Supporting Information

Targeting Cytotoxicity and Tubulin Polymerization by Metal-Carbene Complexes on a Purine Tautomer Platform

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Materials:

6-Chloropurine was purchased from SRL, benzyl bromide from Avra Synthesis, potassium carbonate from Rankem and silver oxide was purchased from Sigma Aldrich. O-methoxy hydroxylamine hydrochloride and dimethyl acetamide (DMA) were purchased from Spectrochem. Dimethyl sufoxide (DMSO), triethyl amine and sodium bicarbonate were purchased from Merck. Mercuric acetate and butanol were purchased from SD-fine. Dulbecco Modified Eagle Medium (DMEM), Cell culture dimethyl sulfoxide (DMSO), 4′, 6-diamidino-2-phenylindole (DAPI), 3- (4, 5-dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium bromide (MTT), Kanamycin sulfate, Trypsin-EDTA solution, Sodium Chloride, Potassium Chloride, ATP, GTP, Curcumin and fetal bovine serum were purchased from Sigma Aldrich. 2-[4-(2-hydroxyethyl)

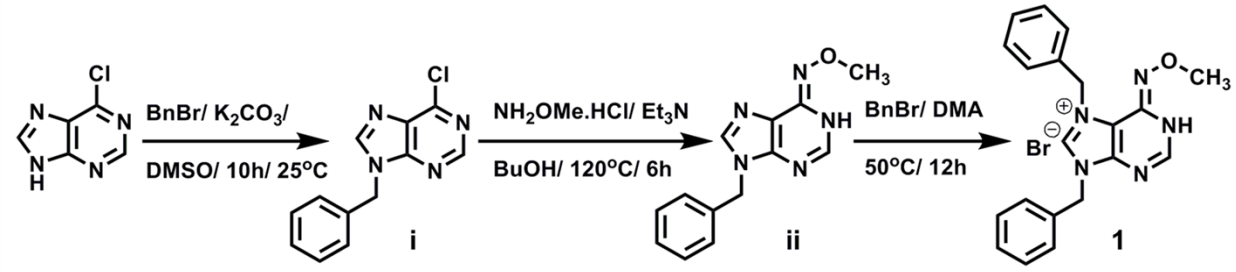
piperazin-1-yl] ethanesulfonic acid (HEPES) was purchased from Himedia. Penicillin-Streptomycin was purchased from Invitrogen. Anti-alpha Tubulin antibody and Goat Anti-Rabbit IgG H&L (Cy3.5 ®) preadsorbed were purchased from Abcam. All compounds were used without further purification. Tubulin was isolated and purified from goat brain in our lab. A549 (adenocarcinomic human alveolar basal epithelial cells) cell line and MCF-7 (human breast cancer cell line) were purchased from NCCS, Pune (India) and cultured in Dulbecco Modified Eagle medium (DMEM) containing 10% (v/v) heat-inactivated fetal bovine serum at 37 °C and 5% CO_2 atmosphere in our lab.

Experimental

General:

^1H and ^{13}C NMR spectra were recorded on JEOL-JNM LAMBDA 400 model operating at 500 and 125 MHz, respectively. Analysis of ^1H and ^{13}C NMR of final product was done by JEOL ECX-500 model operating at 500 MHz and 125 MHz respectively. HRMS was recorded at IIT Kanpur, India, on Waters, Q-Tof Premier Micromass HAB 213 mass spectrometer using capillary voltage 2.6-3.2 kV.

Synthesis of N7, N9-dibenzyl-N^6-methoxyadenine (1): Ligand **1** was synthesized in three steps starting from 6-chloropurine by the following procedure (Scheme 1). Compound **i** and **ii** were synthesized following previously described method.[1]



Scheme 1: Synthesis of N7, N9-dibenzyl-N^6-methoxyadenine (**1**)

N9-benzyl-N^6-methoxyadenine (**ii**) (1 g, 3.92 mmol) was suspended in dimethyl acetamide (DMA) (15 mL). To this reaction mixture, benzyl bromide (2.33 mL, 19.6 mmol) was then added dropwise. After complete addition, reaction was heated at 50 °C under nitrogen atmosphere and was monitored by TLC. After 12 h, TLC showed completion of the reaction. Heating was stopped and reaction mixture was allowed to cool to room temperature. It was then slowly poured over cold ethyl acetate and the obtained white solid was separated. The solvent was decanted and solid was dried in high *vaccuo*. Pure compound was then isolated as a pale white solid. Yield: 1.0 g (2.34 mmol, 60%). HRMS: $[L]^+$ ($C_{20}H_{20}N_5O$): 346.1667 (calcd: 346.1662). ^{1}H NMR: (500 MHz, CD_3OD, 25 °C, TMS) δ (ppm) 3.90 (s, 3H, O-CH_3), 5.45 (s, 2H, CH_2), 5.63 (s, 2H, CH_2) 7.37-7.41 (m, 10H, Ar-H), 7.76 (s, 1H, C2-H), 9.26 (s, 1H, C8-H). ^{13}C NMR (125 MHz, CD_3OD, 25 °C, TMS); δ (ppm) 48.86, 52.97, 61.53, 111.33, 128.01, 128.40, 128.54, 128.90, 128.92, 128.96, 133.70, 133.87, 136.37, 136.71, 141.35, 148.62.

Crystals of **1** were obtained by slow evaporation of its methanolic solution. Refinement data suggests that **1** crystallizes as its bromide salt in a triclinic unit cell system with *P-1* space group (Figure S1). The crystal structure refinement parameters and selected bond lengths and bond angles are given in Table S1 and S2, respectively.

Synthesis of silver carbene complex, 1A: Ligand **1** (50 mg, 0.117 mmol) and silver oxide (17 mg, 0.073 mmol) were suspended in 1:1 DCM: acetonitrile (12 mL) solvent system and stirred in dark under nitrogen atmosphere for 16 h at 25 °C. The reaction mixture was then filtered through a celite bed and the filterate was concentrated under high *vaccuo* affording a yellow powder. Yield: 40 mg (0.045 mmol, 77.7%). HRMS: $[L_2Ag]^+$ ($C_{40}H_{38}AgN_{10}O_2$): 797.2230 (Calcd.: 797.2219), $[L]^+$ ($C_{20}H_{20}N_5O$): 346.1375 (Calcd.: 346.1662). ^{1}H NMR: (500 MHz, CD_3OD, 25 °C, TMS) δ (ppm) 3.80 (s, 3H, O-CH_3), 5.36 (s, 2H, CH_2), 5.65 (s, 2H, CH_2) 7.35-7.43 (m, 10H, Ar-H), 7.68 (s, 1H, C2-H). ^{13}C NMR (125 MHz, d_6-DMSO, 25 °C, TMS); δ (ppm) 47.70, 52.04, 60.90, 108.51, 128.57, 128.81, 128.89, 128.95, 129.27, 129.35, 133.59, 135.76, 136.38, 145.07, 156.58, 178.52.

Synthesis of mercury carbene complex, 1B: Ligand **1** (50 mg, 0.117 mmol) and mercuric acetate (46 mg, 0.144 mmol) were suspended in DCM (10 mL) and stirred under nitrogen atmosphere at 25 °C for 24 h. Reaction mixture was then concentrated under high *vaccuo*

affording a pale yellow powder. Yield: 40 mg (0.038 mmol, 65%). HRMS: $[L_2HgBr_2 + H]^+$ ($C_{40}H_{39}Br_2HgN_{10}O_2$): 1051.11 (Calcd: 1051.1330), $[L_2HgBr]^+$ ($C_{40}H_{38}BrHgN_{10}O_2$): 971.21 (Calcd: 971.2068), $[LHgBr]^+$ ($C_{20}H_{19}BrHgN_5O$): 626.0489 (Calcd.: 626.0479), $[L_2Hg]^{2+}/2$ ($C_{20}H_{19}Hg_{0.5}N_5O$): 446.1507 (Calcd.: 446.1442) and $[L]^+$ ($C_{20}H_{20}N_5O$): 346.1647 (Calcd.: 346.1662). ^{1}H NMR: (500 MHz, d_6-DMSO, 25 °C, TMS) δ (ppm) 3.30 (merged with d_6-DMSO, 3H, O-CH_3), 5.54 (s, 2H, CH_2), 5.72 (s, 2H, CH_2) 7.20-7.23 (m, 10H, Ar-H), 7.71 (s, 1H, C2-H). ^{13}C NMR (125 MHz, d_6-DMSO, 25 °C, TMS); δ (ppm) 49.51, 53.94, 61.45, 112.02, 127.88, 127.93, 128.36, 128.46, 128.98, 129.13, 136.19, 136.78, 140.38, 144.47, 156.40, 175.80.

Methods:

Cytotoxicity study:

Inhibition of cancer cells (adenocarcinomic human alveolar basal epithelial cell line (A549 cell line) and breast cancer cell line (MCF-7 cell line)) proliferation were evaluated by 3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium bromide (MTT) reduction.[2] Both A549 and MCF-7 cells were seeded at a density of 10000 cells per well in a 96-well plate separately for 18-24 h prior to their treatment with compounds and curcumin. Cell lines were then treated with various concentrations of curcumin (control) and the compounds (stock concentration was 10 mg/mL in cell culture DMSO) in DMEM containing 10% fetal bovine serum for 24 h in different 96-well plate. Following the termination of experiment, cells were washed and assayed for viability using MTT. Results were expressed as percent viability = [A550 (treated cells)-background/A550 (untreated cells)-background] x 100.

Study of change in the cellular morphology after the compounds' treatment:

Change in cellular morphologies of A549 and MCF-7 cells after the compounds and curcumin treatment were evaluated by following method. Both A549 and MCF-7 cells were seeded at a density of 50000 cells per well in a 6-well plate separately for 18-24 h. Both the cell lines were then treated with 40 μM concentration of each compound as well as curcumin (stock concentration was 10 mg/mL in cell culture DMSO) in DMEM containing 10% fetal bovine serum for 24 h in different 6-well plate. Following the termination of the experiment, cells were observed in the inverted microscope (Model Nikon Eclipse Ti-U) in DIC mode.

Study the effect of 1, 1A, 1B and curcumin on the microtubule network of A549 and MCF-7 cell lines:

Change in the microtubule network of a lung cancer cell line (A549 cell line) and breast cancer cell line (MCF-7 cell line) after compounds' treatment was studied by following method.[3] Both A549 and MCF-7 cells were seeded at a density of 5000 cells per cover glass bottom dish in 5 cover glass bottom dish for each cell line for 18-24 h. After washing, the cells were treated with 40 μM concentration of each compound as well as curcumin (stock concentration was 10 mg/mL in cell culture DMSO) in DMEM containing 10% fetal bovine serum for 24 h in different cover glass bottom dish keeping one dish as a control for each case. The cells were washed with 1X Phosphate Buffer Saline (PBS) and fixed with 4% paraformaldehyde solution. These fixed cells were then treated with primary antibody (Anti-alpha Tubulin (1:300)) for 1 h followed by secondary antibody (Goat Anti-Rabbit IgG H&L (1:500)) treatment for 1 h. Finally the cells were treated with 4,6-diamidino-2-phenylindole (DAPI) at a concentration of 3 μM for 30 minutes. Following the termination of the experiment, the cells were washed with 1X PBS and observed in the inverted microscope (Model Nikon Eclipse Ti-U) in DIC mode.

Tubulin Polymerization Assay:

Turbidity experiment was carried out with 20 μM tubulin and 40 μM of **1**, **1A**, **1B** and curcumin. For this experiment, 100 μL of 20 μM tubulin solution in Brinkley Reassembly Buffer 80 (BRB 80) containing 2 mM ATP and 4 mM GTP used as a control. 10% dimethyl sulfoxide was used for initiating the polymerization.[4] All the components were mixed in ice, kept for 5 minutes and injected into 37 °C heated quartz cuvettes and the polymerization of tubulin was performed at 37 °C and the turbidity was measured by measuring absorbance at 350 nm monitored at 0.1 min intervals in the UV Spectrophotometer (Shimadzu UV-2401PC). Now inhibition of tubulin polymerization was assessed using 50 μM of **1**, **1A**, **1B** and curcumin.

Docking Simulation:

Autodock-Vina version 1.1.2 was used for docking simulation.[5] 29x30x28 affinity grids were centered on the receptor (1sa02) at 79.52, 69.51 and 4.77 of X, Y, Z axis respectively.

Density Functional Theoretical (DFT) Studies:

Geometry optimizations were carried out for both silver carbene complex, **1A** and mercury carbene complex, **1B** using Gaussian 09 package.[6]

Figures:

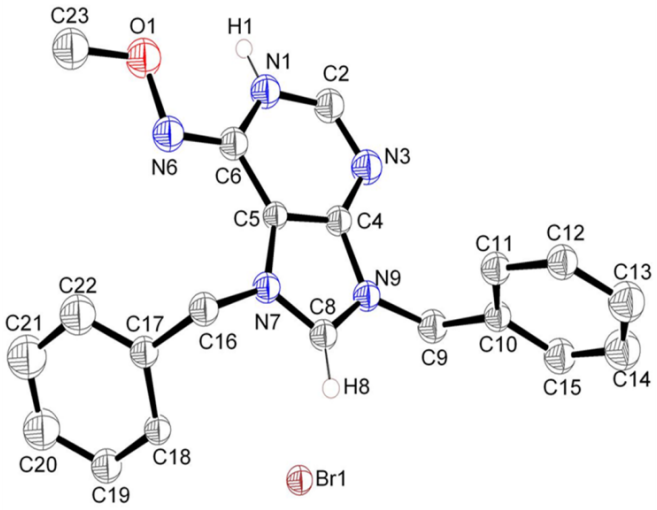


Figure S1: ORTEP diagram of **1** showing asymmetric unit of the cell at 50% probability level (hydrogen atoms are omitted for clarity).

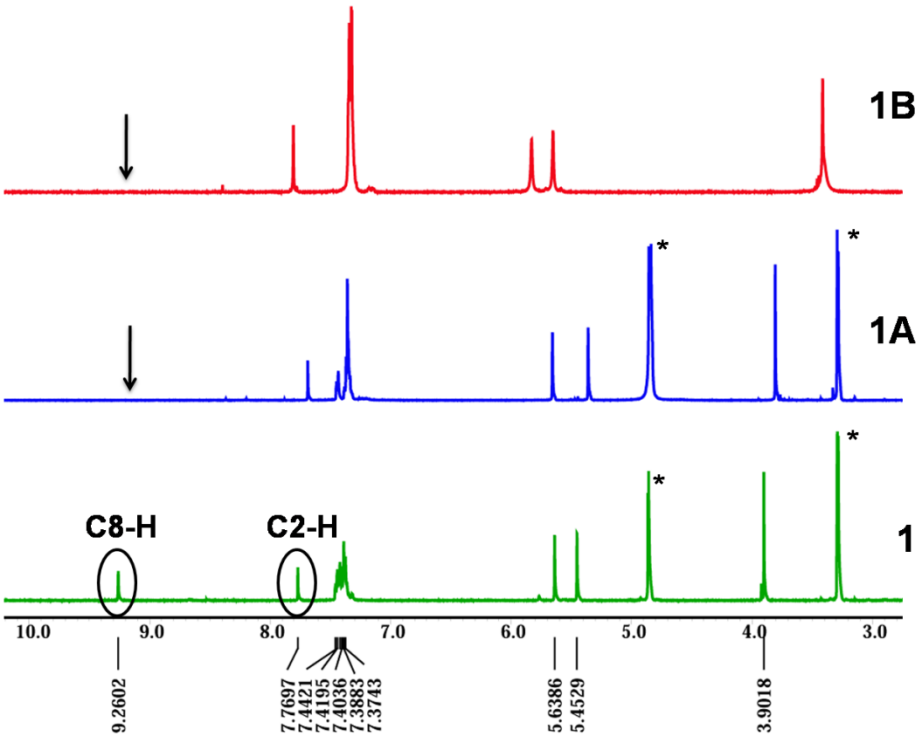


Figure S2: ^{1}H NMR spectra for **1** (CD_3OD), **1A** (CD_3OD) and **1B** (d_6-DMSO) illustrating the disappearance of peak corresponding to C8-H in **1A** and **1B**. (*: residual solvent)

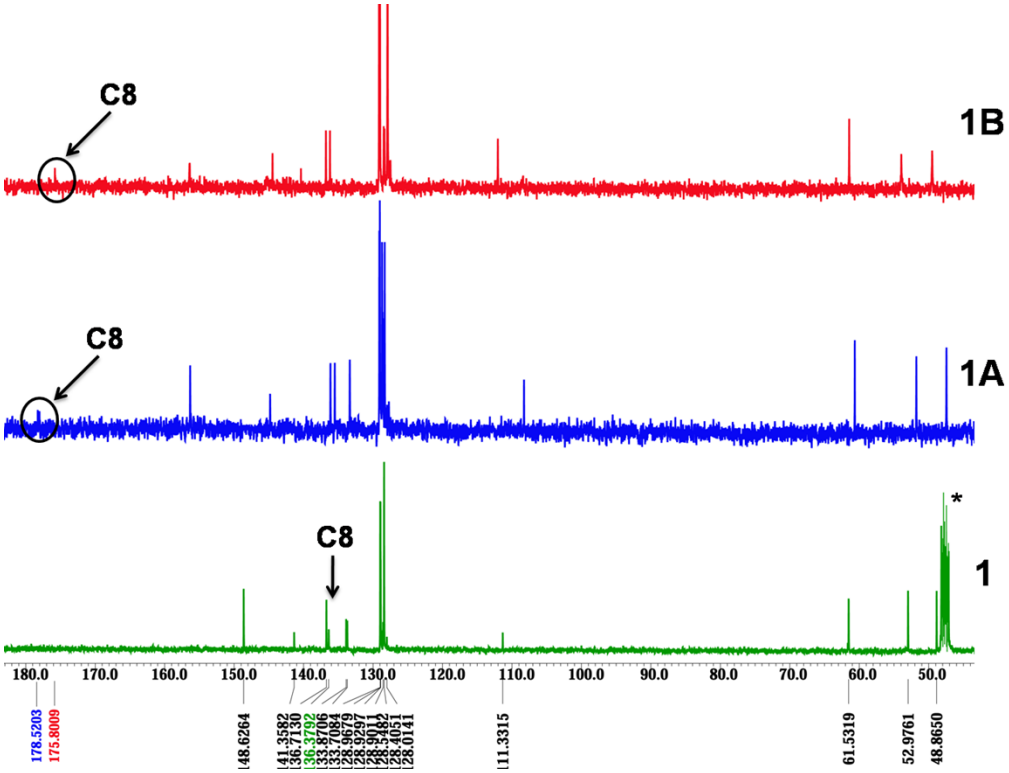
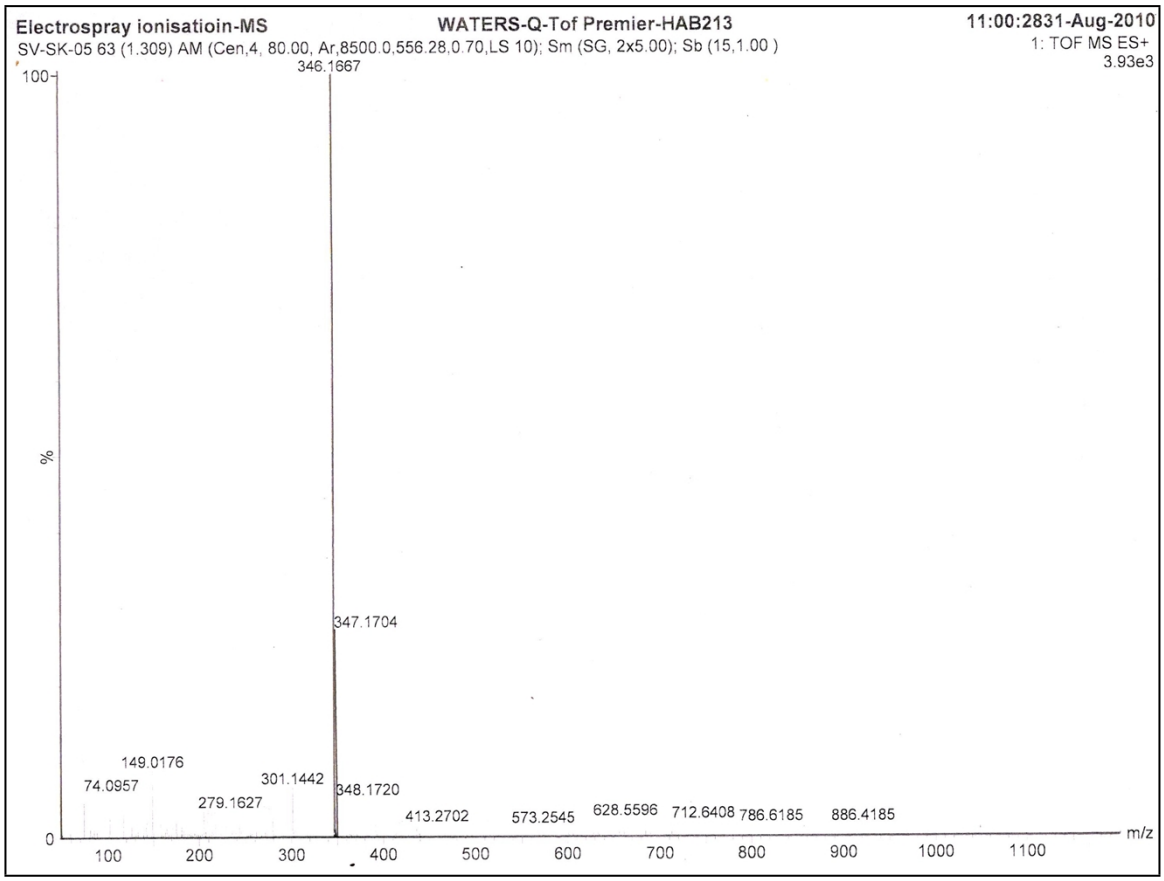


Figure S3: ^{13}C NMR spectra for **1** (CD_3OD), **1A** (d_6-DMSO) and **1B** (d_6-DMSO) demonstrating the shifting of peak corresponding to C8 in **1A** and **1B**. (*: residual solvent)

(Note: Orginal ^{1}H and ^{13}C NMR spectra are provided in the last)

a)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WATERS-Q-Tof Premier-HAB213
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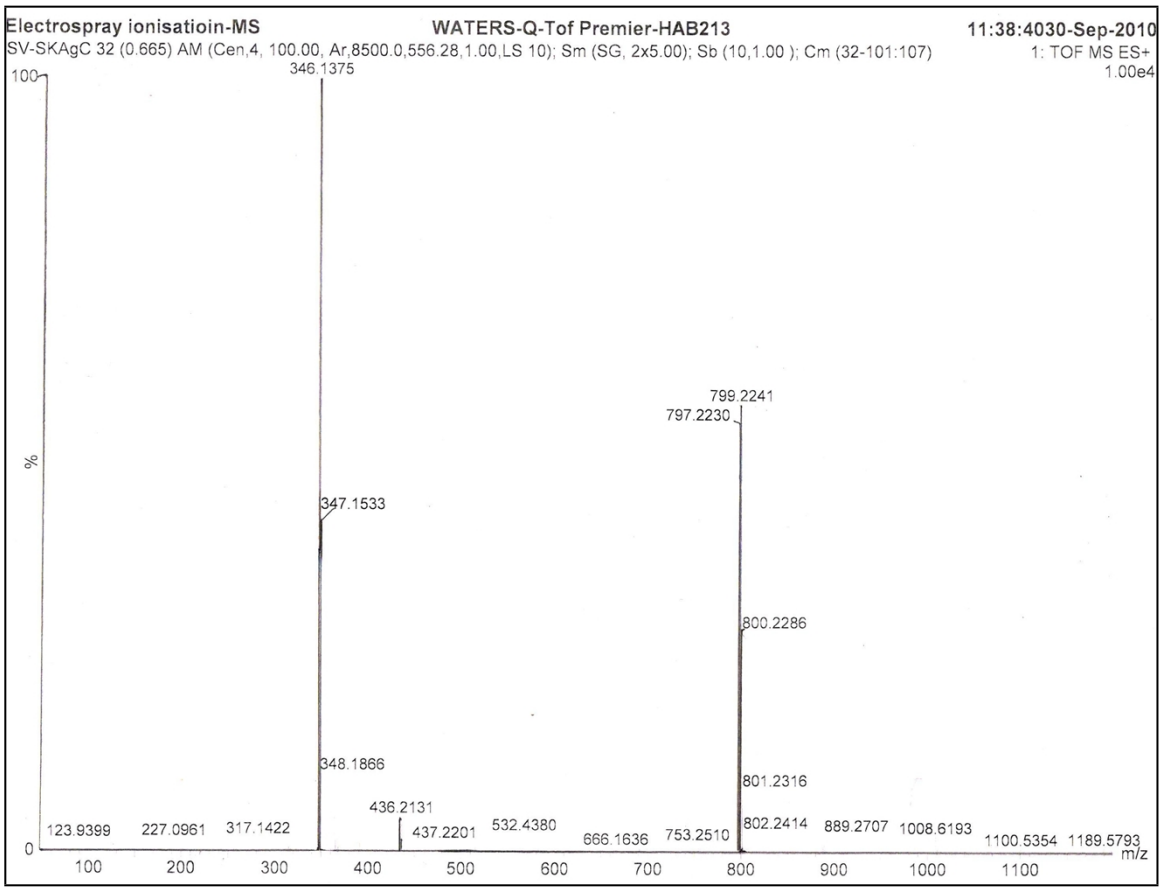
SV-SK-05 63 (1.309) AM (Cen,4, 80.00, Ar,8500.0,556.28,0.70,LS 10); Sm (SG, 2x5.00); Sb (15,1.00)
1: TOF MS ES+
3.93e3
346.1667
347.1704
149.0176
74.0957
301.1442
279.1627
348.1720
413.2702
573.2545
628.5596
712.6408
786.6185
886.4185
%
m/z

b)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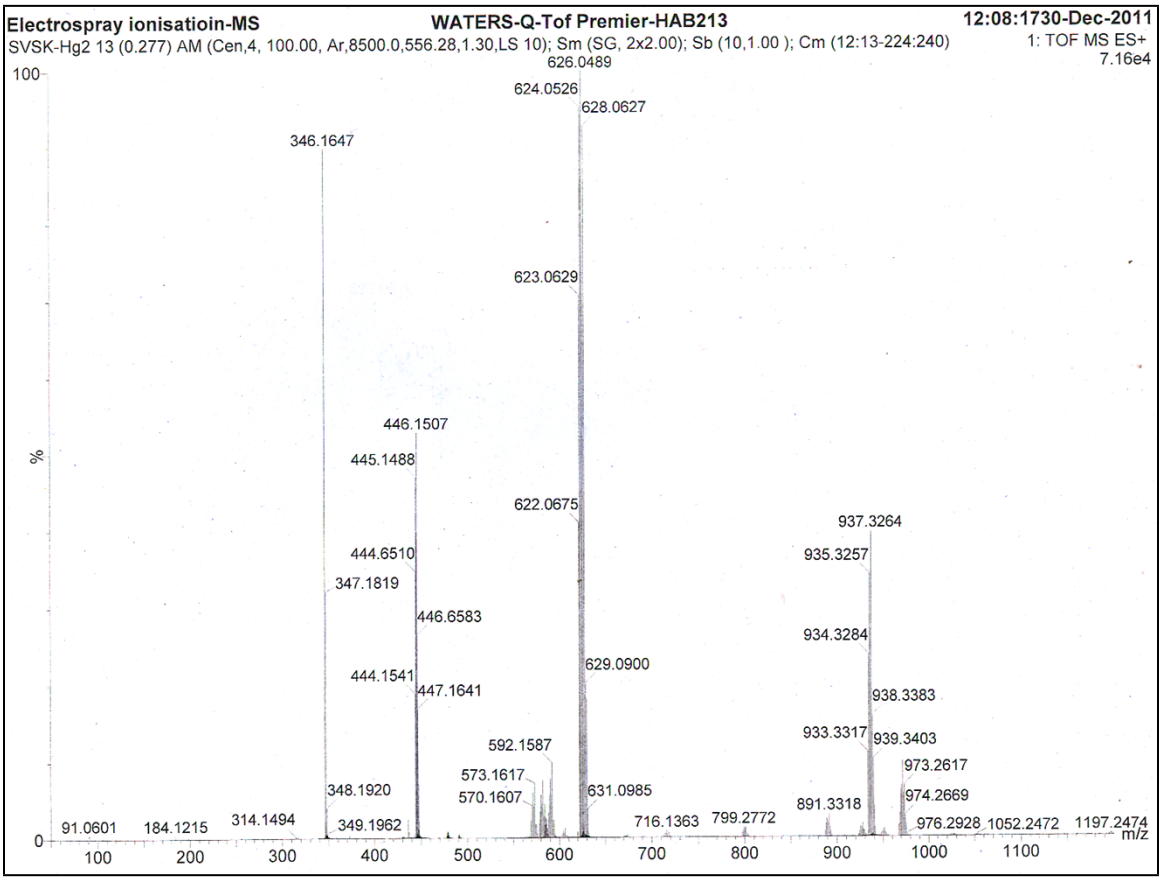
WATERS-Q-Tof Premier-HAB213
11:38:4030-Sep-2010
SV-SKAgC 32 (0.665) AM (Cen,4, 100.00, Ar,8500.0,556.28,1.00,LS 10); Sm (SG, 2x5.00); Sb (10,1.00); Cm (32-101:107)
1: TOF MS ES+
1.00e4
346.1375
799.2241
797.2230
347.1533
800.2286
348.1866
801.2316
436.2131
123.9399
227.0961
317.1422
437.2201
532.4380
666.1636
753.2510
802.2414
889.2707
1008.6193
1100.5354
1189.5793
%
m/z

c)



Figures S4: HRMS of (a) **1**; (b) **1A** and (c) **1B**.

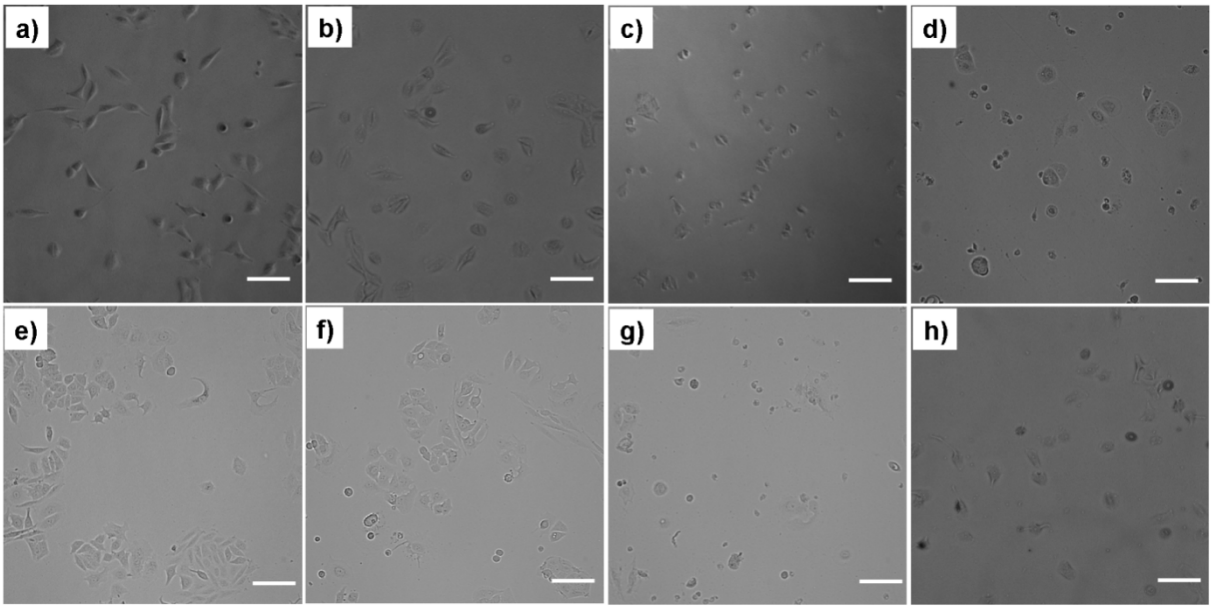


Figure S5: Morphological changes of A549 and MCF7 cells after treatment with conjugates for 24 h. Upper panel: (a) Untreated A549 cells; (b) with **1**; (c) with **1A**; (d) with **1B**. Lower panel: (e) Untreated MCF7 cells; (f) with **1**; (g) with **1A**; (h) with **1B**. Scale bar corresponds to 100 μm.

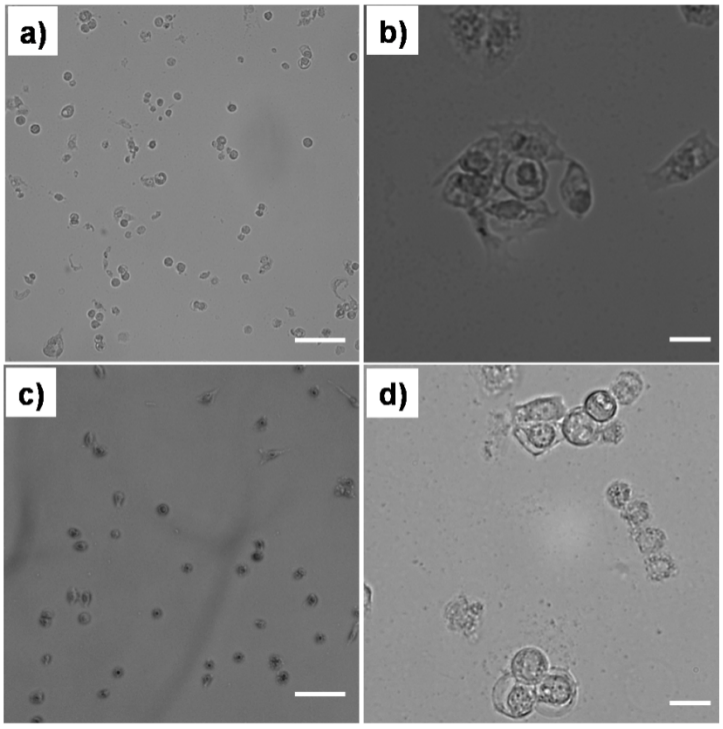


Figure S6: Morphologies of the A549 (a, b) and MCF7 (c, d) cells after treatment with curcumin (control) for 24 h. Scale bar corresponds to 100 μm for a, c and 20 μm for b, d.

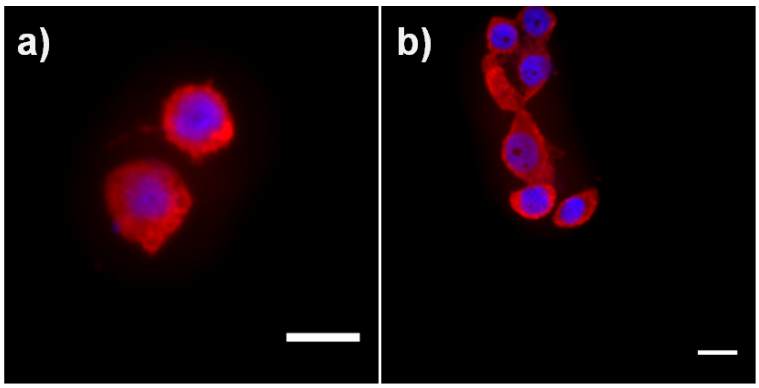


Figure S7: Changes in microtubule networks in (a) A549 and (b) MCF7 cells after treatment with curcumin (control) for 24 h. Scale bar corresponds to 20 µm.

Tables:

Table S1: Crystal structure refinement parameters for **1**

Identification code	**Ligand 1**
Empirical formula	$C_{20}H_{20}BrN_5O$
*M*r	426.32
crystal system	Triclinic
space group	*P -1*
a(Å)	7.283(2)
b(Å)	11.074(3)
c(Å)	13.183(4)
α (deg)	107.84(4)
β (deg)	98.89(2)
γ (deg)	105.76(3)
Volume (Å^3)	940.7(3)
Z	2

Dx (Mg m^{-3})	1.505
F(000)	436
μ (mm^{-1})	2.205
θ range for data collection(deg)	4.11-25.02
Limiting indices	-8<=h<=8, -13<=k<=11, -15<=l<=12
Reflections collected	4788
unique reflections	3245
R(int)	0.0237
Completeness to θ	= 25.02, 97.3
T_{max} / T_{min}	0.6923/ 0.6545
Data / restraints / parameters	3245 / 0 / 245
GOF on F^2	0.649
*R*1 and *R*2 [$I>2\sigma(I)$]	0.0484, 0.1346
*R*1 and *R*2 (all data)	0.0557, 0.1584
Largest diff. peak and hole(e.A^{-3})	0.846 and -0.684

Table S2: Selected Bond Lengths (Å) and Bond Angles (°) for **1**, DFT optimized silver carbene complex, **1A** and mercury carbene complex, **1B.**

Ligand, 1

Bond Lengths (Å)	
N9-C8	1.338
N7-C8	1.329
Bond Angles (°)	
N7-C8-N9	108.9

Silver Carbene Complex, 1A

Bond Lengths (Å)	
Ag-C8	2.137
N9-C8	1.362
N7-C8	1.363
Bond Angles (°)	
C8-Ag-C8’	178.63
N7-C8-N9	105.77

Mercury Carbene Complex, 1B

Bond Lengths (Å)	
Ag-C8	2.250
N9-C8	1.358
N7-C8	1.359
Bond Angles (°)	
C8-Ag-C8’	170.62
N7-C8-N9	107.19

Table S3: Coordinates of DFT optimized structure of **1A**:

H	-3.24055	-4.17326	1.74577
C	-2.76292	-3.97408	0.79113
C	-3.11542	-2.83607	0.06536
C	-1.80985	-4.86363	0.28713

C	-2.50898	-2.56611	-1.16891
H	-3.86952	-2.16004	0.45852
C	-1.20793	-4.60623	-0.94539
H	-1.54415	-5.75339	0.84965
C	-2.92669	-1.37797	-2.01258
C	-1.55181	-3.45898	-1.66590
H	-0.47391	-5.29713	-1.34974
H	-2.19342	-1.19718	-2.80262
H	-3.89437	-1.56555	-2.48542
H	-1.08364	-3.26515	-2.62807
C	-4.28477	0.53206	-1.03621
C	-2.05720	0.57672	-0.69117
C	-5.64897	0.25956	-1.40827
C	-3.99344	1.67226	-0.32362
N	-2.62453	1.67836	-0.12601
N	-6.05220	-0.77482	-2.07192
C	-1.90565	2.74135	0.61066
O	-7.44749	-0.69711	-2.25215
C	-6.10149	2.37574	-0.24703
H	-2.48538	3.65431	0.45641
H	-0.93512	2.86315	0.12715
C	-1.74088	2.45207	2.08848
C	-7.89502	-1.84353	-2.97271

C	-0.48902	2.09058	2.59906
C	-2.83135	2.56619	2.96282
H	-8.97440	-1.71888	-3.07632
H	-7.67648	-2.76248	-2.41906
H	-7.42798	-1.88885	-3.96200
C	-0.32807	1.83601	3.96316
H	0.36725	2.02672	1.93232
C	-2.67058	2.30964	4.32391
H	-3.80089	2.86490	2.57375
C	-1.41894	1.94315	4.82648
H	0.64755	1.55581	4.34797
H	-3.51896	2.40598	4.99507
H	-1.29441	1.75222	5.88836
N	-3.08455	-0.12341	-1.25010
H	0.47402	5.29720	-1.34950
C	1.20812	4.60628	-0.94532
C	1.81038	4.86370	0.28702
C	1.55175	3.45898	-1.66587
C	2.76356	3.97413	0.79080
H	1.54489	5.75350	0.84958
C	2.50900	2.56607	-1.16910
H	1.08331	3.26514	-2.62791
H	3.24146	4.17334	1.74529

C	3.11580	2.83607	0.06498
C	2.92636	1.37785	-2.01282
H	3.86998	2.16002	0.45797
H	2.19288	1.19711	-2.80267
H	3.89395	1.56529	-2.48590
N	3.08425	0.12330	-1.25032
C	4.28449	-0.53211	-1.03638
C	2.05694	-0.57677	-0.69127
C	3.99320	-1.67228	-0.32372
N	2.62430	-1.67837	-0.12605
N	6.05186	0.77468	-2.07230
C	1.90546	-2.74127	0.61080
O	7.44714	0.69695	-2.25261
C	6.10126	-2.37576	-0.24722
H	2.48502	-3.65430	0.45642
H	0.93480	-2.86294	0.12751
C	1.74108	-2.45195	2.08865
C	7.89464	1.84335	-2.97321
C	0.48959	-2.08941	2.59939
C	2.83155	-2.56701	2.96287
H	8.97400	1.71864	-3.07698
H	7.67625	2.76230	-2.41949
H	7.42746	1.88873	-3.96243

C	0.32899	-1.83474	3.96351
H	-0.36669	-2.02481	1.93272
C	2.67113	-2.31039	4.32400
H	3.80080	-2.86649	2.57367
C	1.41986	-1.94285	4.82671
H	-0.64635	-1.55372	4.34843
H	3.51950	-2.40747	4.99506
H	1.29561	-1.75186	5.88860
Ag	-0.00014	-0.00007	-0.66570
H	-6.89085	3.06897	0.02981
H	6.89062	-3.06901	0.02958
C	5.64867	-0.25963	-1.40851
N	4.87309	-2.63116	0.09692
N	-4.87331	2.63114	0.09704
N	6.50668	-1.27778	-0.95016
H	7.48401	-1.14802	-1.18306
N	-6.50695	1.27772	-0.94993
H	-7.48429	1.14797	-1.18279

Table S4: Coordinates of DFT optimized structure of **1B**:

H	2.07188	4.14388	-2.39840
C	1.78926	3.13354	-2.67802
C	2.51914	2.05036	-2.18893

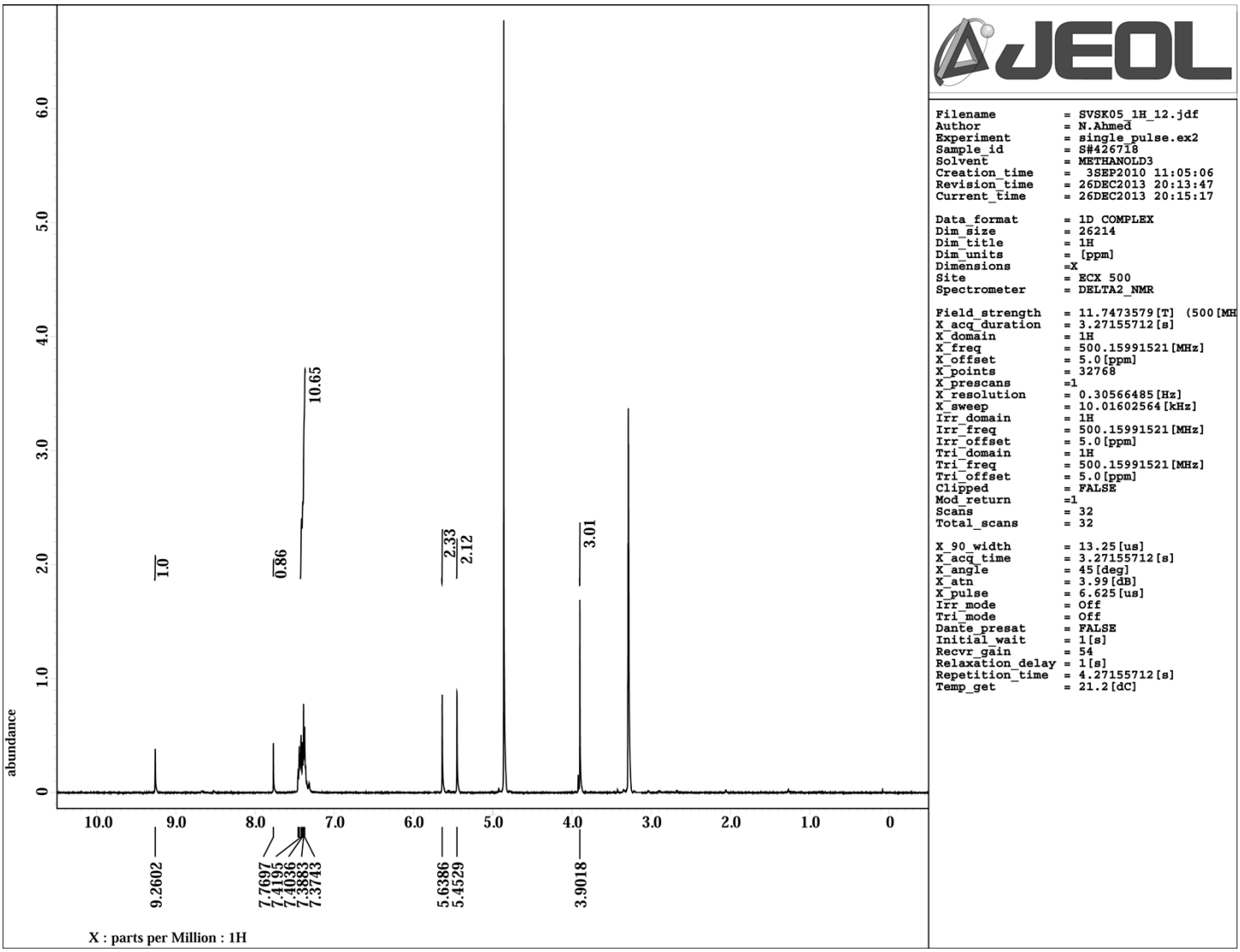
C	0.72076	2.92341	-3.55785
C	2.18466	0.74014	-2.56904
H	3.36957	2.22530	-1.53544
C	0.37757	1.62451	-3.93598
H	0.17340	3.77075	-3.95915
C	3.04669	-0.43486	-2.16089
C	1.10381	0.53652	-3.43926
H	-0.43738	1.45555	-4.63316
H	2.58797	-1.37945	-2.46810
H	4.03057	-0.38207	-2.63503
H	0.85962	-0.47020	-3.77107
C	4.56852	-0.65759	-0.14013
C	2.37402	-0.53379	0.27564
C	5.90608	-0.69879	-0.68039
C	4.39016	-0.77441	1.22061
N	3.02796	-0.69451	1.45217
N	6.20562	-0.58890	-1.93099
C	2.42514	-0.84971	2.80053
O	7.58894	-0.67103	-2.09398
C	6.55372	-0.97371	1.67346
H	3.25914	-0.74806	3.49797
H	2.04518	-1.87195	2.87943
C	1.33313	0.15294	3.08301

C	7.93004	-0.56137	-3.48204
C	-0.00959	-0.26050	3.11212
C	1.64426	1.49196	3.36067
H	9.01761	-0.63415	-3.51430
H	7.60589	0.40328	-3.88297
H	7.48164	-1.37859	-4.05421
C	-1.02533	0.65587	3.41747
H	-0.25417	-1.31078	2.97330
C	0.63015	2.39967	3.66217
H	2.68134	1.81698	3.36299
C	-0.70549	1.98489	3.68987
H	-2.05649	0.31992	3.46768
H	0.88009	3.43070	3.89001
H	-1.48856	2.69661	3.92598
N	3.31415	-0.51054	-0.70275
H	1.20487	-4.47133	1.30458
C	0.21218	-4.05130	1.43598
C	-0.42472	-4.12723	2.67473
C	-0.45109	-3.47559	0.34430
C	-1.72307	-3.62241	2.82413
H	0.07366	-4.59803	3.51646
C	-1.75428	-2.97323	0.48490
H	0.01953	-3.48788	-0.63720

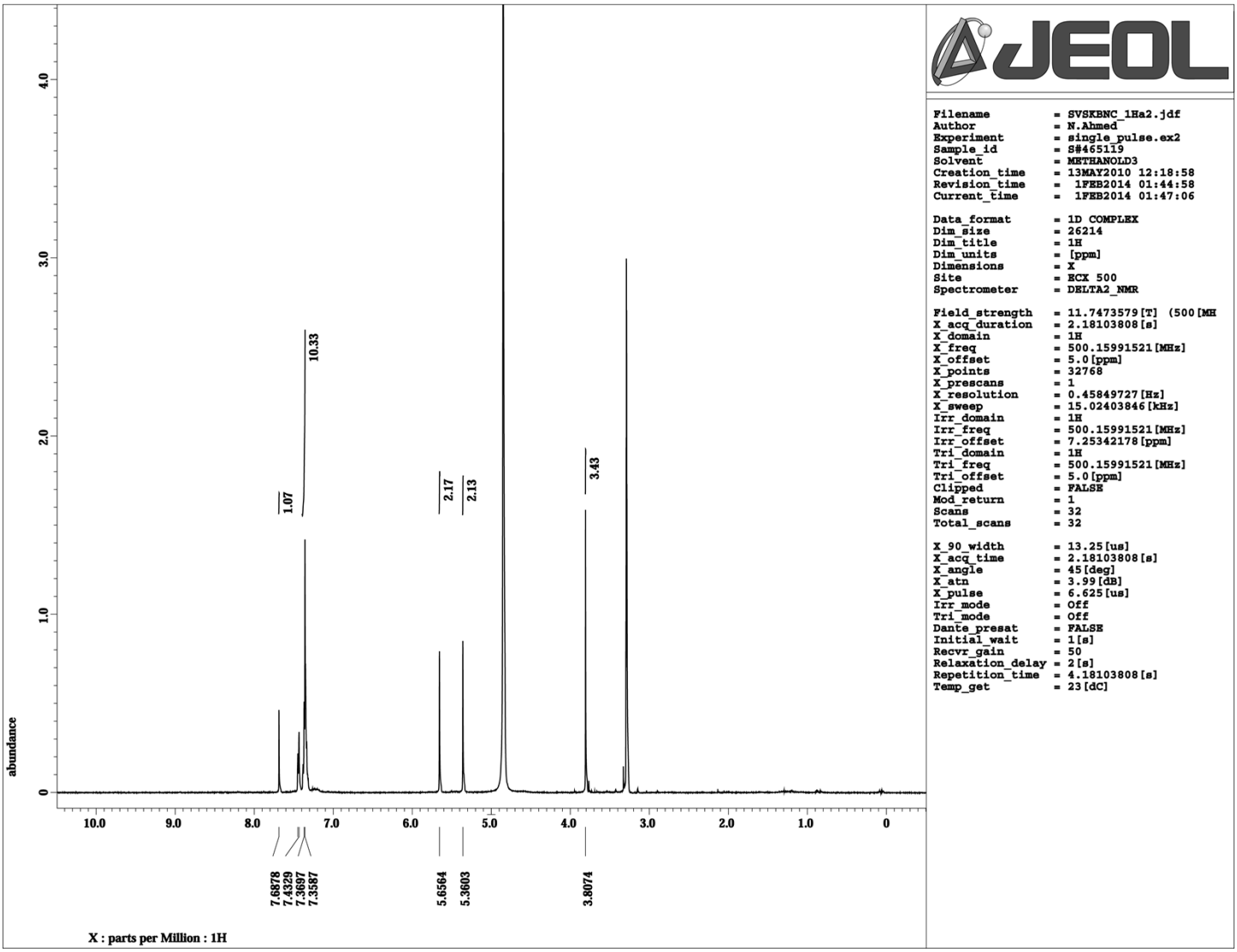
H	-2.22719	-3.69976	3.78244
C	-2.38351	-3.04969	1.73826
C	-2.51051	-2.48440	-0.72806
H	-3.40405	-2.69400	1.85185
H	-1.93559	-2.66688	-1.64067
H	-3.46237	-3.01107	-0.82757
N	-2.86394	-1.03763	-0.70886
C	-4.11993	-0.55071	-1.01848
C	-1.98912	-0.00177	-0.61528
C	-4.00935	0.81695	-1.12275
N	-2.68568	1.13595	-0.86889
N	-5.63914	-2.44003	-1.14851
C	-2.14772	2.50968	-1.02244
O	-6.98329	-2.69041	-1.42824
C	-6.14446	1.12985	-1.65047
H	-2.79104	2.97375	-1.77568
H	-1.15061	2.41654	-1.45730
C	-2.11737	3.36420	0.22784
C	-7.25337	-4.09519	-1.33680
C	-0.95760	4.09470	0.51501
C	-3.25950	3.55254	1.01907
H	-8.31464	-4.19652	-1.56609
H	-7.05081	-4.46129	-0.32618

H	-6.65681	-4.65020	-2.06650
C	-0.94004	5.01189	1.56869
H	-0.07574	3.97551	-0.11055
C	-3.23563	4.45654	2.08091
H	-4.17817	3.02351	0.78446
C	-2.07901	5.19410	2.35369
H	-0.04319	5.59151	1.76539
H	-4.12871	4.60642	2.67988
H	-2.07332	5.91648	3.16416
Hg	0.16066	-0.23305	0.00812
H	7.40302	-1.09778	2.33942
H	-7.00365	1.73996	-1.91471
C	-5.40208	-1.17442	-1.24200
N	-4.99355	1.70581	-1.43637
N	5.34974	-0.93198	2.17396
N	-6.37704	-0.20957	-1.57025
H	-7.30434	-0.58089	-1.74773
N	6.85537	-0.87249	0.34906
H	7.82017	-0.91482	0.03840

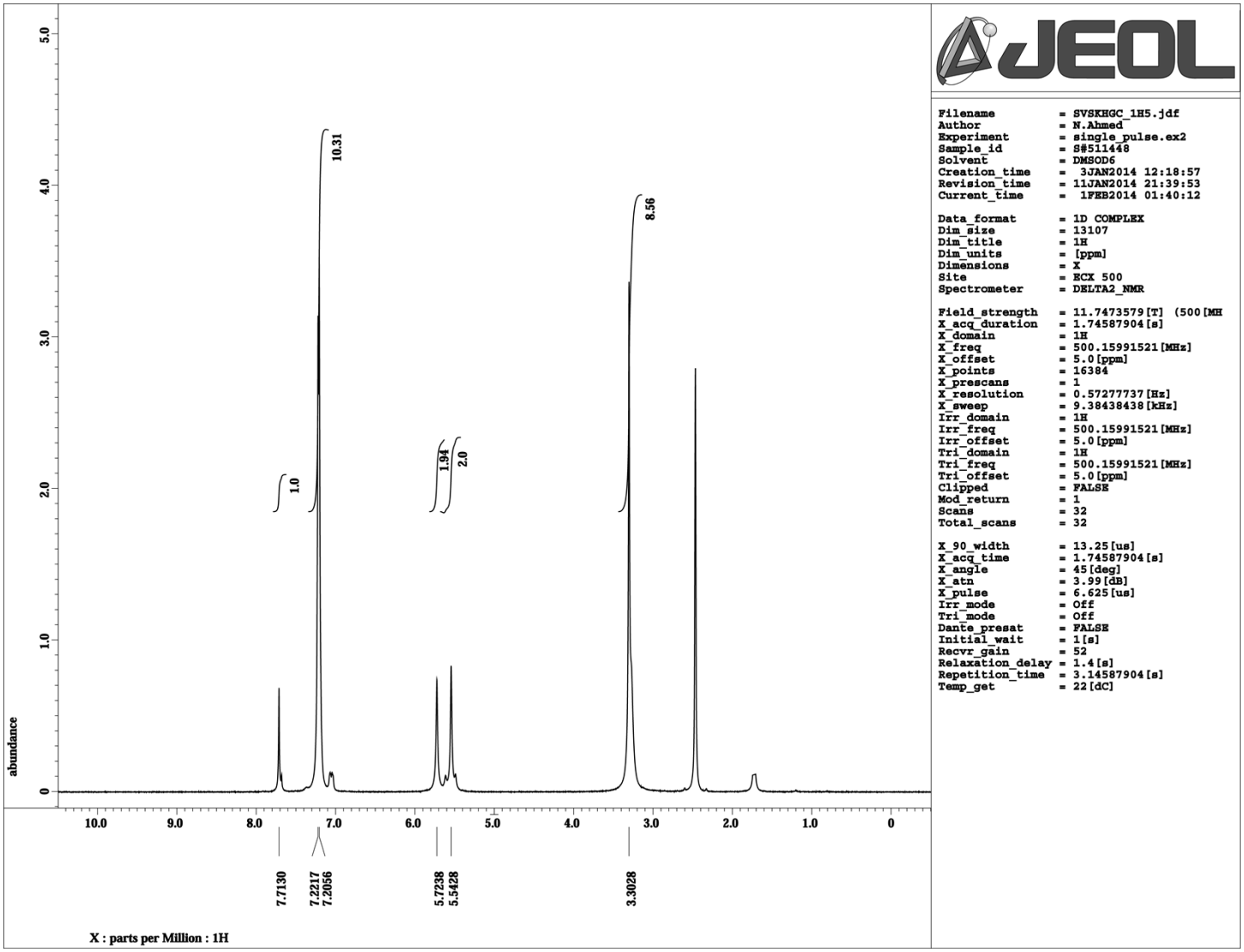
^{1}H NMR of 1:


abundance
0
1.0
2.0
3.0
4.0
5.0
6.0
10.0
9.0
8.0
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0
1.0
0.86
10.65
2.33
2.12
3.01
9.2602
7.7697
7.4195
7.4036
7.3883
7.3743
5.6386
5.4529
3.9018
X : parts per Million : 1H
Filename = SVSK05_1H_12.jdf
Author = N.Ahmed
Experiment = single_pulse.ex2
Sample_id = S#426718
Solvent = METHANOLD3
Creation_time = 3SEP2010 11:05:06
Revision_time = 26DEC2013 20:13:47
Current_time = 26DEC2013 20:15:17
Data_format = 1D COMPLEX
Dim_size = 26214
Dim_title = 1H
Dim_units = [ppm]
Dimensions =X
Site = ECX 500
Spectrometer = DELTA2_NMR
Field_strength = 11.7473579[T] (500[MH
X_acq_duration = 3.27155712[s]
X_domain = 1H
X_freq = 500.15991521[MHz]
X_offset = 5.0[ppm]
X_points = 32768
X_prescans =1
X_resolution = 0.30566485[Hz]
X_sweep = 10.01602564[kHz]
Irr_domain = 1H
Irr_freq = 500.15991521[MHz]
Irr_offset = 5.0[ppm]
Tri_domain = 1H
Tri_freq = 500.15991521[MHz]
Tri_offset = 5.0[ppm]
Clipped = FALSE
Mod_return =1
Scans = 32
Total_scans = 32
X_90_width = 13.25[us]
X_acq_time = 3.27155712[s]
X_angle = 45[deg]
X_atn = 3.99[dB]
X_pulse = 6.625[us]
Irr_mode = Off
Tri_mode = Off
Dante_presat = FALSE
Initial_wait = 1[s]
Recvr_gain = 54
Relaxation_delay = 1[s]
Repetition_time = 4.27155712[s]
Temp_get = 21.2[dC]

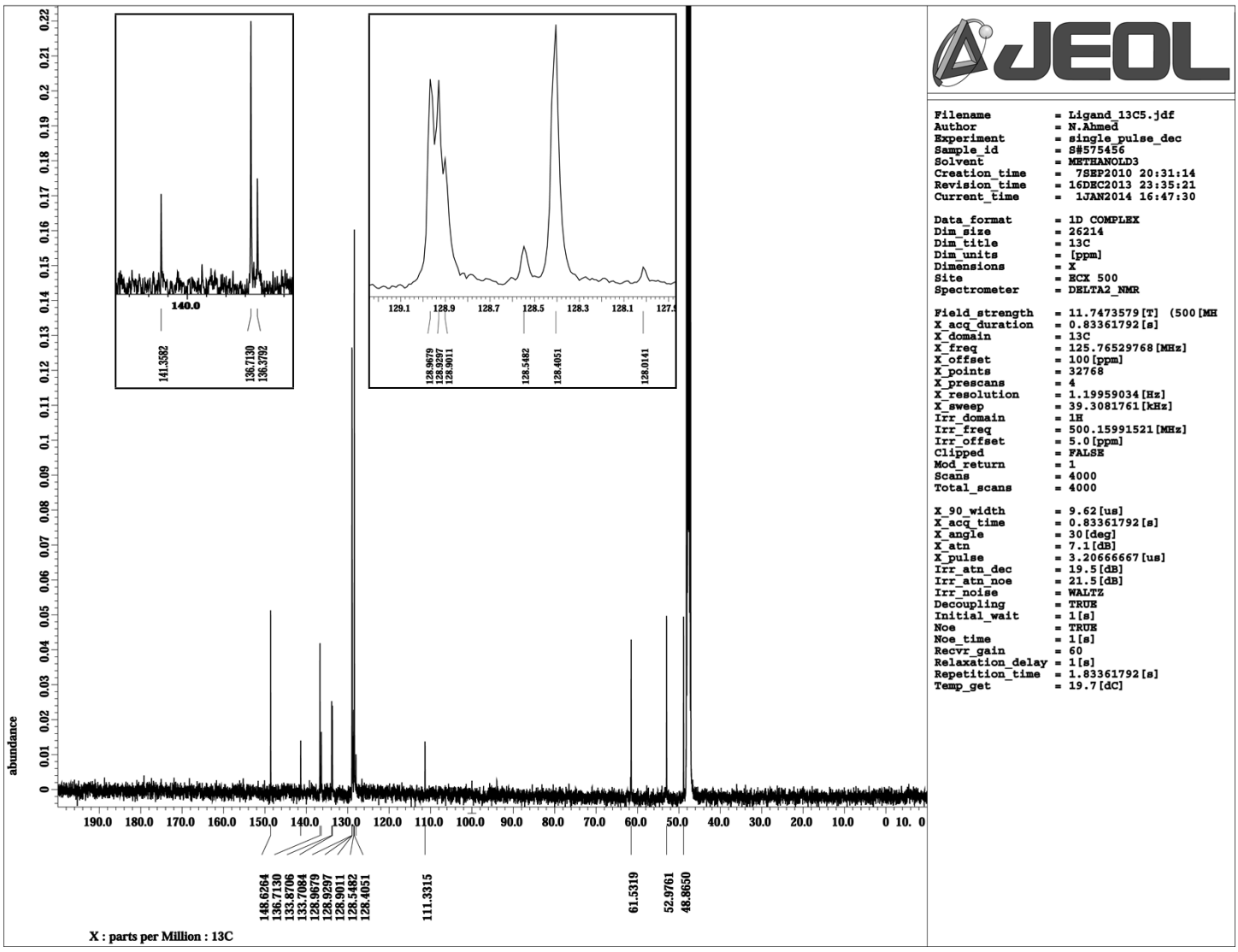
^{1}H NMR of 1A:


abundance
4.0
3.0
2.0
1.0
0
10.33
1.07
2.17
2.13
3.43
10.0
9.0
8.0
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0
7.6878
7.4329
7.3697
7.3587
5.6564
5.3603
3.8074
X : parts per Million : 1H
JEOL
Filename = SVSKBNC_1Ha2.jdf
Author = N.Ahmed
Experiment = single_pulse.ex2
Sample_id = S#465119
Solvent = METHANOLD3
Creation_time = 13MAY2010 12:18:58
Revision_time = 1FEB2014 01:44:58
Current_time = 1FEB2014 01:47:06
Data_format = 1D COMPLEX
Dim_size = 26214
Dim_title = 1H
Dim_units = [ppm]
Dimensions = X
Site = HCX 500
Spectrometer = DELTA2_NMR
Field_strength = 11.7473579[T] (500[MH
X_acq_duration = 2.18103808[s]
X_domain = 1H
X_freq = 500.15991521[MHz]
X_offset = 5.0[ppm]
X_points = 32768
X_prescans = 1
X_resolution = 0.45849727[Hz]
X_sweep = 15.02403846[kHz]
Irr_domain = 1H
Irr_freq = 500.15991521[MHz]
Irr_offset = 7.25342178[ppm]
Tri_domain = 1H
Tri_freq = 500.15991521[MHz]
Tri_offset = 5.0[ppm]
Clipped = FALSE
Mod_return = 1
Scans = 32
Total_scans = 32
X_90_width = 13.25[us]
X_acq_time = 2.18103808[s]
X_angle = 45[deg]
X_atn = 3.99[dB]
X_pulse = 6.625[us]
Irr_mode = Off
Tri_mode = Off
Dante_presat = FALSE
Initial_wait = 1[s]
Recvr_gain = 50
Relaxation_delay = 2[s]
Repetition_time = 4.18103808[s]
Temp_get = 23[dC]

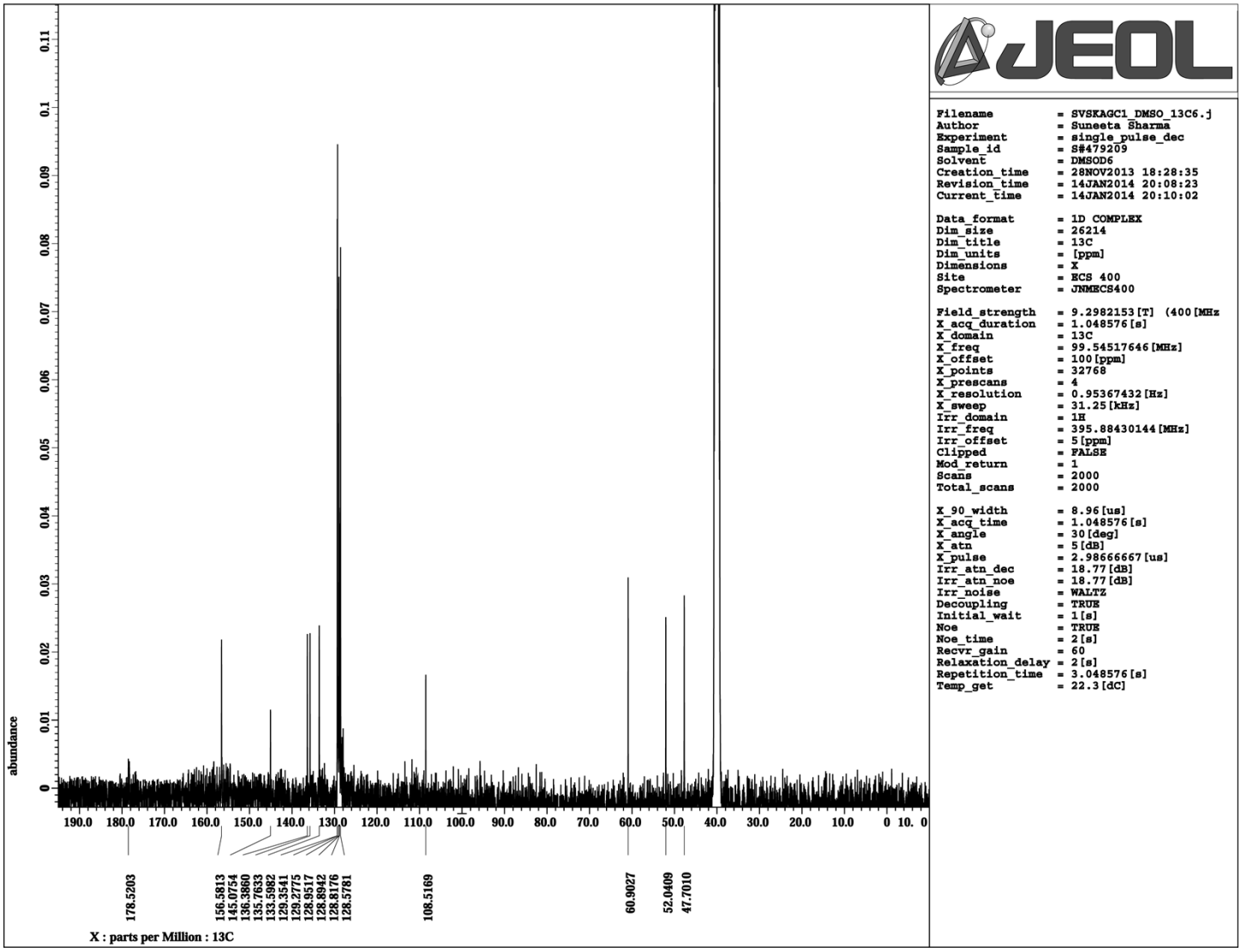
^{1}H NMR of 1B:


abundance
10.31
8.56
1.94
2.0
1.0
7.7130
7.2217
7.2056
5.7238
5.5428
3.3028
X : parts per Million : 1H
Filename = SVSKHGC_1H5.jdf
Author = N.Ahmed
Experiment = single_pulse.ex2
Sample_id = S#511448
Solvent = DMSOD6
Creation_time = 3JAN2014 12:18:57
Revision_time = 11JAN2014 21:39:53
Current_time = 1FEB2014 01:40:12
Data_format = 1D COMPLEX
Dim_size = 13107
Dim_title = 1H
Dim_units = [ppm]
Dimensions = X
Site = ECX 500
Spectrometer = DELTA2_NMR
Field_strength = 11.7473579[T] (500[MH
X_acq_duration = 1.74587904[s]
X_domain = 1H
X_freq = 500.15991521[MHz]
X_offset = 5.0[ppm]
X_points = 16384
X_prescans = 1
X_resolution = 0.57277737[Hz]
X_sweep = 9.38438438[kHz]
Irr_domain = 1H
Irr_freq = 500.15991521[MHz]
Irr_offset = 5.0[ppm]
Tri_domain = 1H
Tri_freq = 500.15991521[MHz]
Tri_offset = 5.0[ppm]
Clipped = FALSE
Mod_return = 1
Scans = 32
Total_scans = 32
X_90_width = 13.25[us]
X_acq_time = 1.74587904[s]
X_angle = 45[deg]
X_atn = 3.99[dB]
X_pulse = 6.625[us]
Irr_mode = Off
Tri_mode = Off
Dante_presat = FALSE
Initial_wait = 1[s]
Recvr_gain = 52
Relaxation_delay = 1.4[s]
Repetition_time = 3.14587904[s]
Temp_get = 22[dC]

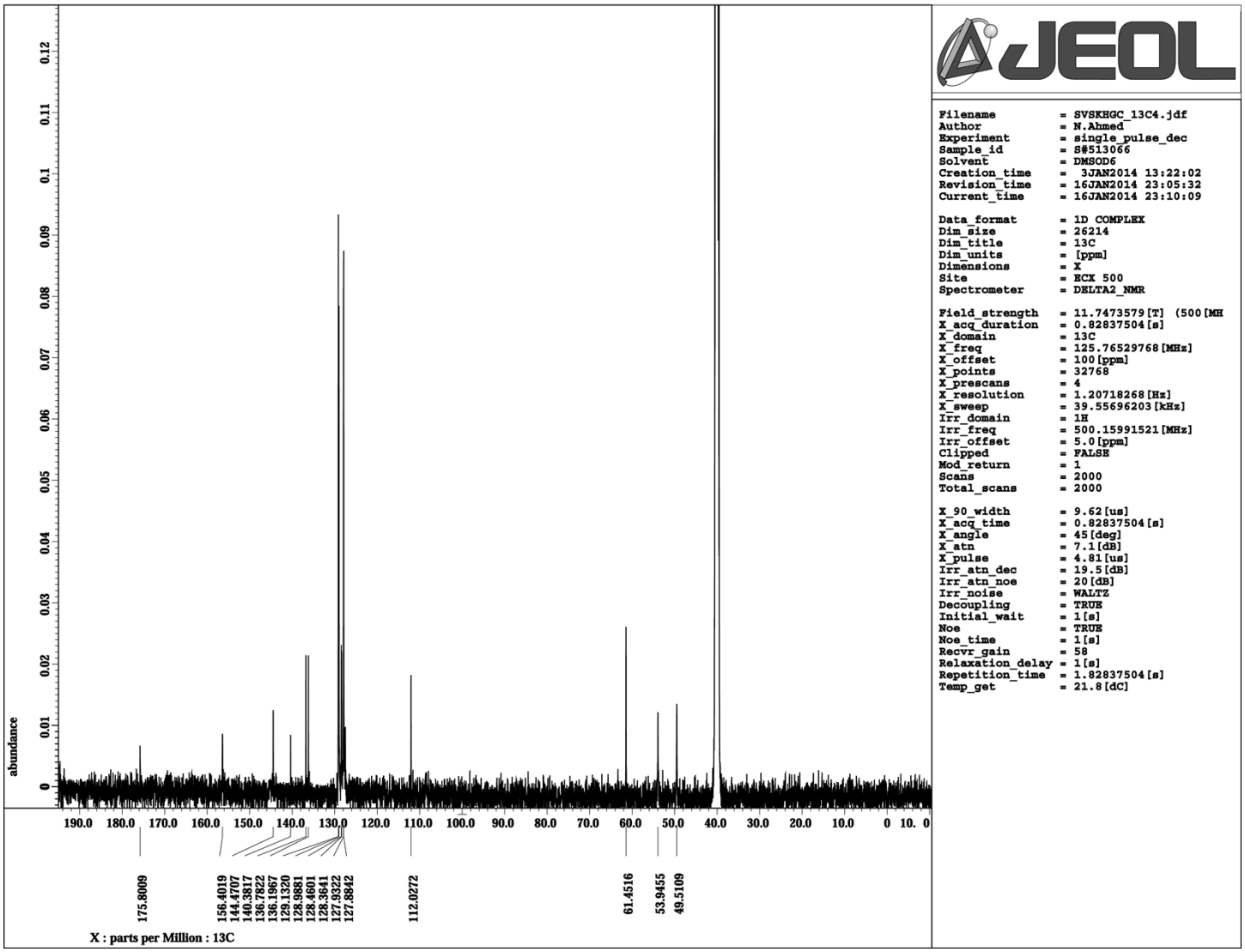
^{13}C NMR of 1:


abundance
X : parts per Million : 13C
148.6264
136.7130
133.8706
133.7084
128.9679
128.9297
128.9011
128.5482
128.4051
111.3315
61.5319
52.9761
48.8650
141.3582
136.7130
136.3792
128.9679
128.9297
128.9011
128.5482
128.4051
128.0141
Filename = Ligand_13C5.jdf
Author = N.Ahmed
Experiment = single_pulse_dec
Sample_id = S#575456
Solvent = METHANOLD3
Creation_time = 7SEP2010 20:31:14
Revision_time = 16DEC2013 23:35:21
Current_time = 1JAN2014 16:47:30
Data_format = 1D COMPLEX
Dim_size = 26214
Dim_title = 13C
Dim_units = [ppm]
Dimensions = X
Site = NCX 500
Spectrometer = DELTA2_NMR
Field_strength = 11.7473579[T] (500[MH
X_acq_duration = 0.83361792[s]
X_domain = 13C
X_freq = 125.76529768[MHz]
X_offset = 100[ppm]
X_points = 32768
X_prescans = 4
X_resolution = 1.19959034[Hz]
X_sweep = 39.3081761[kHz]
Irr_domain = 1H
Irr_freq = 500.15991521[MHz]
Irr_offset = 5.0[ppm]
Clipped = FALSE
Mod_return = 1
Scans = 4000
Total_scans = 4000
X_90_width = 9.62[us]
X_acq_time = 0.83361792[s]
X_angle = 30[deg]
X_atn = 7.1[dB]
X_pulse = 3.20666667[us]
Irr_atn_dec = 19.5[dB]
Irr_atn_noe = 21.5[dB]
Irr_noise = WALTZ
Decoupling = TRUE
Initial_wait = 1[s]
Noe = TRUE
Noe_time = 1[s]
Recvr_gain = 60
Relaxation_delay = 1[s]
Repetition_time = 1.83361792[s]
Temp_get = 19.7[dC]

^{13}C NMR of 1A:


abundance
0.11
0.1
0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
190.0 180.0 170.0 160.0 150.0 140.0 130.0 120.0 110.0 100.0 90.0 80.0 70.0 60.0 50.0 40.0 30.0 20.0 10.0 0 10. 0
178.5203
156.5813
145.0754
136.3860
135.7653
133.3982
129.3541
129.2775
128.9517
128.8942
128.8176
128.5781
108.5169
60.9027
52.0409
47.7010
X : parts per Million : 13C
JEOL
Filename = SVSKAGC1_DMSO_13C6.j
Author = Suneeta Sharma
Experiment = single_pulse_dec
Sample_id = S#479209
Solvent = DMSOD6
Creation_time = 28NOV2013 18:28:35
Revision_time = 14JAN2014 20:08:23
Current_time = 14JAN2014 20:10:02
Data_format = 1D COMPLEX
Dim_size = 26214
Dim_title = 13C
Dim_units = [ppm]
Dimensions = X
Site = ECS 400
Spectrometer = JNMECS400
Field_strength = 9.2982153[T] (400[MHz
X_acq_duration = 1.048576[s]
X_domain = 13C
X_freq = 99.54517646[MHz]
X_offset = 100[ppm]
X_points = 32768
X_prescans = 4
X_resolution = 0.95367432[Hz]
X_sweep = 31.25[kHz]
Irr_domain = 1H
Irr_freq = 395.88430144[MHz]
Irr_offset = 5[ppm]
Clipped = FALSE
Mod_return = 1
Scans = 2000
Total_scans = 2000
X_90_width = 8.96[us]
X_acq_time = 1.048576[s]
X_angle = 30[deg]
X_atn = 5[dB]
X_pulse = 2.98666667[us]
Irr_atn_dec = 18.77[dB]
Irr_atn_noe = 18.77[dB]
Irr_noise = WALTZ
Decoupling = TRUE
Initial_wait = 1[s]
Noe = TRUE
Noe_time = 2[s]
Recvr_gain = 60
Relaxation_delay = 2[s]
Repetition_time = 3.048576[s]
Temp_get = 22.3[dC]

^{13}C NMR of 1B:


abundance
0 0.01 0.02 0.03 0.04 0.05 0.06 0.07 0.08 0.09 0.1 0.11 0.12
190.0 180.0 170.0 160.0 150.0 140.0 130.0 120.0 110.0 100.0 90.0 80.0 70.0 60.0 50.0 40.0 30.0 20.0 10.0 0 10. 0
175.8009
156.4019
144.4707
140.3817
136.7822
136.1967
129.1320
128.9881
128.4601
128.3641
127.9322
127.8842
112.0272
61.4516
53.9455
49.5109
X : parts per Million : 13C
JEOL
Filename = SVSKHGC_13C4.jdf
Author = N.Ahmed
Experiment = single_pulse_dec
Sample_id = S#513066
Solvent = DMSOD6
Creation_time = 3JAN2014 13:22:02
Revision_time = 16JAN2014 23:05:32
Current_time = 16JAN2014 23:10:09
Data_format = 1D COMPLEX
Dim_size = 26214
Dim_title = 13C
Dim_units = [ppm]
Dimensions = X
Site = ECX 500
Spectrometer = DELTA2_NMR
Field_strength = 11.7473579[T] (500[MH
X_acq_duration = 0.82837504[s]
X_domain = 13C
X_freq = 125.76529768[MHz]
X_offset = 100[ppm]
X_points = 32768
X_prescans = 4
X_resolution = 1.20718268[Hz]
X_sweep = 39.55696203[kHz]
Irr_domain = 1H
Irr_freq = 500.15991521[MHz]
Irr_offset = 5.0[ppm]
Clipped = FALSE
Mod_return = 1
Scans = 2000
Total_scans = 2000
X_90_width = 9.62[us]
X_acq_time = 0.82837504[s]
X_angle = 45[deg]
X_atn = 7.1[dB]
X_pulse = 4.81[us]
Irr_atn_dec = 19.5[dB]
Irr_atn_noe = 20[dB]
Irr_noise = WALTZ
Decoupling = TRUE
Initial_wait = 1[s]
Noe = TRUE
Noe_time = 1[s]
Recvr_gain = 58
Relaxation_delay = 1[s]
Repetition_time = 1.82837504[s]
Temp_get = 21.8[dC]

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