77	6	0	6.37203	-2.67126	-1.743977
78	1	0	2.447224	-2.260903	-1.689691
79	6	0	4.135394	-3.413911	-2.381519
80	6	0	7.415239	2.754738	1.462502
81	1	0	3.665862	2.053761	1.486353
82	6	0	5.201802	3.427057	2.077957
83	6	0	5.539515	-3.557748	-2.411156
84	1	0	7.448343	-2.757773	-1.796947
85	1	0	3.518632	-4.130032	-2.915286
86	6	0	6.570211	3.68559	2.057738
87	1	0	8.483849	2.913351	1.424138
88	1	0	4.512581	4.116828	2.55437
89	1	0	5.974323	-4.374627	-2.978205
90	1	0	6.986627	4.584756	2.498043
91	1	0	9.537469	-3.084799	-1.589578
92	6	0	10.07206	-2.136955	-1.687313
93	6	0	9.879753	-1.2575	-0.485495
94	1	0	11.135588	-2.381044	-1.803675
95	1	0	9.741322	-1.642703	-2.605318
96	6	0	10.469826	0.06225	-0.346064
97	6	0	9.348587	-1.635074	0.812427
98	6	0	10.248904	0.51706	0.991063
99	6	0	11.220251	0.781104	-1.422119
100	6	0	9.540943	-0.534889	1.717776
101	6	0	8.766127	-2.967158	1.175304

102	6	0	10.817973	1.768117	1.592216
103	1	0	11.269391	1.85626	-1.238499
104	1	0	10.757561	0.630042	-2.399643
105	1	0	12.24806	0.395834	-1.462273
106	6	0	9.234113	-0.525373	3.185536
107	1	0	9.566899	-3.632913	1.522797
108	1	0	8.280369	-3.449801	0.325003
109	1	0	8.032028	-2.882565	1.98059
110	1	0	11.856442	1.587936	1.89879
111	1	0	10.273056	2.081659	2.486796
112	1	0	10.829697	2.596448	0.878251
113	1	0	8.973442	0.476156	3.539423
114	1	0	10.110229	-0.857809	3.757521
115	1	0	8.405258	-1.194697	3.4294
116	17	0	7.846955	1.348765	-2.053522
117	77	0	-8.249052	-0.186713	0.080331
118	77	0	8.259828	0.152126	0.026062
Rotational constants (GHz)			0.0978516	0.0070092	0.0069022
E (a.u.)			-3398.35628365		



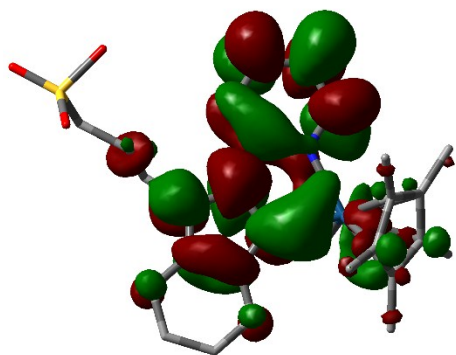
a)



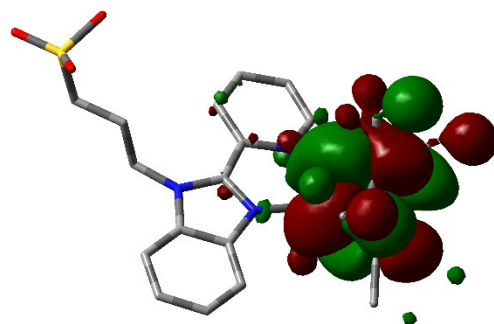
b)

Figure S6 Absorption spectra of complex a) **1** and b) **2** in Tris-buffer (in 20% (v/v) DMSO/tris-buffer (NaCl 50 mM, Tris-HCl 5 mM, pH = 7.4)), in absence ($R = 0.0$) and presence ($R > 0.0$) of increasing amounts of calf-thymus DNA ($R = [\text{DNA}]/[\text{complex}]$, $[\text{complex}] = 3.22 \times 10^{-5} \text{ M}$ (**1**) and $2.80 \times 10^{-5} \text{ M}$ (**2**)).

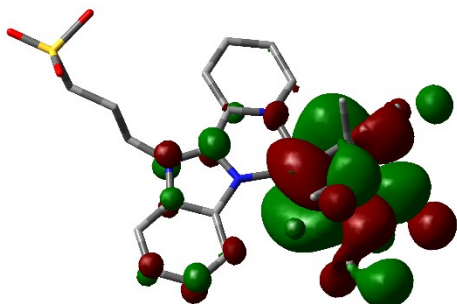
Table S4†: Computed excitation energies (eV), electronic transition configurations and oscillator strengths (f) of the studied complexes (selected).			
Energy (cm ⁻¹)	Wavelength (nm)	f	Major contributions (> 20 %)
• 1			
30153	331	0.0512	HOMO-1→LUMO+3 (22%), HOMO→LUMO (59%)
32233	310	0.1064	HOMO-1→LUMO (53%)
34784	287	0.4916	HOMO-2→LUMO (80%)
37681	265	0.0555	HOMO-3→LUMO (81%)
47453	210	0.1526	HOMO-2→LUMO+2 (22%), HOMO-2→LUMO+3 (26%)
48997	204	0.2137	HOMO-8→LUMO (34%)
• 2			
30093	332	0.0553	HOMO-1→LUMO+3 (22%), HOMO→LUMO (56%)
31693	315	0.0479	HOMO-1→LUMO (49%)
32235	310	0.0795	HOMO-1→LUMO (29%)
34797	287	0.5136	HOMO-2→LUMO (85%)
37703	265	0.0638	HOMO-3→LUMO (79%)
47506	210	0.2002	HOMO-2→L+3 (31%)
49067	203	0.1724	HOMO-8→LUMO (25%)



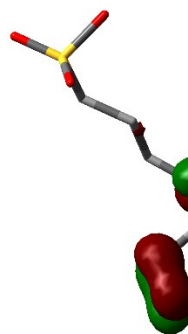
LUMO+3



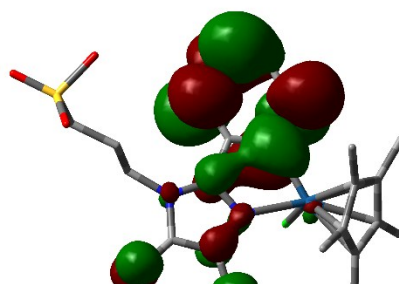
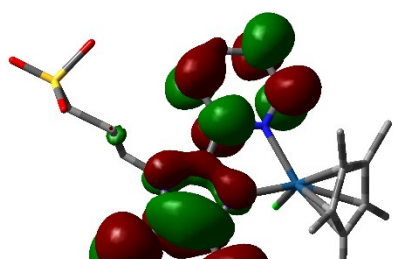
LUMO+2



LUMO+1



LUMO



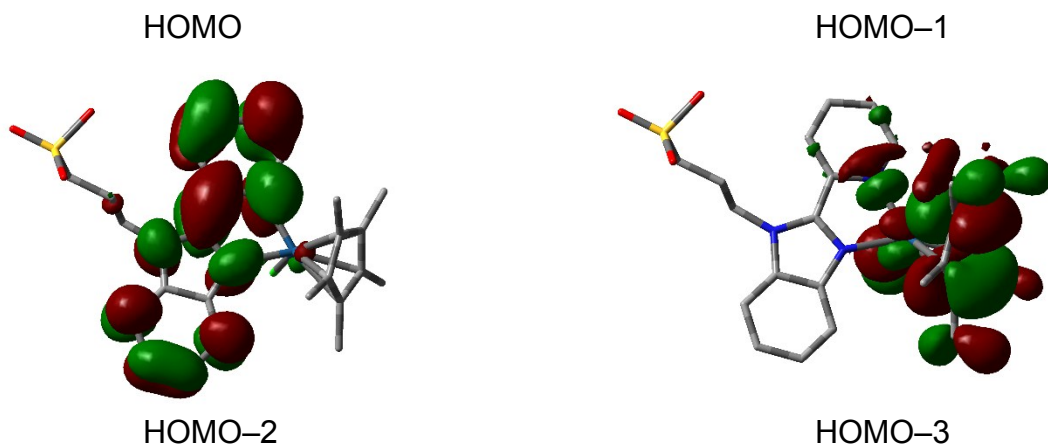
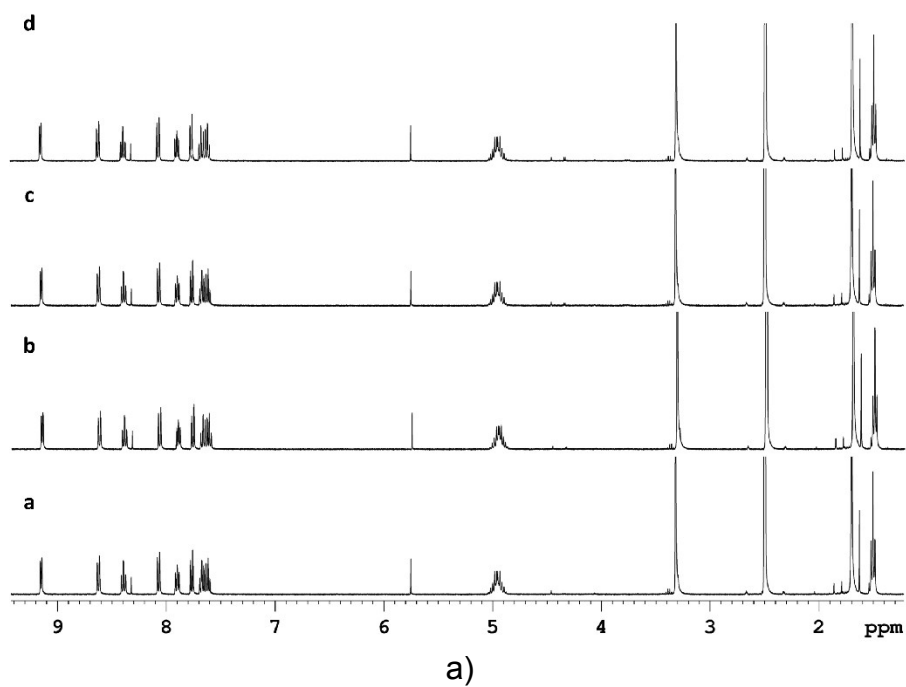
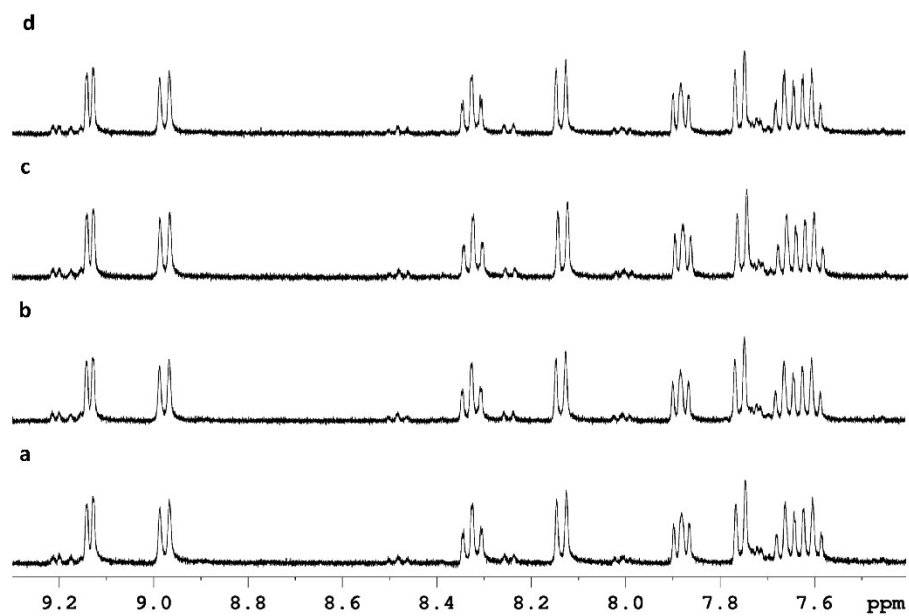


Figure S7 Selected Frontiers molecular orbitals of **2** calculated at B3LYP/LANL2DZ level of theory.

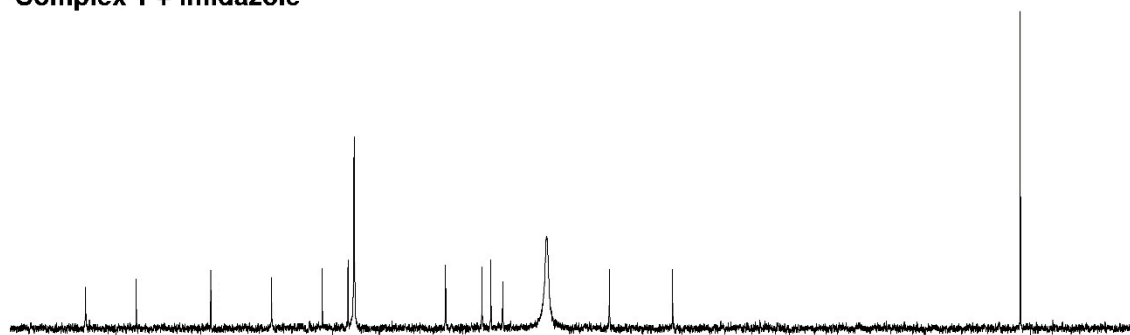




b)

Figure S8 Stability of a) **1** and b) **2** (aromatic region) in [D₆] DMSO followed by ¹H NMR at different time interval [a (10 min), b (1 h), c (6 h) and d (24 h)].

Complex 1 + Imidazole



Complex 1

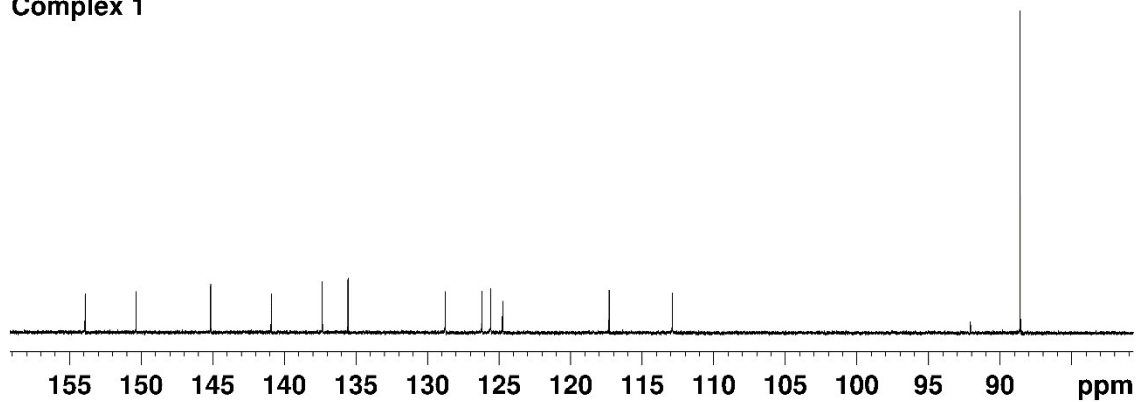


Figure S9 ^{13}C NMR spectra of complex 1 ($[\text{D}_6]$ DMSO) in presence and absence of imidazole.

Biological activity testing

Evaluation of antimicrobial properties

The antimicrobial activities of the synthesized ligands and complexes were evaluated against cultures of *Staphylococcus aureus* ATCC 43300, *Escherichia coli* ATCC 25922, *Klebsiella pneumoniae* ATCC 700603, *Acinetobacter baumannii* ATCC 19606, *Pseudomonas aeruginosa* ATCC 27853, as well as two fungi, *Candida albicans* ATCC 90028 and *Cryptococcus neoformans var. grubii* H99; ATCC 208821. The samples were prepared in DMSO to a final testing concentration of 32 µg/mL and serially diluted 1:2 fold for 8 times. Each concentration was prepared in 384-well plates, non-binding surface plate (NBS; Corning 3640) for each bacterial/fungal strain, all in duplicate (n=2), and keeping the final DMSO concentration to a maximum of 0.5%. All bacteria were cultured in Cation-adjusted Mueller Hinton broth at 37 °C overnight. A sample of each culture was then diluted 40-fold in fresh broth and incubated at 37 °C for 1.5-3 h. The resultant mid-log phase cultures were diluted (CFU/mL, measured the absorbance at 600 nm), then added to each well of the compound containing plates, giving a cell density of 5×10^5 CFU/mL and a total volume of 50 µL. All the plates were covered and incubated at 37 °C for 18 h without shaking. The inhibition of the bacterial growth was determined by OD₆₀₀ using a Tecan M1000 Pro monochromator plate reader. The percentage of growth inhibition was calculated for each well, using the negative control (media only) and positive control (bacteria without inhibitors) on the same plate as references. The MIC was determined as the lowest concentration at which the growth was fully inhibited, defined by an inhibition $\geq 80\%$. In addition, the maximal percentage of growth inhibition is reported as D_{Max}, indicating any compounds with partial activity plates.

Fungi strains were cultured for 3 days on Yeast Extract-peptone Dextrose agar at 30 °C. A yeast suspension of 1×10^6 to 5×10^6 CFU/mL (determined by OD₆₀₀) was prepared from five colonies. The suspension was subsequently diluted and added to each well of the sample-containing plates giving a cell density of fungi suspension of 2.5×10^3 CFU/mL and total volume of 50 µL. All plates were covered and incubated at 35 °C for 36 h without shaking. The growth inhibition of *Candida albicans* was measured at 630 nm, while that of *Cryptococcus neoformans* was determined by measuring the difference in

absorbance at 600 and 570 nm, after the addition of resazurin (0.001%, final concentration) and incubation at 35 °C for 2 h. The absorbance was measured using a Biotek Multiflo Synergy HTX plate reader and controls. The MIC was determined as the lowest concentration at which the growth was fully inhibited, defined by an inhibition = 80% for *Candida albicans* and an inhibition = 70% for *Cryptococcus neoformans*. Due to a higher variance in the growth and inhibition, a lower threshold was applied to the data for *Cryptococcus neoformans*. In addition, the maximal percentage of growth inhibition is reported as D_{Max} , indicating any compounds with marginal activity.

Cytotoxicity Assay

Human embryonic kidney HEK293 cells were counted manually in a Neubauer haemocytometer and then plated in the 384-well plates containing the compounds to give a density of 5000 cells/well in a final volume of 50 μ L. Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% FBS was used as growth media and the cells were incubated together with the compounds for 20 h at 37 °C in 5% CO₂. Cytotoxicity (or cell viability) was measured by Fluorescence (excitation 560/10, emission 590/10 nm) ($F_{560/590}$), after addition of 5 μ L of 25 μ g/mL resazurin (2.3 μ g/mL final concentration) and after incubation for further 3 h at 37 °C in 5% CO₂. The intensity was measured using Tecan M1000 Pro monochromator plate reader, using automatic gain calculation. CC₅₀ (the concentration at 50% cytotoxicity) was calculated by curve fitting the inhibition values vs. logC using a sigmoidal dose-response function, with variable fitting values for bottom, top and slope. The curve fitting was implemented using Pipeline Pilot's dose-response component, resulting in similar values to curve fitting tools such as GraphPad's Prism and IDBS's XIFit.