Electronic Supplementary Material (ESI) for Organic & Biomolecular Chemistry.

Supporting Information

Sulfonic Nucleic Acids (SNA): A New Class of Substrate Mimic for Ribonuclease A Inhibition

Dhrubajyoti Datta, Swagata Dasgupta* and Tanmaya Pathak*
Department of Chemistry, Indian Institute of Technology Kharagpur, Kharagpur, India, 721302

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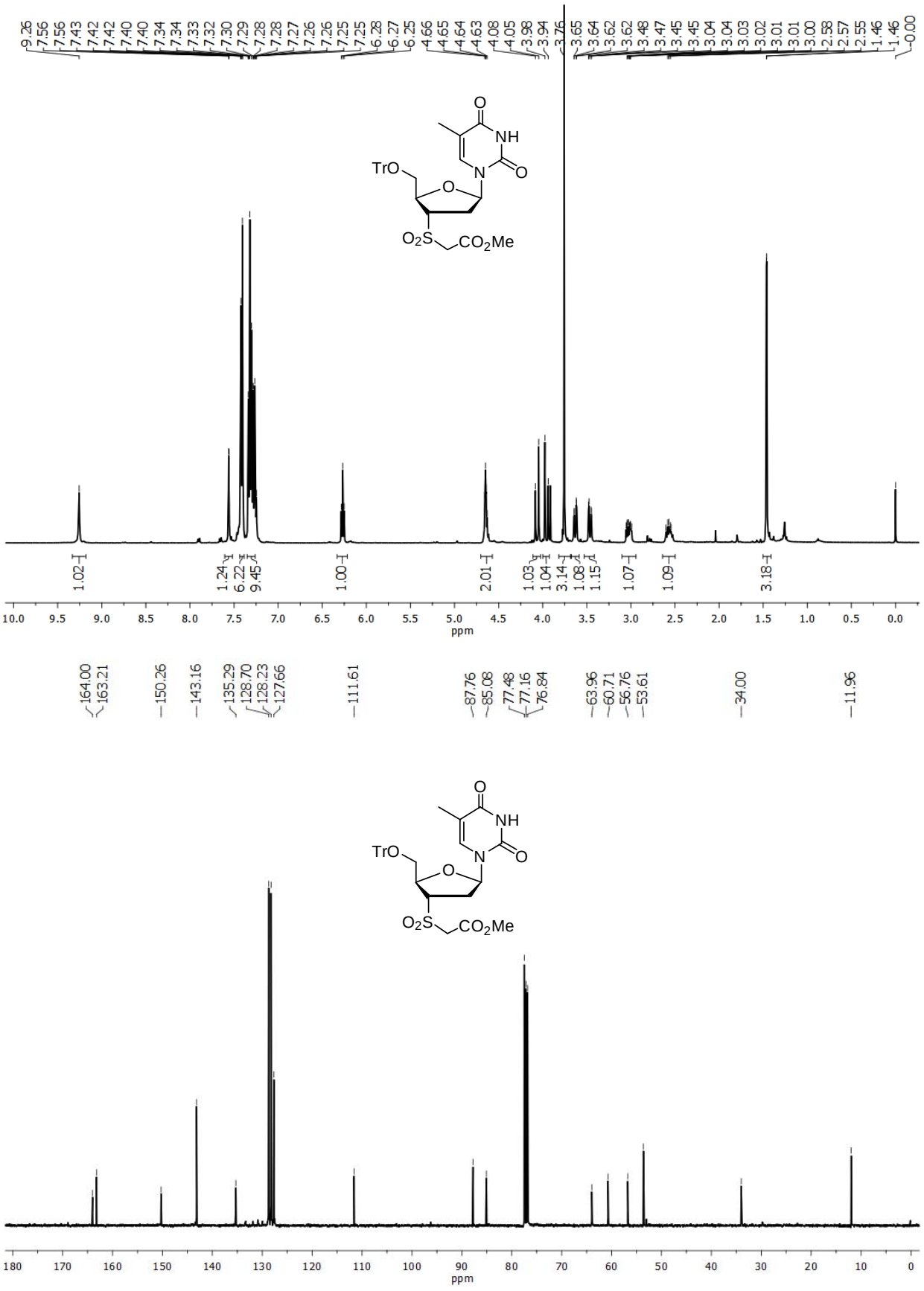


Figure S1: (A) ^{1}H (400 MHz) and (B) ^{13}C NMR (100 MHz) of **1**

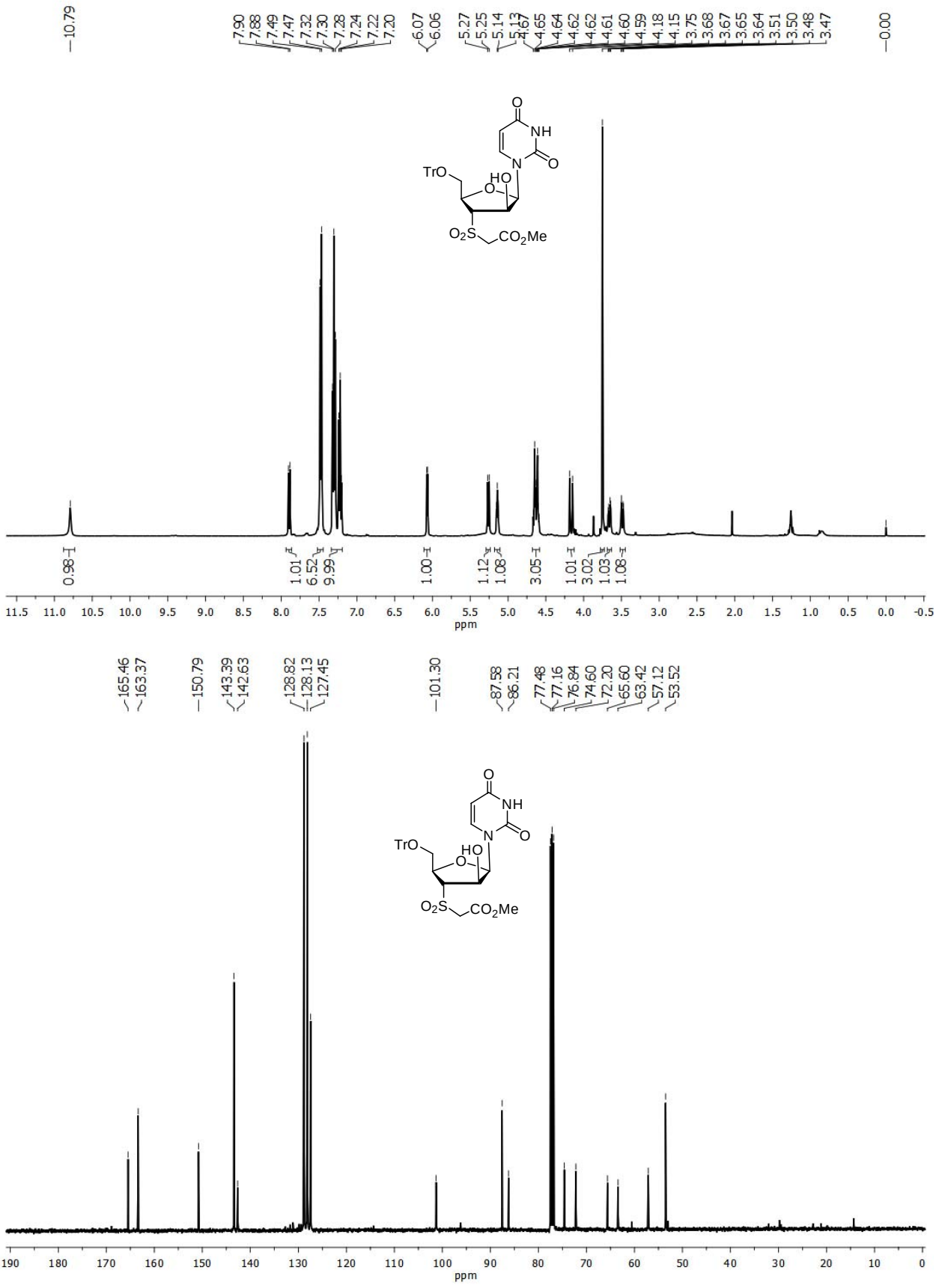


Figure S2: (A) ^{1}H (400 MHz) and (B) ^{13}C NMR (100 MHz) of **3**

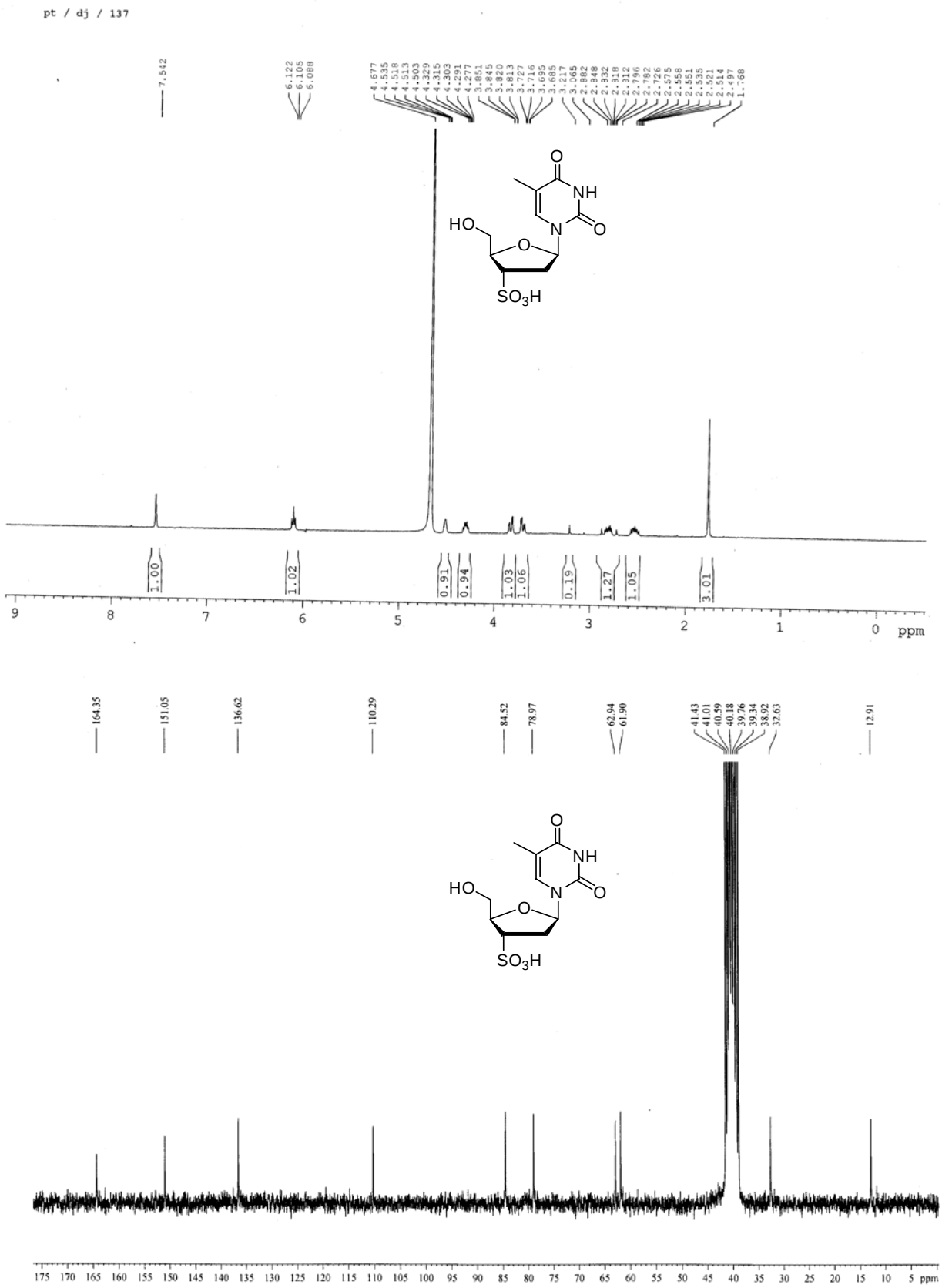
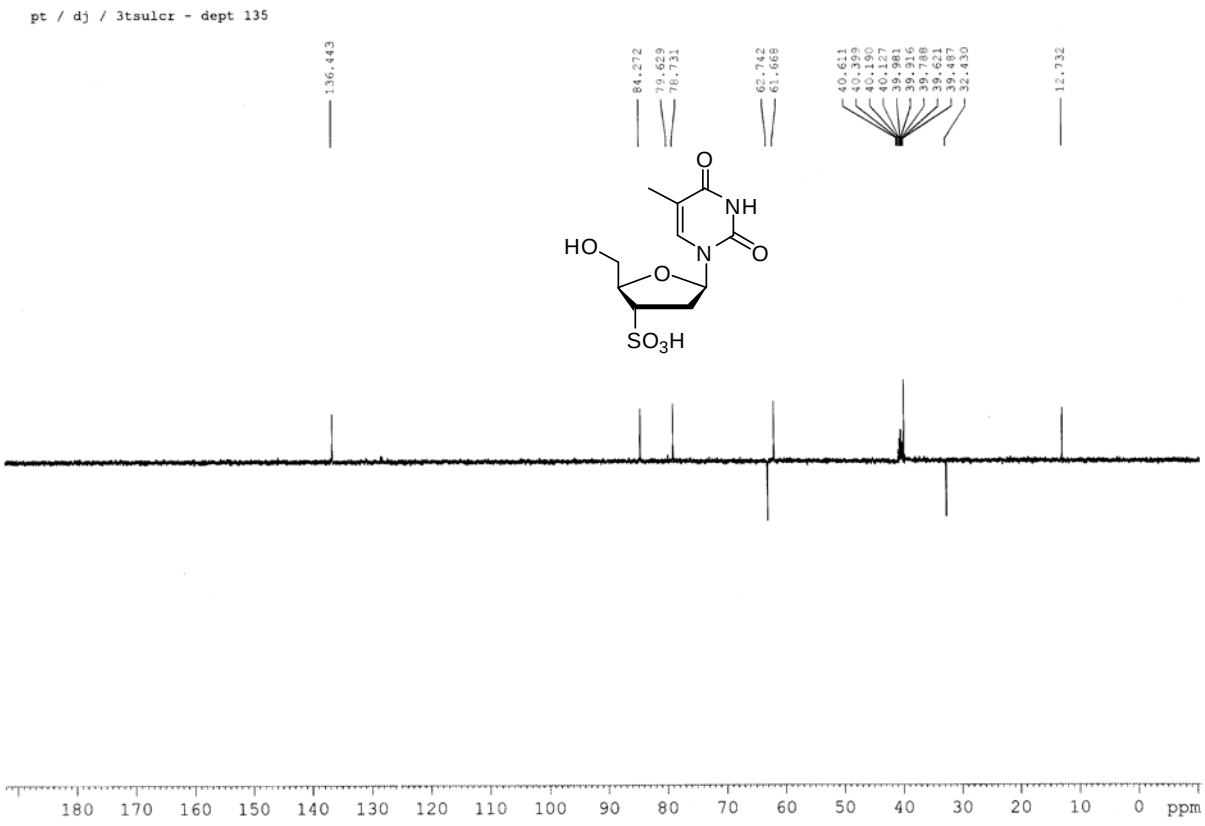


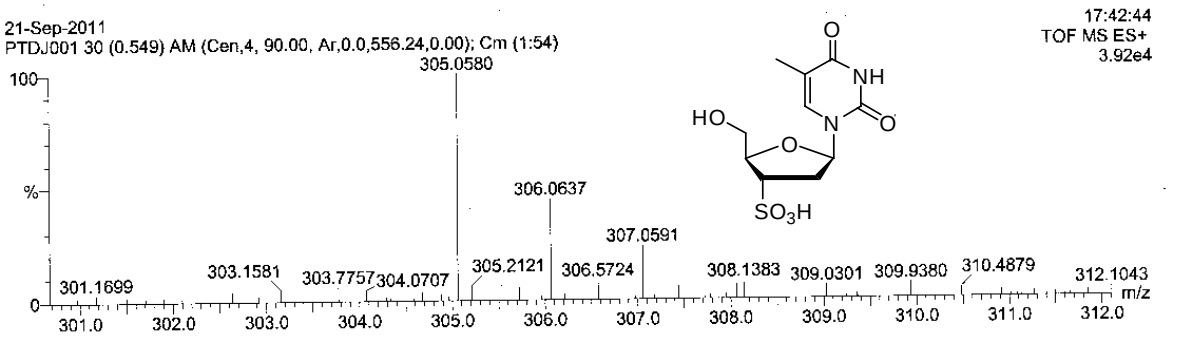
Figure S3: (A) ^{1}H (400 MHz) and (B) ^{13}C NMR (100 MHz) of **2**



Elemental Composition Report **Page 1**

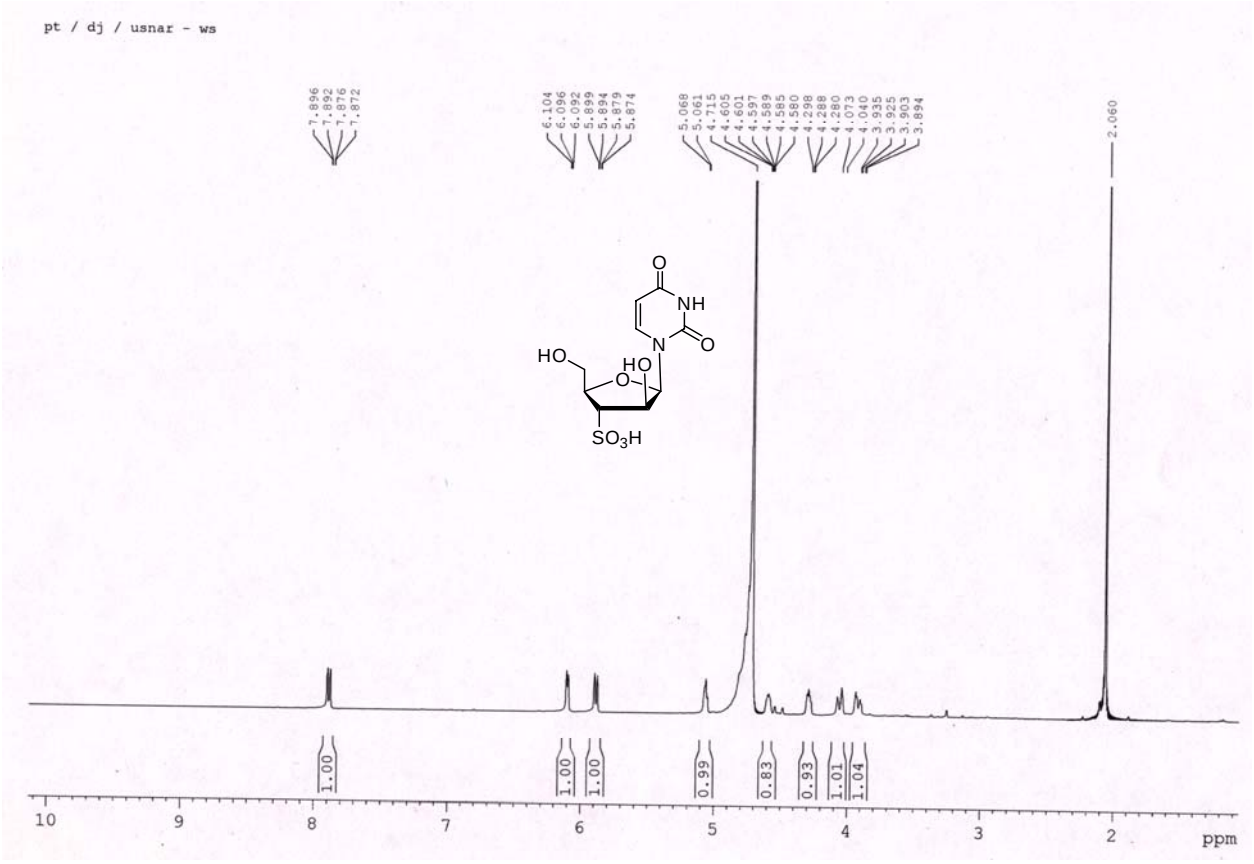
Single Mass Analysis (displaying only valid results)
Tolerance = 20.0 PPM / DBE: min = -1.5, max = 50.0
Isotope cluster parameters: Separation = 1.0 Abundance = 1.0%

Monoisotopic Mass, Odd and Even Electron Ions
139 formula(e) evaluated with 3 results within limits (up to 50 closest results for each mass)



Minimum:				-1.5		
Maximum:		200.0	20.0	50.0		
Mass	Calc. Mass	mDa	PPM	DBE	Score	Formula
307.0591	307.0600	-0.9	-2.9	4.5	1	C10 H15 N2 O7 S ✓ [M+H]+
	307.0539	5.2	16.8	5.0	2	C10 H13 N O10
	307.0652	-6.1	-19.8	5.0	3	C9 H13 N3 O9

Figure S4: (A) DEPT 135 (100 MHz) and (B) Elemental composition of **2**



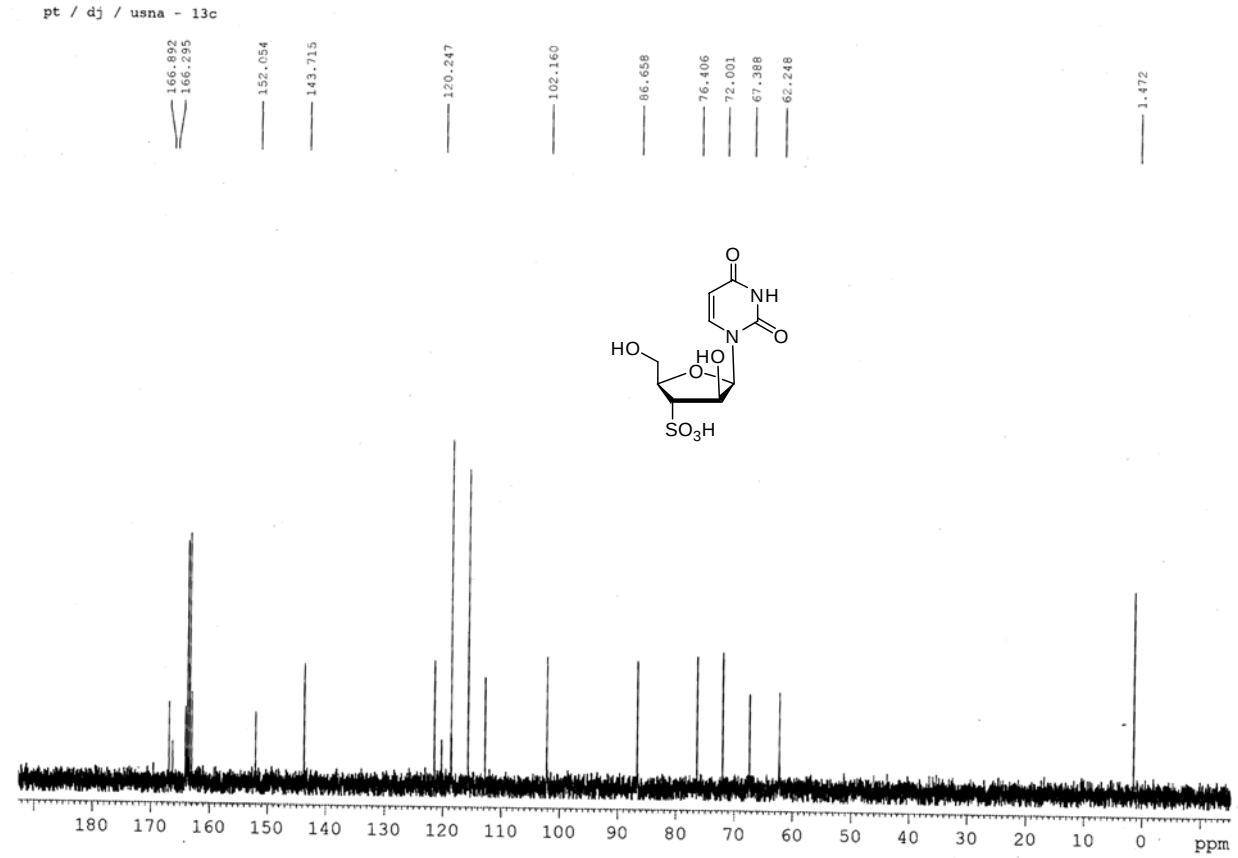


Figure S5: (A) ^{1}H (400 MHz) and (B) ^{13}C NMR (100 MHz) of **4**

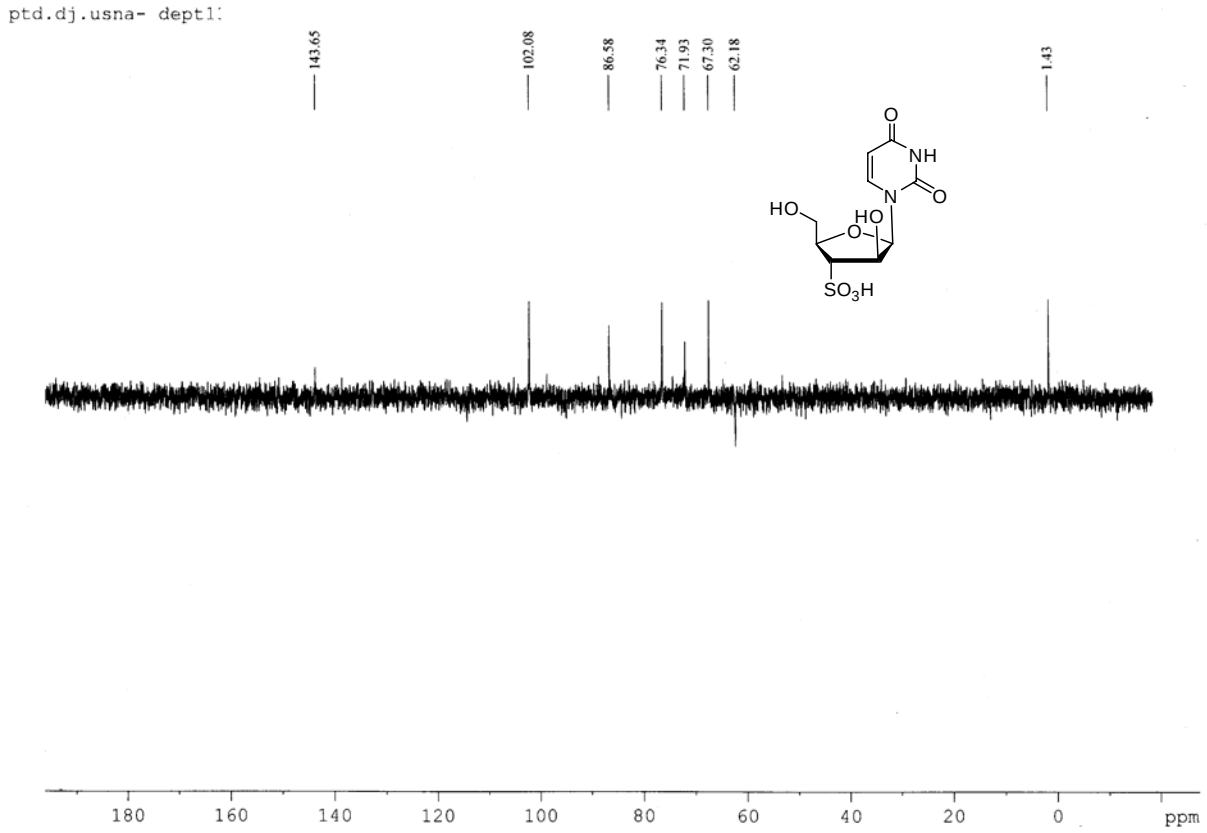


Figure S6: DEPT 135 (50 MHz) of **4**.

Biophysical assays:

Lineweaver-Burk plots:

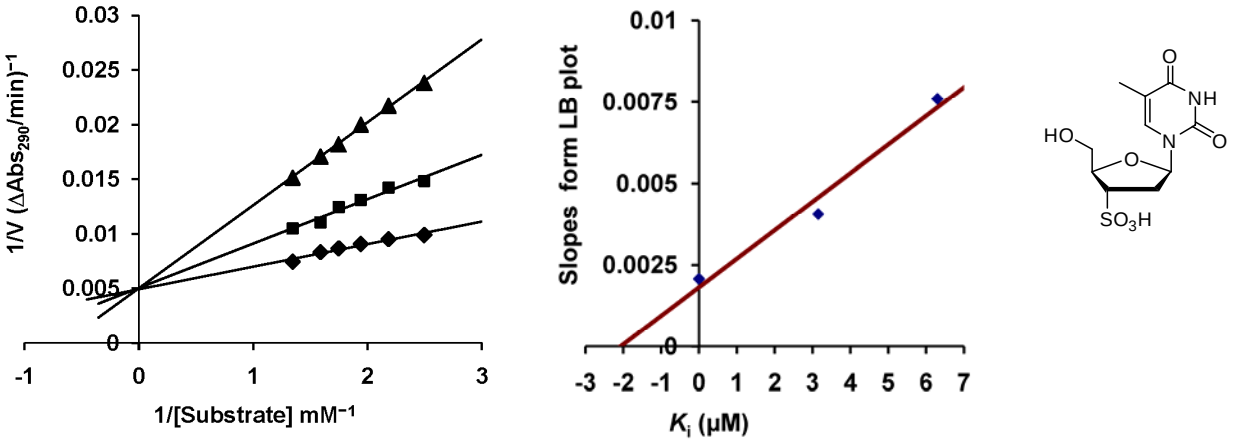


Figure S7: Lineweaver-Burk plot for inhibition of RNase A by inhibitor **2** of 6.30 (▲), 3.15 (■), 0.0 (♦) μM with 2′,3′-cCMP as substrate (0.74-0.40 μM) and RNase A concentration of 10.0 μM.

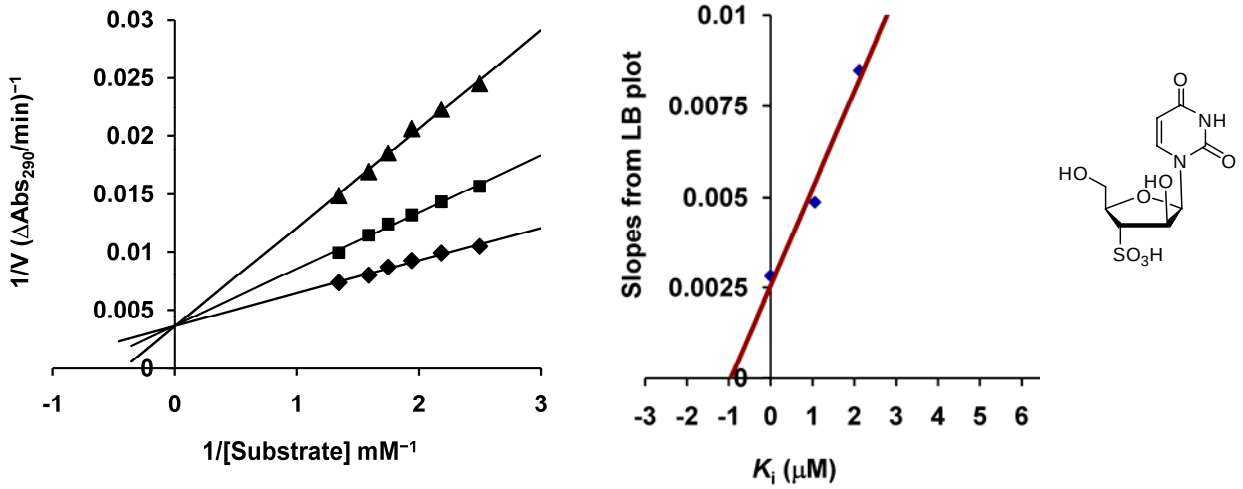


Figure S8: Lineweaver-Burk plot for inhibition of RNase A by inhibitor **4** of 2.16 (▲), 1.06 (■), 0.0 (♦) μM with 2′,3′-cCMP as substrate (0.74-0.40 μM) and RNase A concentration of 10.0 μM.

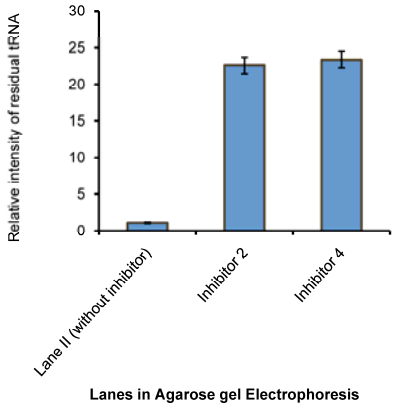


Figure S9: Relative intensity of residual tRNA in Agarose Gel electrophoresis for inhibitor **2** and **4** considering Lane IV.

Docking Studies:

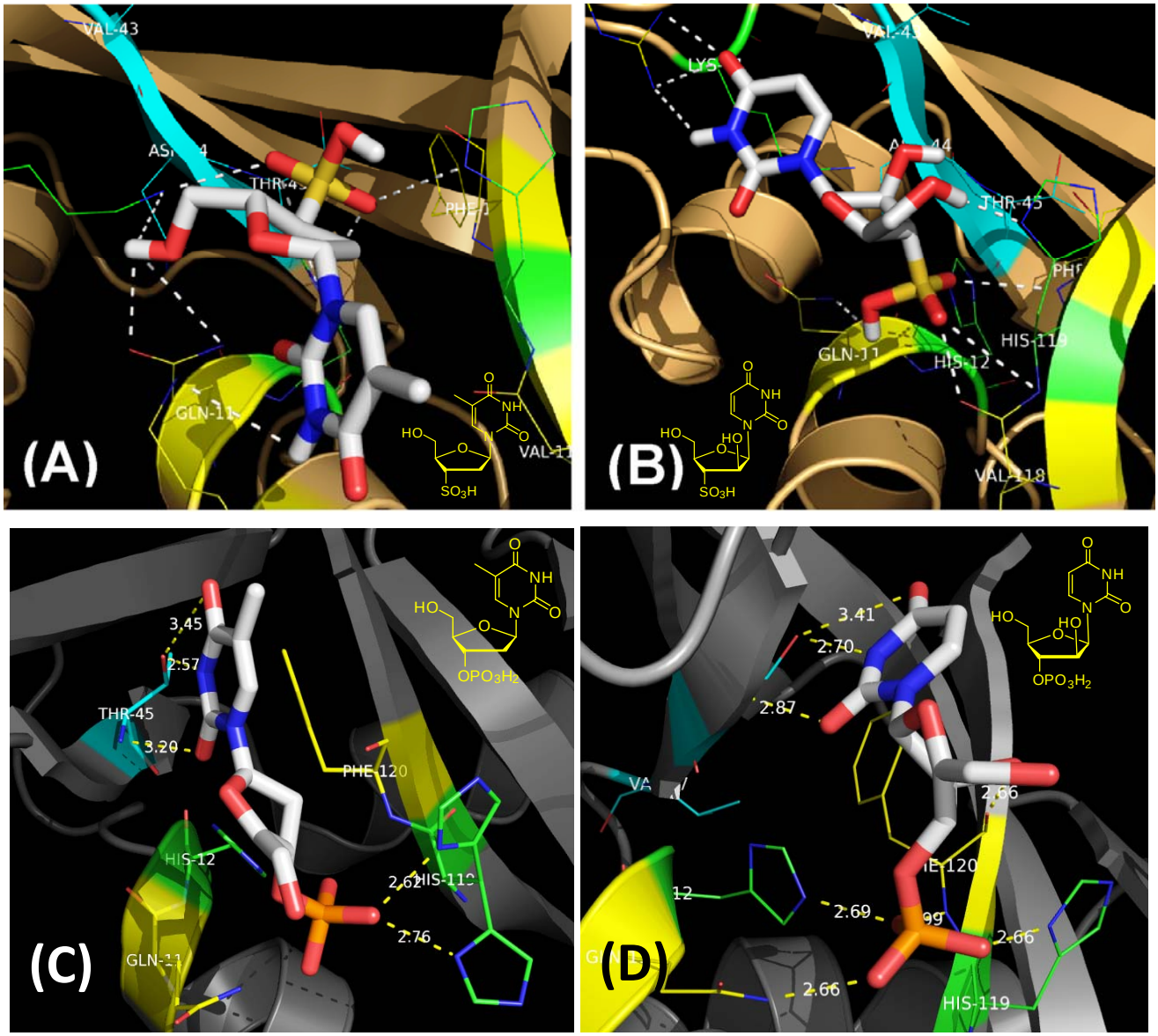
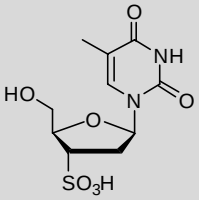
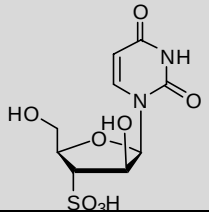
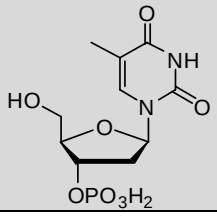
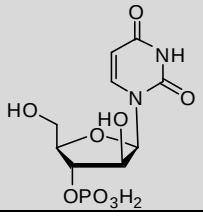


Figure S10: Docked poses of compound (A) **2**, (B) **4**, (C) inhibitor **B** and (D) inhibitor **L** with RNase A (1FS3) where cyan, green and yellow colored amino-acid residues are of B_1, P_1 and other subsites respectively.

Table S1: Hydrogen bonding distance (Å) of compound **2** and **4** with amino acid residues of RNase A (1FS3)

RNase A (PDB ID: **1FS3**) Amino acid residues				
Lys7 Nζ	3.11 [NH] of Thymine N3			
Glu11 Nε2	3.35 [5′-OH]	2.45 [OH] of SO_3H group		2.66 [O1] of OPO_3H_2 group
Glu11 Oε1	2.61 [5′-OH]			
Arg39 NH1		2.53 [O] of Thymine C4		
Arg39 NH2		2.97 [NH] of Thymine N3 2.85 [O] of Thymine C4		
His12 Nε2	3.15 [O] of SO_3H group 3.89 [O] of SO_3H group	2.70 [O] of SO_3H group		2.69 [O3] of OPO_3H_2 group
His119 Nδ1	3.48 [O] of SO_3H group	1.89 [5′-OH]	2.62 [O1] of OPO_3H_2 group **His119 Nδ1 A** form 2.76 [O1] of OPO_3H_2 group **His119 Nδ1 B** form	2.66 [O2] of OPO_3H_2 group
Lys41 Nζ	3.16 [O] of SO_3H group 3.26 [5′-OH]			
Val118 amide C=O		2.43 [O] of SO_3H group		
Val118 amide NH		3.44 [O] of SO_3H group		
Phe120 C=O				2.66 [ara-2′-OH]
Phe120 NH		3.18 [O] of SO_3H group		2.99 [O3] of OPO_3H_2 group
Thr45 Oγ1			3.45 [O] of Thymine C4 2.57 [N] of Thymine N3	3.41 [O] of Thymine C4 2.70 [N] of Thymine N3
Thr45 NH			3.20 [O] of Thymine C2	2.87 [O] of Thymine C2