Supplementary Material (ESI) for Chemical Communications

Communication:

Supporting Information

Novel helical foldamers: Organized heterogeneous backbone folding in 1:1 α/Nucleoside-derived-β-amino acid sequences

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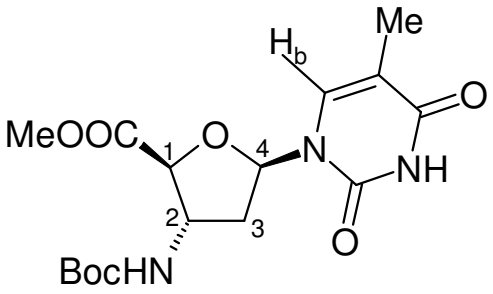
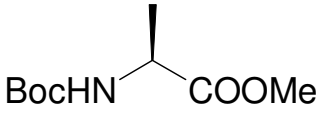
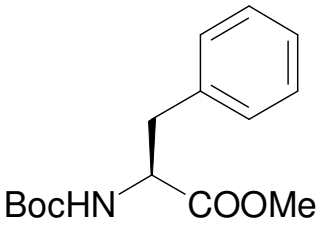
Supporting Figure-01: Monomer units used.



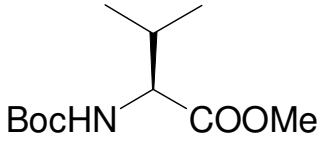
(**NDA**)
Nucleoside **D**erived **A**mino acid



(**Ala**)



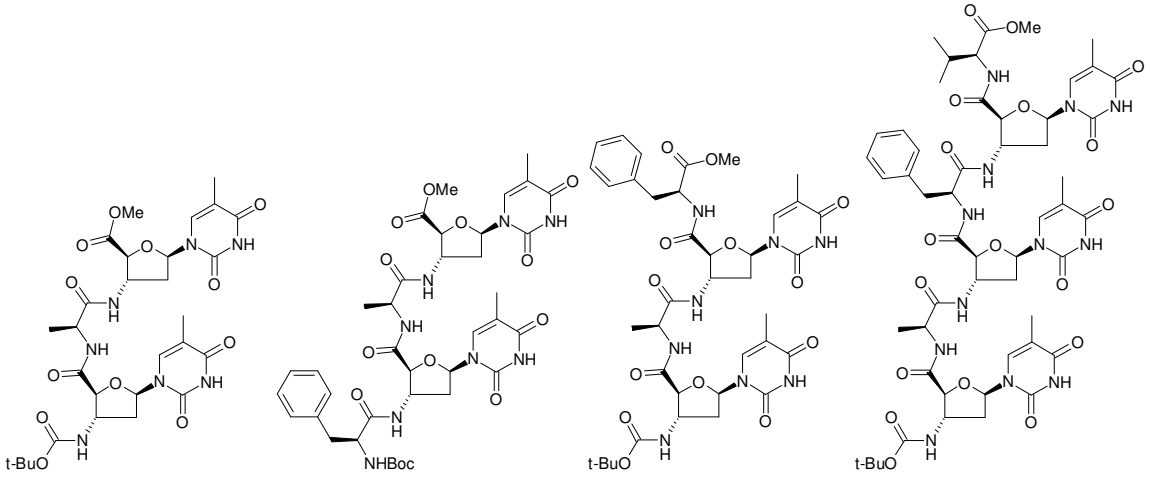
(**Phe**)



(**Val**)

Supporting Figure-02: Oligomers that are characterized.

Boc-NDA-Ala-NDA-OMe; **2**
Boc-Phe-NDA-Ala-NDA-OMe; **3**
Boc-NDA-Ala-NDA-Phe-OMe; **4**
Boc-NDA-Ala-NDA-Phe-NDA-Val-OMe; **5**



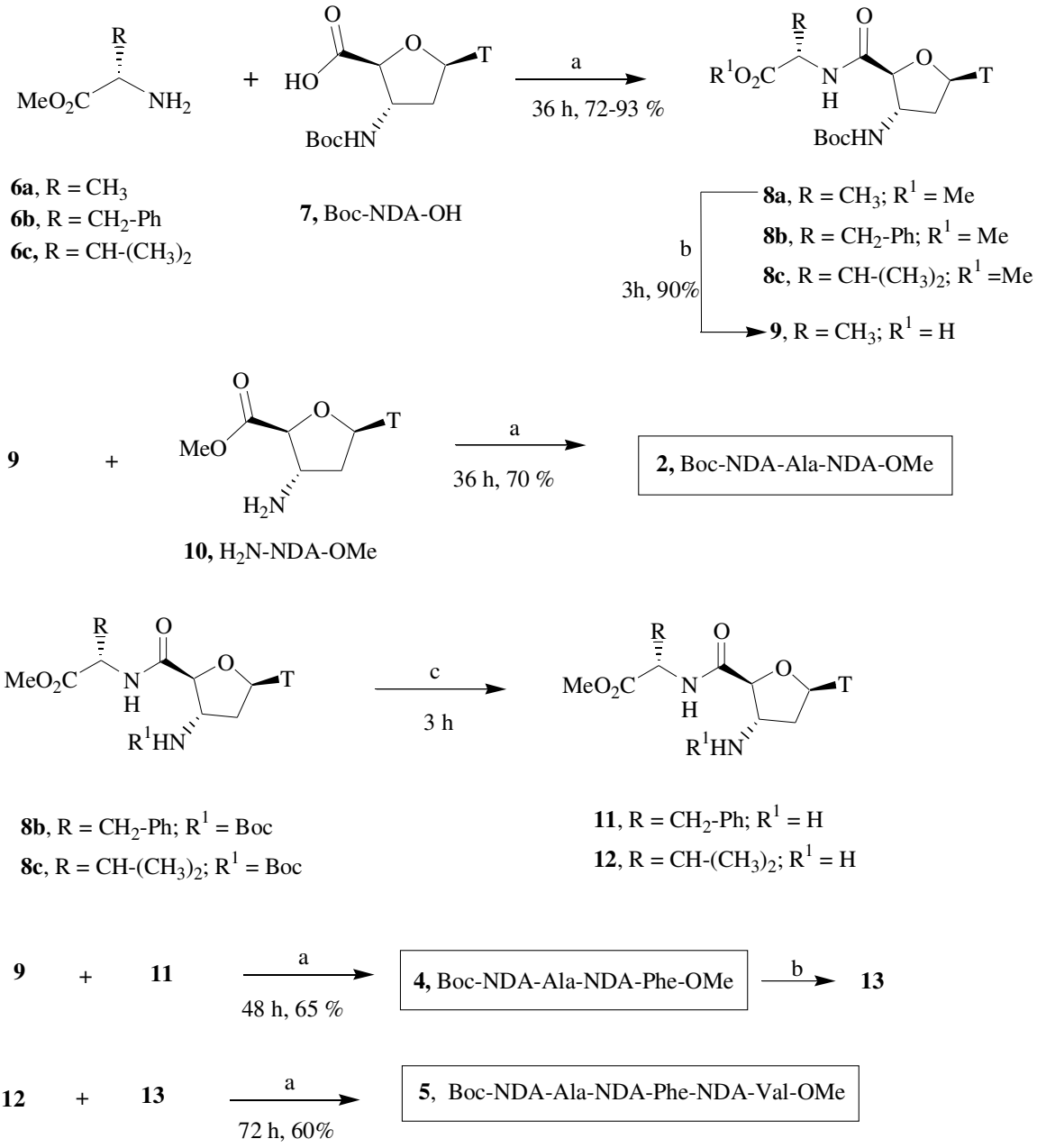
Trimer, **2** Tetramer, **3** Tetramer, **4** Hexamer, **5**

SYNTHESIS

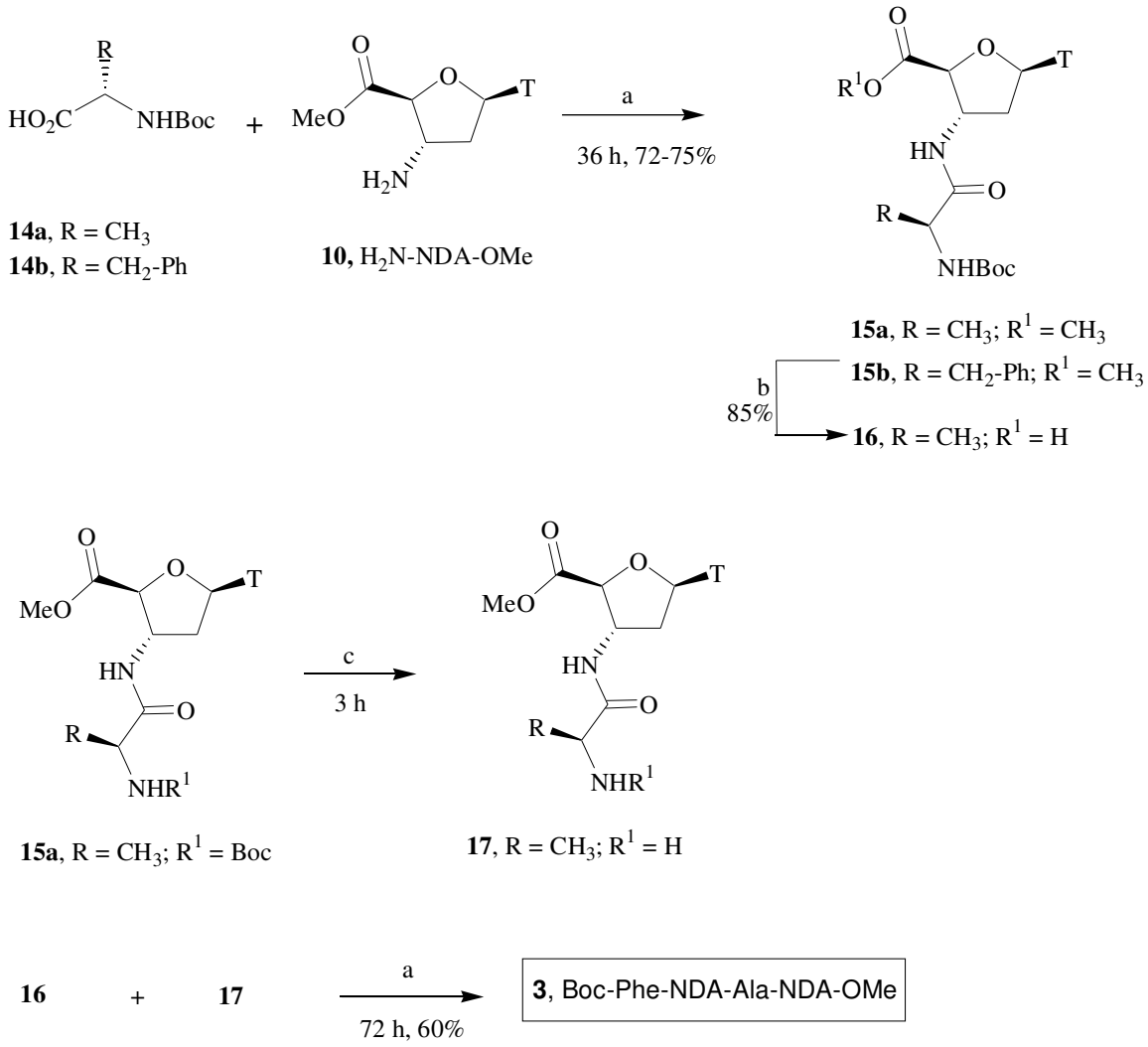
Our synthetic efforts culminated in preparation of four oligomers viz., trimer **2** (Boc-NDA-Ala-NDA-OMe); tetramer **3** (Boc-Phe-NDA-Ala-NDA-OMe); tetramer **4** (Boc-NDA-Ala-NDA-Phe) and hexamer **5** (Boc-NDA-Ala-NDA-Phe-NDA-Val-OMe). Interestingly all the oligomers were synthesized with excellent purity in solution phase which is generally a tough challenge in nucleoside synthesis.

NDA was obtained from the commercially available drug, AZT (for synthesis of NDA, please refer to S. Chandrasekhar, G. P. K. Reddy, M. U. Kiran, Ch. Nagesh and B. Jagadeesh, *Tetrahedron Letters*, 2008, **49**, 2969). AZT was oxidized in CH_3CN/H_2O with BAIB and TEMPO to afford the acid which was immediately esterified to azido methyl ester. This was reduced via hydrogenation to give amino ester monomer (H_2N-NDA-OMe) **10**. The other monomer (Boc-NDA acid) **7** was obtained from **10** in two steps involving protection of the amino group as *tert*-butyl carbamate followed by mild ester hydrolysis using LiOH.

Dimer **8a** was synthesized by straight forward peptidation between NDA acid **7** and L-Alanine methyl ester **6a** using EDCI-HOBt as coupling reagent in 72 % yield. The other dimer **8b** was prepared using similar conditions by reaction between NDA acid **7** and L-Phenylalanine methyl ester **6b** with 90% yield. Dimer **8a** was treated with LiOH in THF/H_2O to afford dimer acid **9** which when coupled with H_2N-NDA-OMe **10** gave trimer **2** (Boc-NDA-Ala-NDA-OMe). The second dimer **8b** was treated with trifluoroacetic acid in CH_2Cl_2 to give **11** with free amino functionality. Finally tetramer **4** was obtained from coupling of **9** and **11** in 65 % yield. The NDA acid **7** was coupled with L-Valine methyl ester **6c** to give another dimer **8c**. Tetramer **4** was treated with LiOH to give tetramer acid **13** which was coupled with **12** using EDCI and HOBt protocol to get hexamer **5**. The required amine functionality in **12** was obtained from **8c** by treatment with TFA (Supporting scheme 1). Similarly, tetramer **3** was synthesized using the similar reaction conditions (Supporting scheme 2).



Supporting scheme 1: Reagents and conditions: (a) EDCI, HOBt, DIPEA, DMF, rt; (b) LiOH, THF/H_2O, 0°C, 3 h; (c) TFA, CH_2Cl_2,0°C, 3h.



Supporting scheme 2: Reagents and conditions: (a) EDCI, HOBt, DIPEA, DMF, rt; (b) LiOH, THF/H_2O, 0°C, 3 h; (c) TFA, CH_2Cl_2, 0°C, 3h.

NMR EXPERIMENTS

The NMR data for all the compounds in the present study were obtained on Bruker Avance-II 600 MHz NMR spectrometer equipped with cryoprobe and by using standard pulse sequences. The pulse widths and power levels are properly calibrated for all the experiments.

The samples were studied at the temperature 300K.

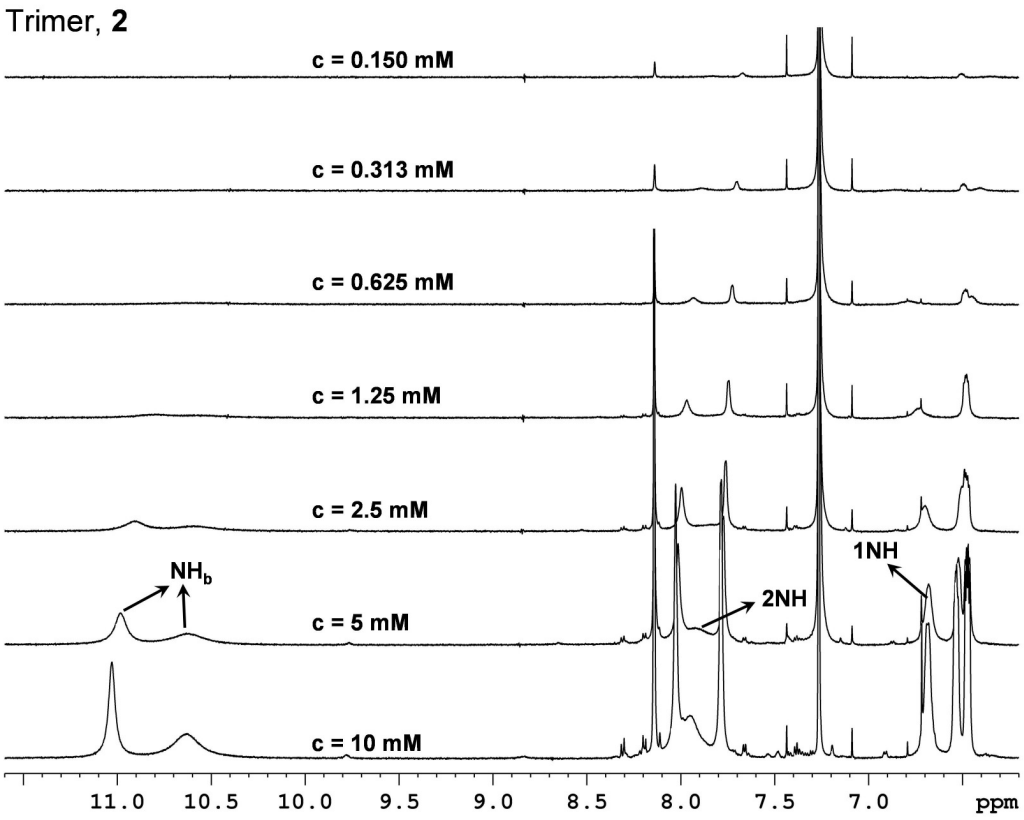
Concentration of the samples: ~5 mM

Solvent medium: $CDCl_3$ for **2** and **3**; mixture of $CDCl_3$+DMSO-d_6 (10 µL for **4** or 90 µL for **5**).

EXPERIMENTAL DATA & STRUCTURAL INFERENCES OF TRIMER 2

Supporting Figure-03: **Concentration Dependency Studies of 2**

Stacked plot of the expanded regions from the ^{1}H-NMR spectra (64 scans) of **2** acquired at different concentrations (ranging from 0.15 mM – 10 mM) in $CDCl_3$ is shown. The backbone NHs are indicated with their corresponding residue number in the oligomer and NHs in thymidine bases are denoted as NH_b.



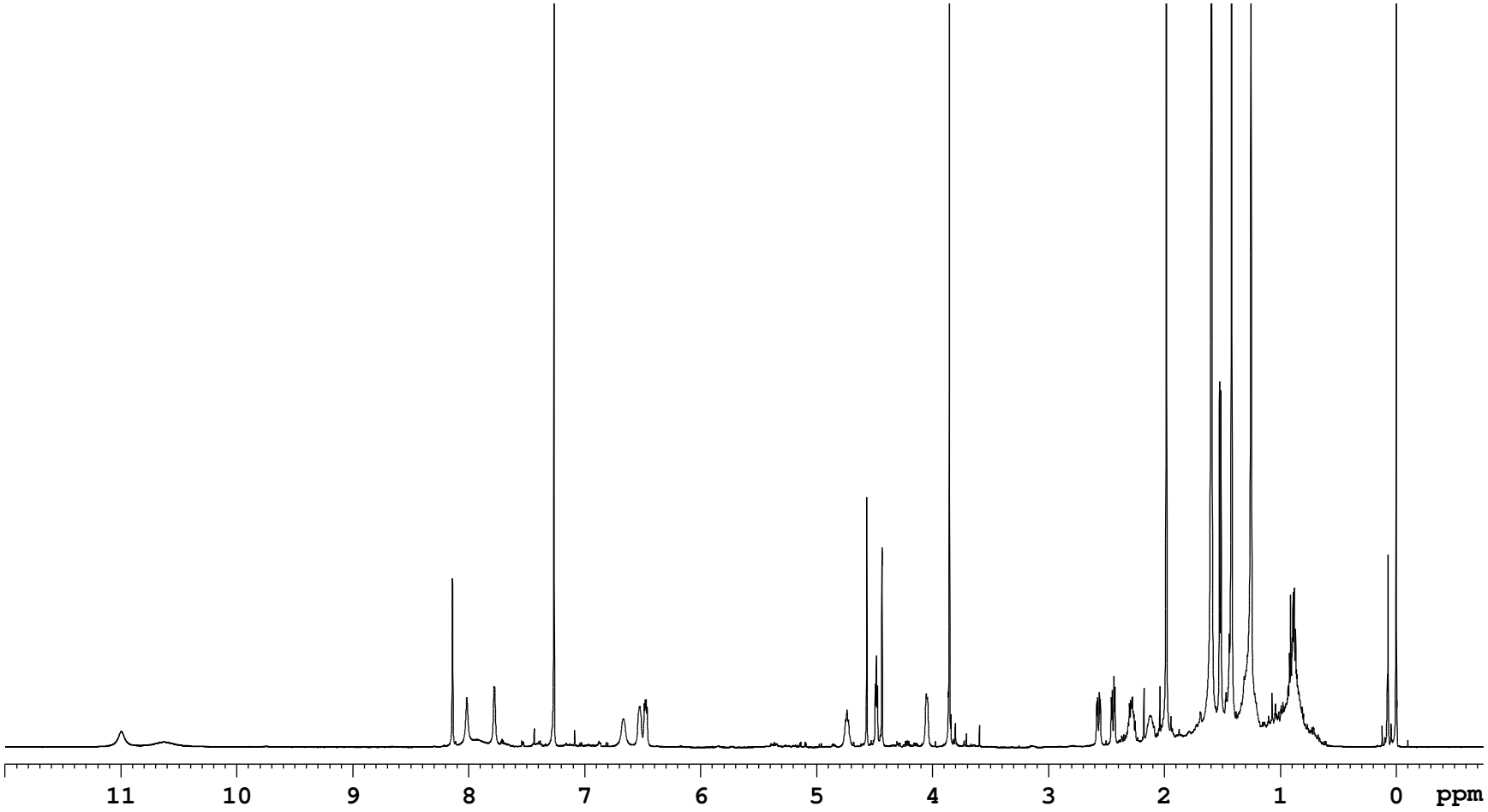
The experimental results show complete independency of the NH chemical shifts of **2** on the variation of sample concentration, which suggest that the compound is not aggregating in the concentration range 0.15 mM – 10 mM. The structural characterization of the trimer **2** is carried out at a concentration of ~5 mM in $CDCl_3$. Similar information has been obtained for other peptides, as shown in the following.

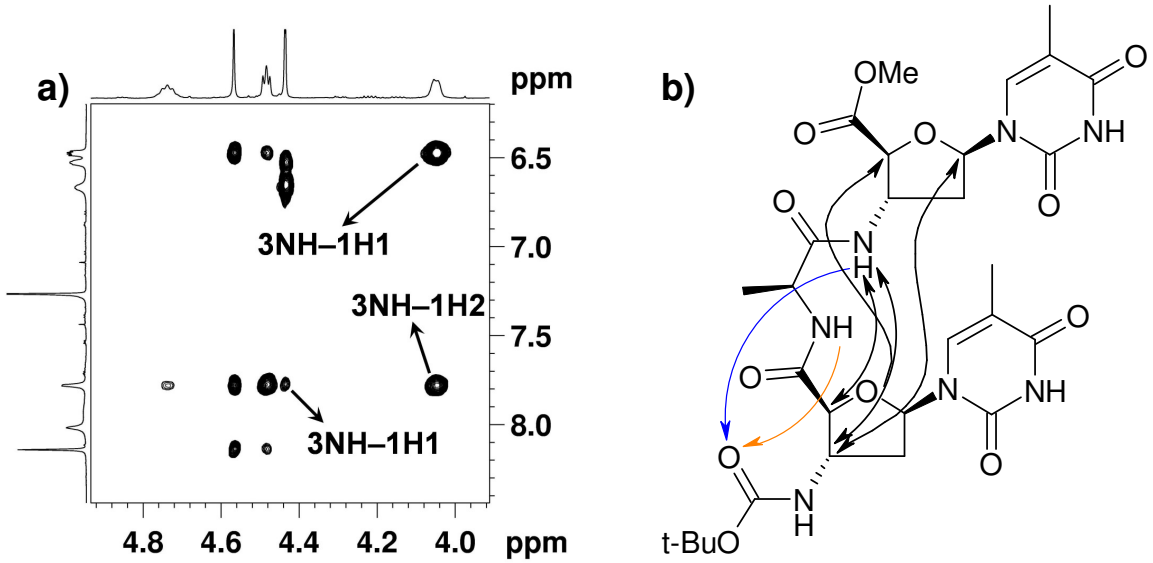
Supporting Table-01: ^{1}H-Chemical shift assignment for trimer **2** in $CDCl_3$ (concentration ~5 mM) at 300 K. (600 MHz)

Residue	NH	C1H (α)	C2H (β)	C3H (γ) (pro-*R*)	C3'H (γ') (pro-*S*)	C4H (δ)	H_b	Me_b	NH_b
1	-- (exchanged with residual water)	4.43 (d) $J_{H1, H2}$=2.0	4.05 (m) $J_{H1, H2}$=2.0	2.57(dd) $J_{H3, H3'}$=13.5 $J_{H3, H4}$=5.3	2.13(m) $J_{H3, H3'}$=13.5 $J_{H3, H4}$ =10.2	6.53 (dd) $J_{H3', H4}$=10.2 $J_{H3, H4}$=5.3	8.01 (s)	1.98 (s)	10.6 (s)
2	6.66 (d) $J_{NH, H1}$=7.0	4.73 (dq) $J_{NH, H1}$=7.0 $J_{H1, H2}$=7.5	1.52 (d) $J_{H1, H2}$=7.5	--	--	--	--	--	--
3	7.78 (d) $J_{NH, H2}$=5.0	4.57 (bs)	4.49 (dd) $J_{NH, H2}$=5.0 $J_{H2, H3'}$=6.9	2.45 (dd) $J_{H3, H3'}$=13.5 $J_{H3, H4}$=5.3	2.28 (ddd) $J_{H3, H3'}$=13.5 $J_{H3, H4'}$=10.2 $J_{H2, H3'}$=6.9	6.49 (dd) $J_{H3', H4}$=10.2 $J_{H3, H4}$=5.3	8.14 (s)	1.98 (s)	11.0 (s)

Multiplicity of the resonances is indicated as: multiplet (m), doublet of doublet (dd), doublet (d), singlet (s), and broad singlet (bs) etc.

Supporting Figure-04: ^{1}H NMR spectrum of **2** in $CDCl_3$ (concentration ~5 mM) at 300 K. (600MHz)

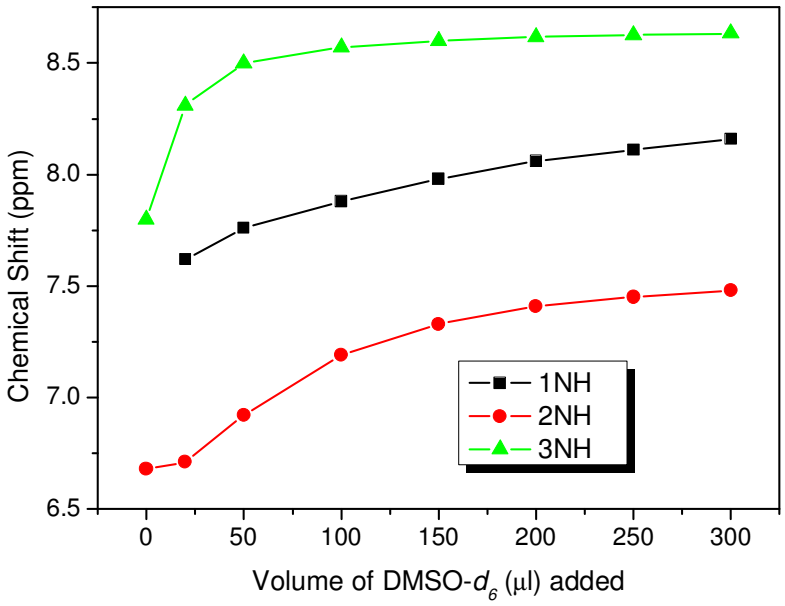




Supporting Figure-05: (a) Expanded region from ROESY spectrum of trimer **2** showing the characteristic ROEs that support a $^{i}NH_{n}$–$^{(i-3)}CO_{\alpha}$ 11-membered hydrogen bonded turn. (b) Schematic representation of characteristic ROEs (solid curves) and hydrogen bonding for **2** (11-mr and 8-mr hydrogen bonds are shown in dotted blue and orange curves, respectively).

Supporting Table-02: DMSO-Titration: NH chemical shifts of trimer **2** observed at different volumes of DMSO-d_6 added to a 500 µL solution of **2** in $CDCl_3$ at 300 K.

Volume of DMSO-d_6 added (µL)	NH chemical shifts in (ppm).		
	1NH	2NH	3NH
0	--	6.68	7.80
20	7.62	6.71	8.31
50	7.76	6.92	8.50
100	7.88	7.19	8.57
150	7.98	7.33	8.60
200	8.06	7.41	8.62
250	8.11	7.45	8.63
300	8.16	7.48	8.63
Δδ over 250 µL DMSO-d_6 addition	--	0.8	0.8

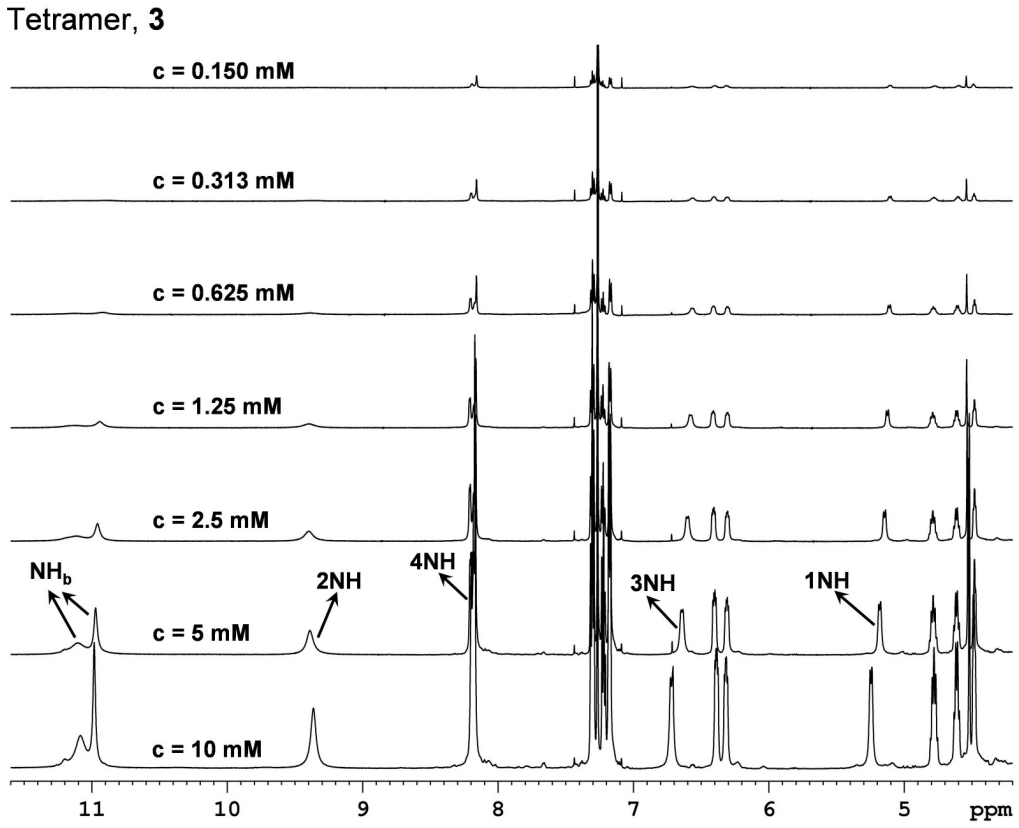


Supporting Figure-06: Variation of NH chemical shifts of **2** with respect to the sequential addition of DMSO-d_6 fractions (in aliquots of 50 µL) at 300 K to an initial 500 µL solution of **2** in $CDCl_3$. The data suggest that the 2NH and 3NH are participating in h-bonding of moderate strength.

EXPERIMENTAL DATA & STRUCTURAL INFERENCES OF TETRAMER 3

Supporting Figure-07: **Concentration Dependency Studies of 3**

Stacked plot of the expanded regions from the ^{1}H-NMR spectra (64 scans) of tetramer **3** acquired at different concentrations (ranging from 0.15 mM – 10 mM) in $CDCl_3$ is shown. The backbone NHs are indicated with their corresponding residue number in the oligomer and NHs in thymidine bases are denoted as NH_b.

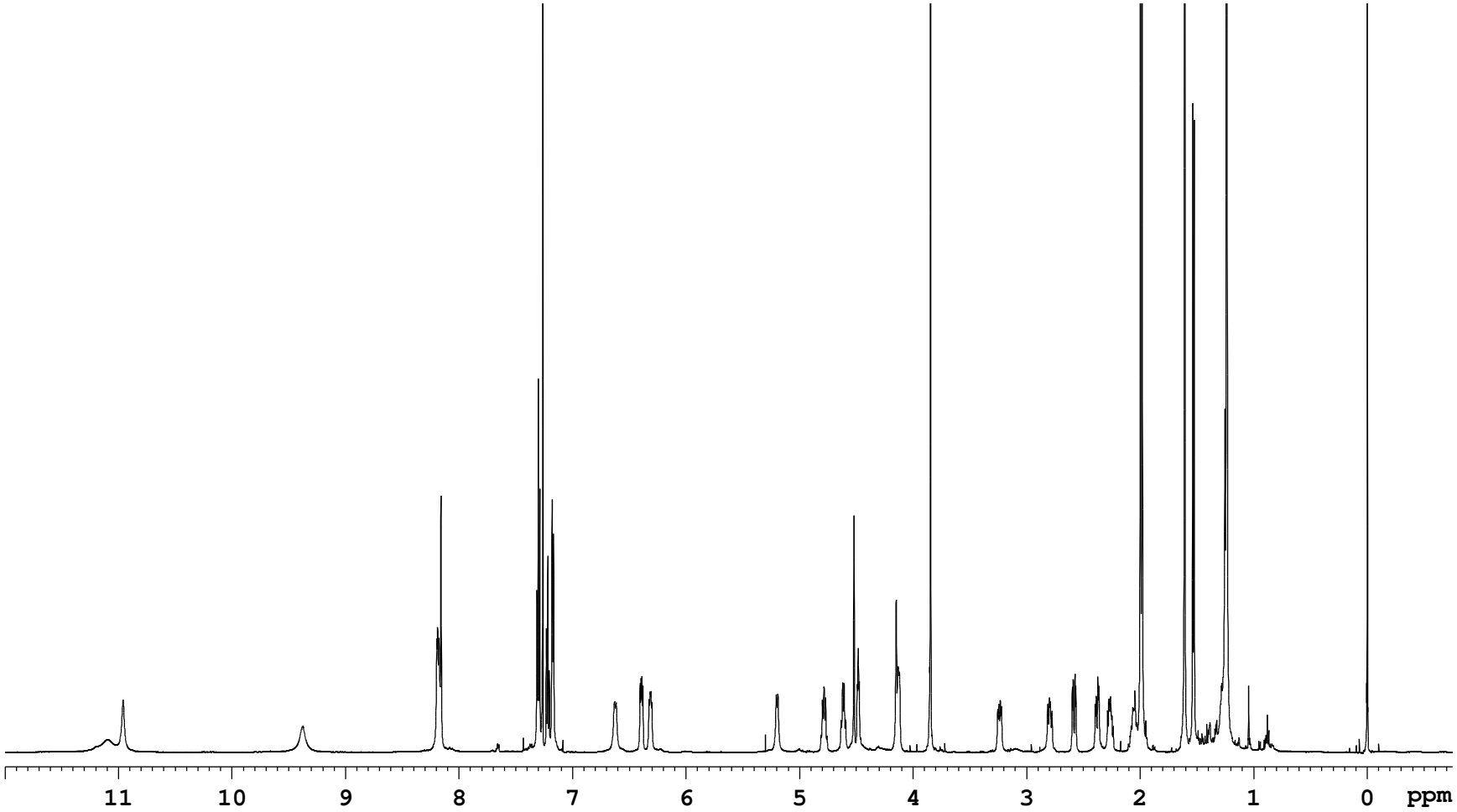


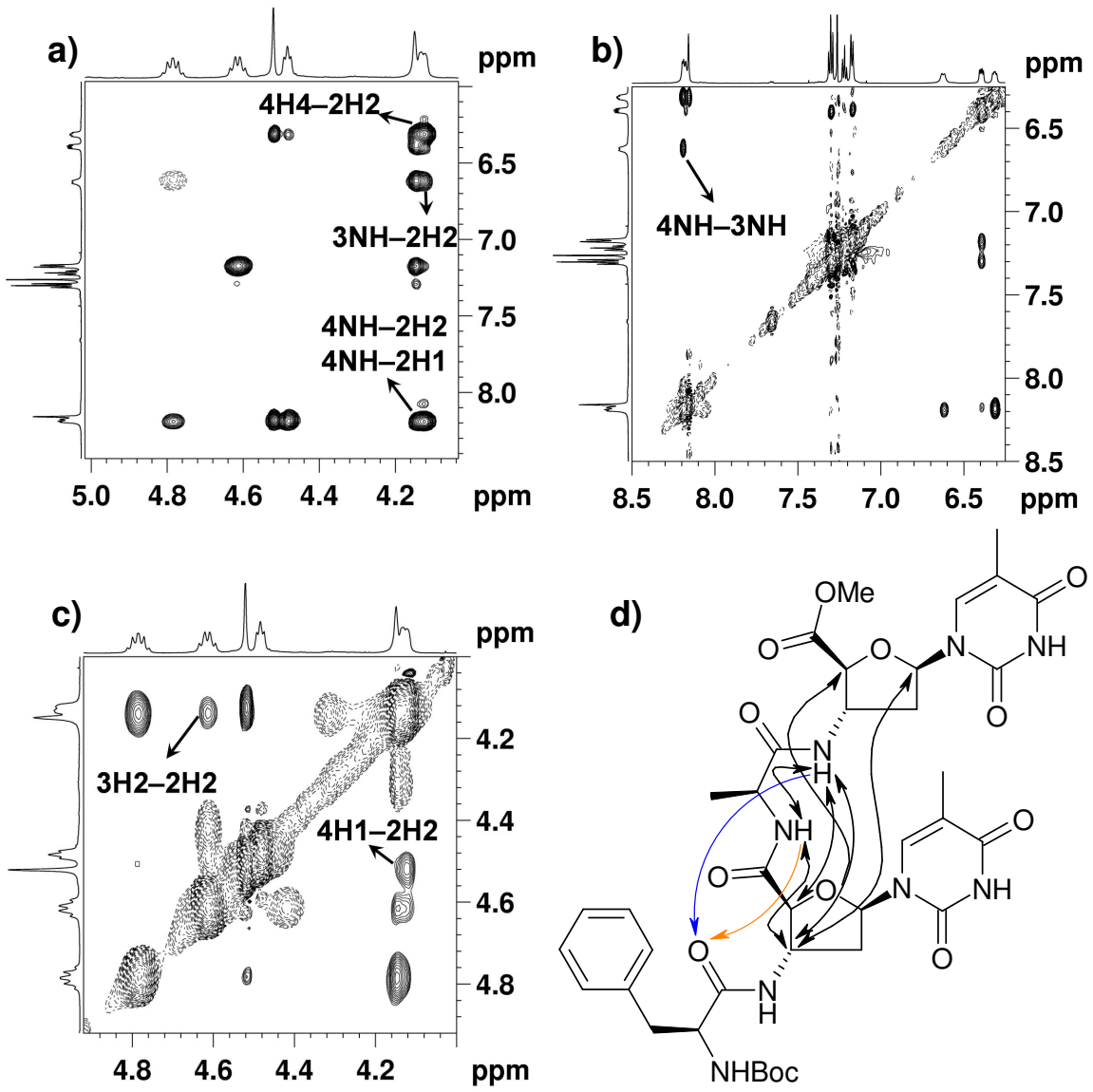
The experimental results show complete independency of the NH chemical shifts of **3** on the variation of concentration, which suggests that the compound is not aggregating in the concentration range 0.15 mM – 10 mM. The structural characterization of the tetramer **3** is carried out at a concentration of ~5 mM in $CDCl_3$.

Supporting Table-03: ^{1}H-Chemical shift assignment for tetramer **3** in $CDCl_3$ (concentration ~5 mM) at 300 K. (600 MHz)

Residue	NH	C1H (α)	C2H (β)	C3H (γ) (pro-*R*)	C3'H (γ') (pro-*S*)	C4H (δ)	H_b	Me_b	NH_b
1	5.20 (d) $J_{NH, H1}$=8.4	4.61 (ddd) $J_{NH, H1}$=8.4 $J_{H1, H2}$=6.4 $J_{H1, H2'}$=8.7	3.24 (dd) $J_{H1, H2}$=6.4 $J_{H2, H2'}$=13.7 2.79 (dd) $J_{H1, H2'}$=8.7 $J_{H2, H2'}$=13.5	--	--	--	--	--	--
2	9.37 (d) (bs)	4.14 $J_{H1, H2}$=2.0	4.12 (m) $J_{H1, H2}$=2.0	2.58 (dd) $J_{H3, H3'}$=13.7 $J_{H3, H4}$=4.8	2.06 (m) $J_{H3, H3'}$=13.7 $J_{H3', H4}$=9.8	6.39 (dd) $J_{H4, H3'}$=9.8 $J_{H4, H3}$=4.8	8.17 (s)	1.99 (s)	10.4 (s)
3	6.62 (d) $J_{NH, H1}$=10.3	4.78 (qd) $J_{NH, H1}$=10.3 $J_{H1, H2}$=7.2	1.53 (d) $J_{H1, H2}$=7.2	--	--	--	--	--	--
4	8.18 (d) $J_{NH,H2}$=5.2	4.52 (bs)	4.48 (dd) $J_{NH, H2}$=5.2 $J_{H2, H3'}$=7.0	2.39 (dd) $J_{H3, H3'}$=13.7 $J_{H3, H4}$=5.2	2.27 (ddd) $J_{H3, H3'}$=13.7 $J_{H3', H4}$=9.7 $J_{H2, H3'}$=7.0	6.31 (dd) $J_{H4, H3'}$=9.7 $J_{H4, H3}$=5.2	8.15 (s)	1.98 (s)	10.4 (s)

Supporting Figure-08: ^{1}H-NMR spectrum of tetramer **3** recorded in $CDCl_3$ (concentration ~5 mM) at 300 K. (600 MHz)

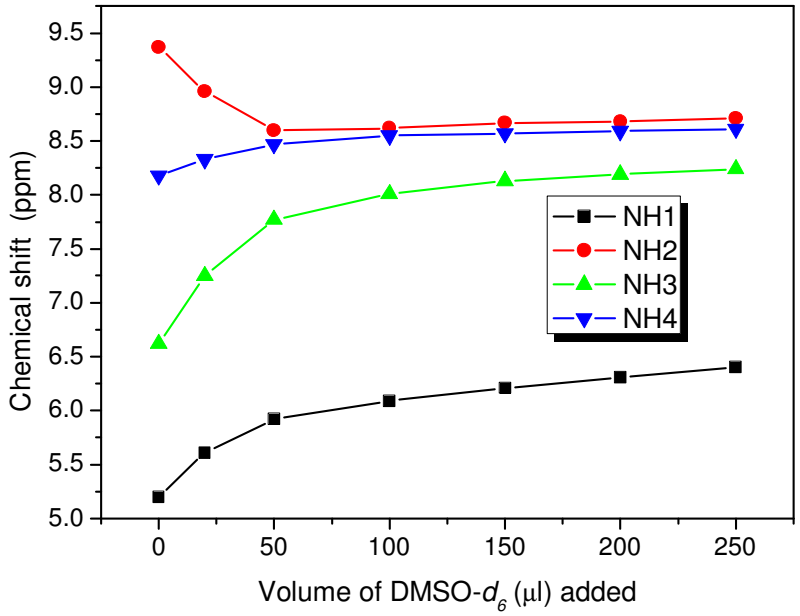




Supporting Figure-09: Expanded regions (a, b and c) of ROESY spectrum of tetramer **3** showing the characteristic ROEs that support 11/8-membered hydrogen bonded turn. (d) Schematic representation of observed ROEs (solid curves) and hydrogen bonding for **3** (11-mr and 8-mr hydrogen bonds are shown in dotted blue and orange curves, respectively).

Supporting Table-04: DMSO-Titration: NH chemical shifts of tetramer **3** observed at different volumes of DMSO-d_6 added to a 500 µL solution of **3** in $CDCl_3$ at 300 K.

Volume of DMSO-d_6 added (µL)	NH chemical shifts in (ppm).			
	1NH	2NH	3NH	4NH
0	5.20	9.37	6.62	8.18
20	5.61	8.96	7.25	8.33
50	5.92	8.60	7.77	8.47
100	6.09	8.62	8.01	8.55
150	6.21	8.67	8.13	8.57
200	6.31	8.68	8.19	8.59
250	6.40	8.71	8.24	8.61
Δδ over 250 µL DMSO-d_6 addition	1.2	–0.7	1.62	0.43



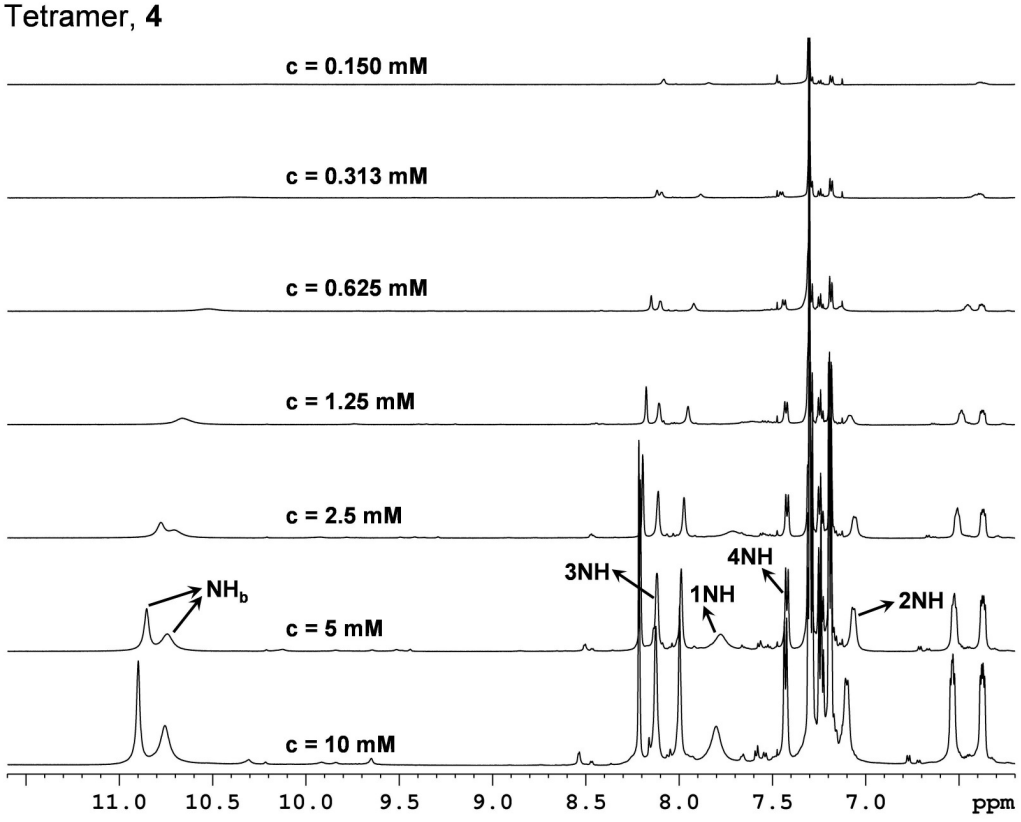
Supporting Figure-10: Variation of NH chemical shifts of **3** with respect to the sequential addition of DMSO-d_6 fractions (in aliquots of 50 µL) at 300 K to an initial 500 µL solution of **3** in $CDCl_3$.

A $\Delta\delta$ shift of 0.43 ppm for 4NH indicates very strong hydrogen bonding for it. The $\Delta\delta$ of 1.62 ppm for 3NH is against its participation in h-bonding. However, the presence of 3NH–4NH and 3NH–2H2 ROEs (Supporting Figure-09) from 3NH support its non-exchangeable behaviour unlike 2NH and further indicate the possibility of an 8mr h-bonded turn involving 3NH. Such contradictions can be expected when the conformation of the molecule is affected during the coarse of titration. In support of this, analysis of the data obtained for **3** in pure DMSO and in the presence of large % of DMSO have not shown any long range ROEs, which can be a result of conformation alteration into an extended fold.

EXPERIMENTAL DATA & STRUCTURAL INFERENCES OF TETRAMER 4

Supporting Figure-11: **Concentration Dependency Studies of 4**

Stacked plot of the expanded regions from the ^{1}H-NMR spectra (64 scans) of tetramer **4** acquired at different concentrations (ranging from 0.15 mM – 10 mM) in (500 µl $CDCl_3$ + 10 µL DMSO-d_6) is shown. The backbone NHs are indicated with their corresponding residue number in the oligomer and NHs in thymidine bases are denoted as NH_b.

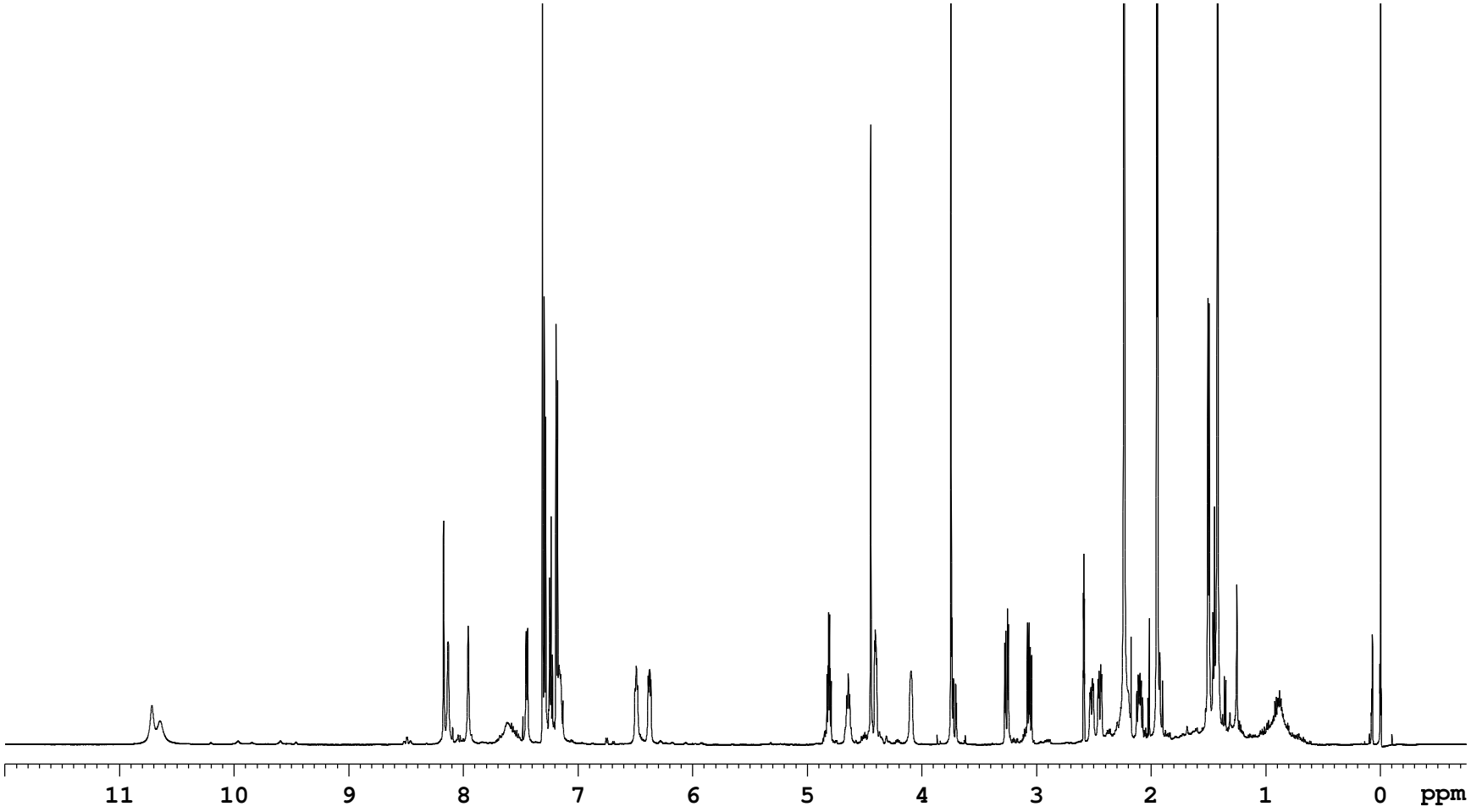


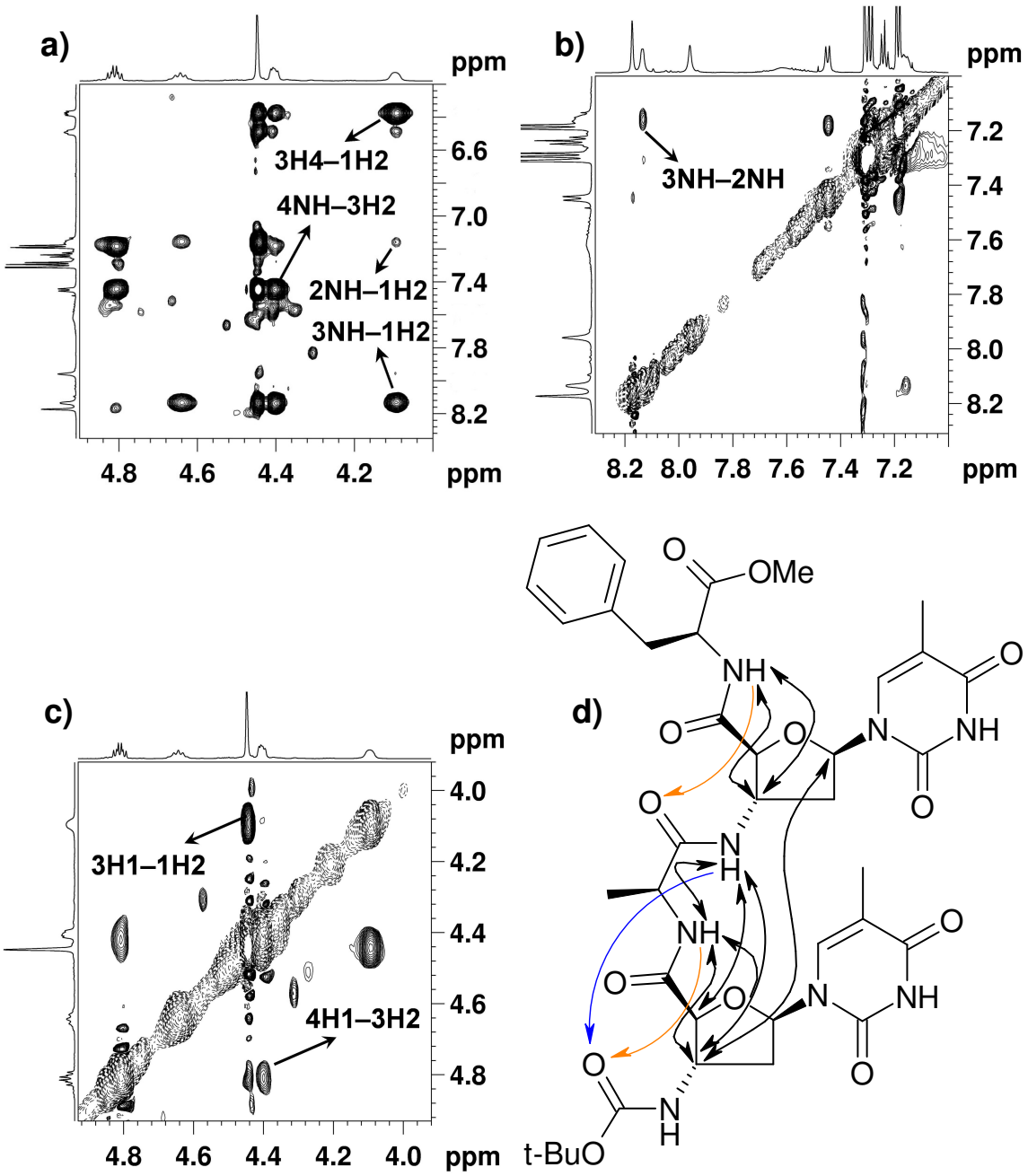
The experimental results show complete independency of the NH chemical shifts of **4** on the variation of concentration, which suggests that the compound is not aggregating in the concentration range 0.15 mM – 10 mM. The structural characterization of the tetramer **4** is carried out at a concentration of ~5 mM in (500 µl $CDCl_3$ + 10 µL DMSO-d_6).

Supporting Table-05: Chemical shift assignment for **4** in (500 µl $CDCl_3$ + 10µL DMSO-d_6) (concentration ~5 mM) at 300 K. (600 MHz)

Residue	NH	C1H (α)	C2H (β)	C3H (γ) (pro-*R*)	C3' (Hγ') (pro-*S*)	C4H (δ)	H_b	Me_b	NH_b
1	7.62 (d) $J_{NH, H2}$=7.0	4.44 (d) $J_{H1, H2}$=5.0	4.09 (m) $J_{NH, H2}$=7.0 $J_{H1, H2}$=5.0	2.52 (dd) $J_{H3, H3'}$=13.7 $J_{H3, H4}$=6.0	2.19 (m) $J_{H3, H3'}$=13.7 $J_{H3', H4}$=8.7	6.50 (dd) $J_{H4, H3'}$=8.7 $J_{H4, H3}$=6.0	7.95 (s)	1.95 (s)	10.4 (s)
2	7.15 (d) $J_{NH, H1}$=8.1	4.64 (qd) $J_{NH, H1}$=8.1 $J_{H1, H2}$=5.1	1.50 (d) $J_{H1, H2}$=5.1	--	--	--	--	--	--
3	8.13 (d) $J_{NH, H2}$=3.9	4.44 (bs)	4.40 (dd) $J_{NH, H2}$=3.9 $J_{H2, H3'}$=7.0	2.45 (dd) $J_{H3, H3'}$=13.7 $J_{H3, H4}$=5.1	2.10 (ddd) $J_{H3, H3'}$=13.7 $J_{H3', H4}$=9.7 $J_{H2, H3'}$=7.0	6.38 (dd) $J_{H4, H3'}$=9.7 $J_{H4, H3}$=5.1	8.17 (s)	1.94 (s)	10.4 (s)
4	7.44 (d) $J_{NH, H1}$=8.2	4.81 (ddd) $J_{NH, H1}$=8.2 $J_{H1, H2'}$=8.0 $J_{H1, H2}$=5.1	3.26 (dd) $J_{H1, H2}$=5.1 $J_{H2, H2'}$=14.0 3.07 (dd) $J_{H1, H2'}$=8.0 $J_{H2, H2'}$=14.0	--	--	--	--	--	--

Supporting Figure-12: (a) ^{1}H-NMR spectrum of tetramer **4** recorded in (500 µl $CDCl_3$ + 10 µL DMSO-d_6) (concentration ~5 mM) at 300 K.

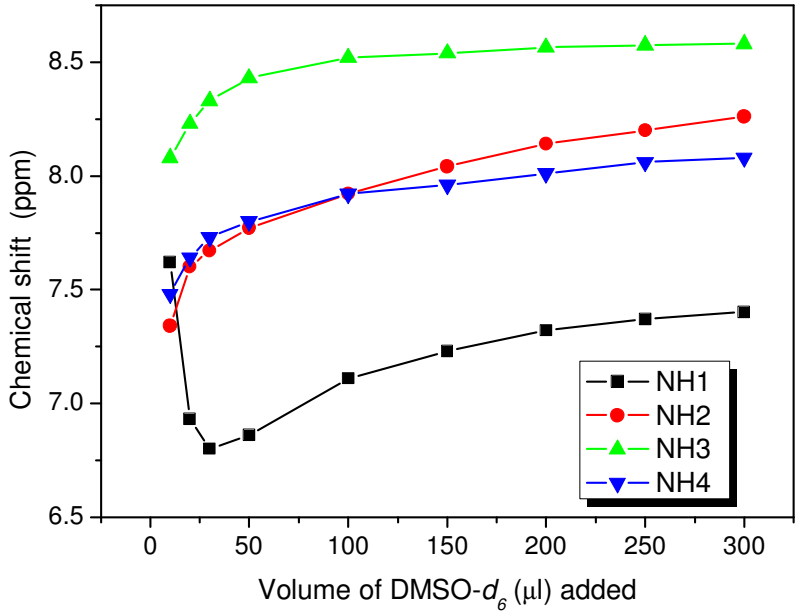




Supporting Figure-13: Expanded regions (a to c) of ROESY spectrum of **4** showing the characteristic ROEs that support 11/8-membered hydrogen bonded helix. (d) Schematic representation of all the observed ROEs (solid curves) and hydrogen bonding for **4** (11-mr and 8-mr hydrogen bonds are shown in dotted blue and orange curves, respectively).

Supporting Table-06: DMSO-Titration: NH chemical shifts of tetramer **4** observed at different volumes of DMSO-d_6 added to a 500 µL solution of **4** in $CDCl_3$ at 300 K.

Volume of DMSO-d_6 added (µL)	NH chemical shifts in (ppm).			
	1NH	2NH	3NH	4NH
0	--	7.34	8.08	7.48
20	6.93	7.60	8.23	7.64
50	6.80	7.67	8.33	7.73
100	6.86	7.77	8.43	7.80
150	7.11	7.92	8.52	7.92
200	7.23	8.04	8.54	7.96
250	7.32	8.14	8.56	8.01
300	7.37	8.20	8.58	8.06
Δδ over 250 µL DMSO-d_6 addition	--	0.92	0.50	0.60



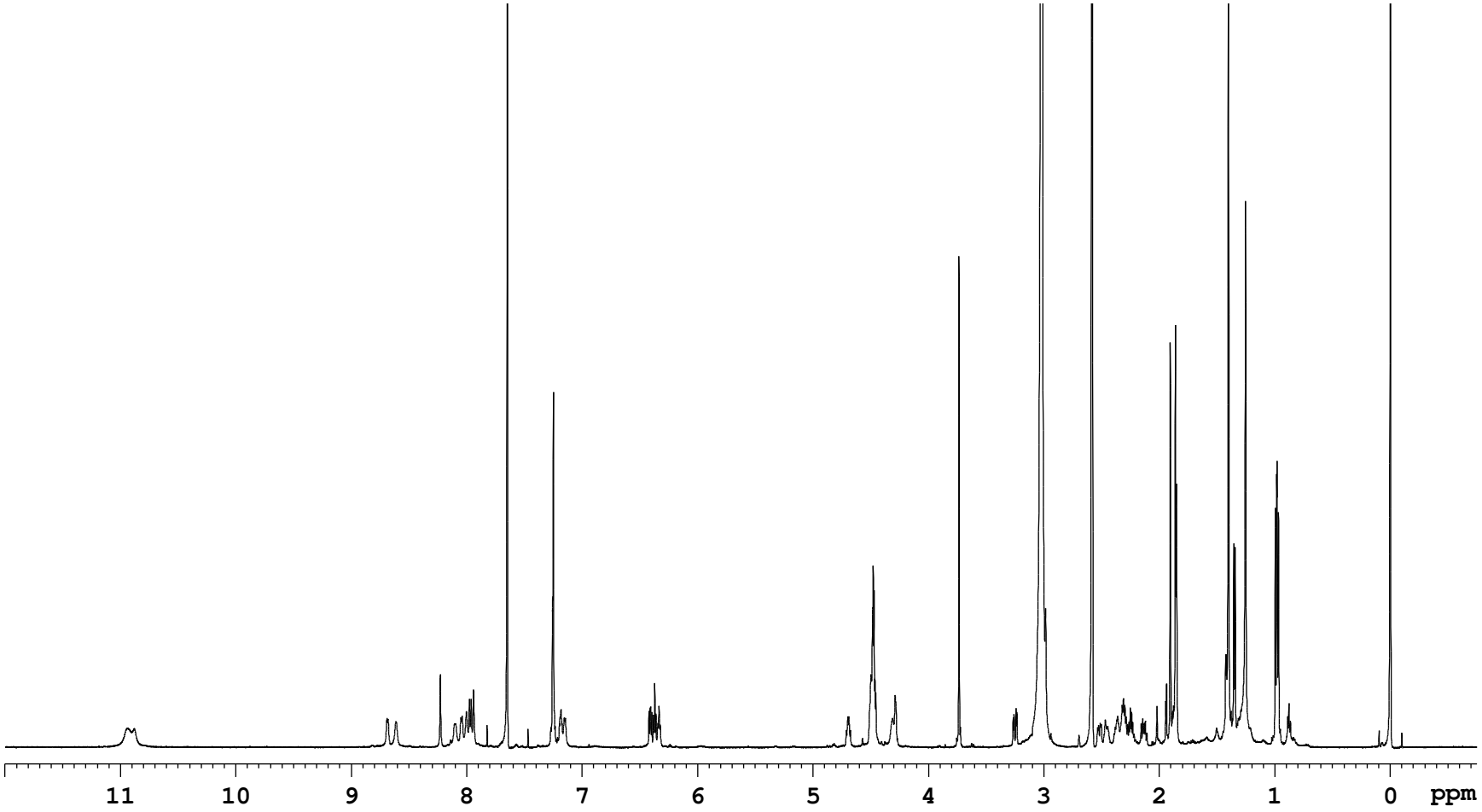
Supporting Figure-14: Variation of NH chemical shifts of **4** with respect to the sequential addition of DMSO-d_6 fractions (in aliquots of 50 µL) at 300 K to an initial 500 µL solution of **4** in $CDCl_3$. The Δδ shifts of <1 ppm for all the NH's except for the 1NH indicates their participation in h-bonding. However, 2NH is involved in 8mr h-bond of moderate strength in 11/8 bifurcated h-bonding compared to the 4NH, which is participating in a stronger h-bonding, in the isolated 8mr ring at the C-terminus.

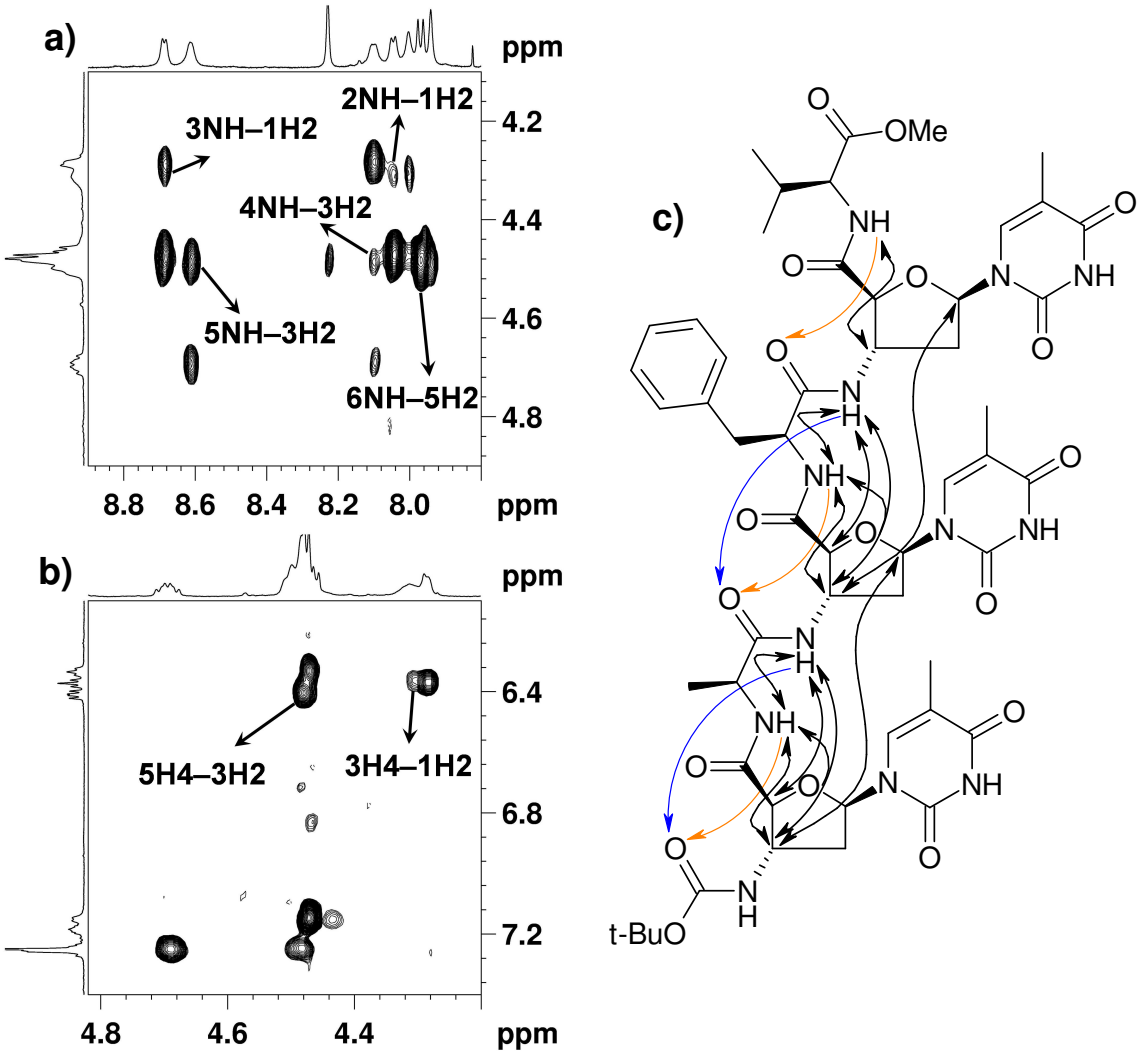
EXPERIMENTAL DATA & STRUCTURAL INFERENCES OF HEXAMER 5

Supporting Table-07: Chemical shift assignment for hexamer **5** in (500 µL $CDCl_3$ + 90 µL DMSO-d_6) (concentration ~5 mM) at 300 K. (600 MHz)

Residue	NH	C1H (α)	C2H (β)	C3H (γ) (pro-*R*)	C3'H (γ') (pro-*S*)	C4H (δ)	H_b	Me_b	NH_b
1	7.15 (d) $J_{NH, H2}$=7.0	4.48 (d) $J_{H1, H2}$=5.0	4.31 (dt) $J_{NH, H2}$=7.0 $J_{H1, H2}$=5.0 $J_{H2, H3}$=7.0	2.36 (dd) $J_{H3, H3'}$=13.7 $J_{H4, H3}$=6.6	2.31 (ddd) $J_{H3, H3'}$=13.7 $J_{H4, H3'}$=6.6 $J_{H2, H3}$=7.0	6.33 (t) $J_{H4, H3}$=6.6 $J_{H4, H3'}$=6.6	7.99 (s)	1.85 (s)	11.9 (s)
2	8.04 (d) $J_{NH, H1}$=6.8	4.46 (qd) $J_{NH, H1}$=6.8 $J_{H1, H2}$=7.0	1.35 (d) $J_{H1, H2}$=7.0	--	--	--	--	--	--
3	8.69 (d) $J_{NH, H2}$=6.6	4.28 (d) $J_{H1, H2}$=5.0	4.49 (ddd) $J_{NH, H2}$=6.6 $J_{H1, H2}$=5.0 $J_{H2, H3}$=7.0	2.45 (dd) $J_{H3, H3'}$=13.7 $J_{H4, H3}$=6.6	2.28 (ddd) $J_{H3, H3'}$=13.7 $J_{H4, H3'}$=6.6 $J_{H2, H3}$=7.0	6.37 (t) $J_{H4, H3}$=6.6 $J_{H4, H3'}$=6.6	7.94 (s)	1.86 (s)	10.9 (s)
4	8.10 (d) $J_{NH,H1}$=7.5	4.69 (ddd) $J_{NH,H2}$=7.5 $J_{H1, H2}$=5.0 $J_{H1, H2}$=8.0	3.24 (dd) $J_{H1, H2}$=5.0 $J_{H2, H2'}$=14.2 3.01 (dd) $J_{H1, H2'}$=8.0 $J_{H2, H2'}$=14.2	--	--	--	--	--	--
5	8.61 (d) $J_{NH, H2}$=-- (broad)	4.49 overlap	4.49 (m) $J_{H2, H3}$=7.0	2.52 (dd) $J_{H3, H3'}$=13.7 $J_{H3, H4}$=5.7	2.12 (ddd) $J_{H3, H3'}$=13.7 $J_{H3', H4}$=8.8 $J_{H2, H3}$=7.0	6.41 (dd) $J_{H4, H3'}$=8.8 $J_{H4, H3}$=5.7	8.22 (s)	1.90 (s)	10.9 (s)
6	7.98 (d) $J_{NH, H1}$=8.6	4.46 (dd) $J_{NH, H1}$=8.6	2.24 (m) $J_{H2, H3}$=7.0 $J_{H2, H3'}$=7.0	0.98 (d) $J_{H2, H3}$=7.0 0.97 (d) $J_{H2, H3'}$=7.0	--	--	--	--	--

Supporting Figure-15: ^{1}H NMR spectrum of **5** in (500 µL $CDCl_3$ + 90 µL DMSO-d_6) (concentration ~5 mM) at 300 K. (600MHz)





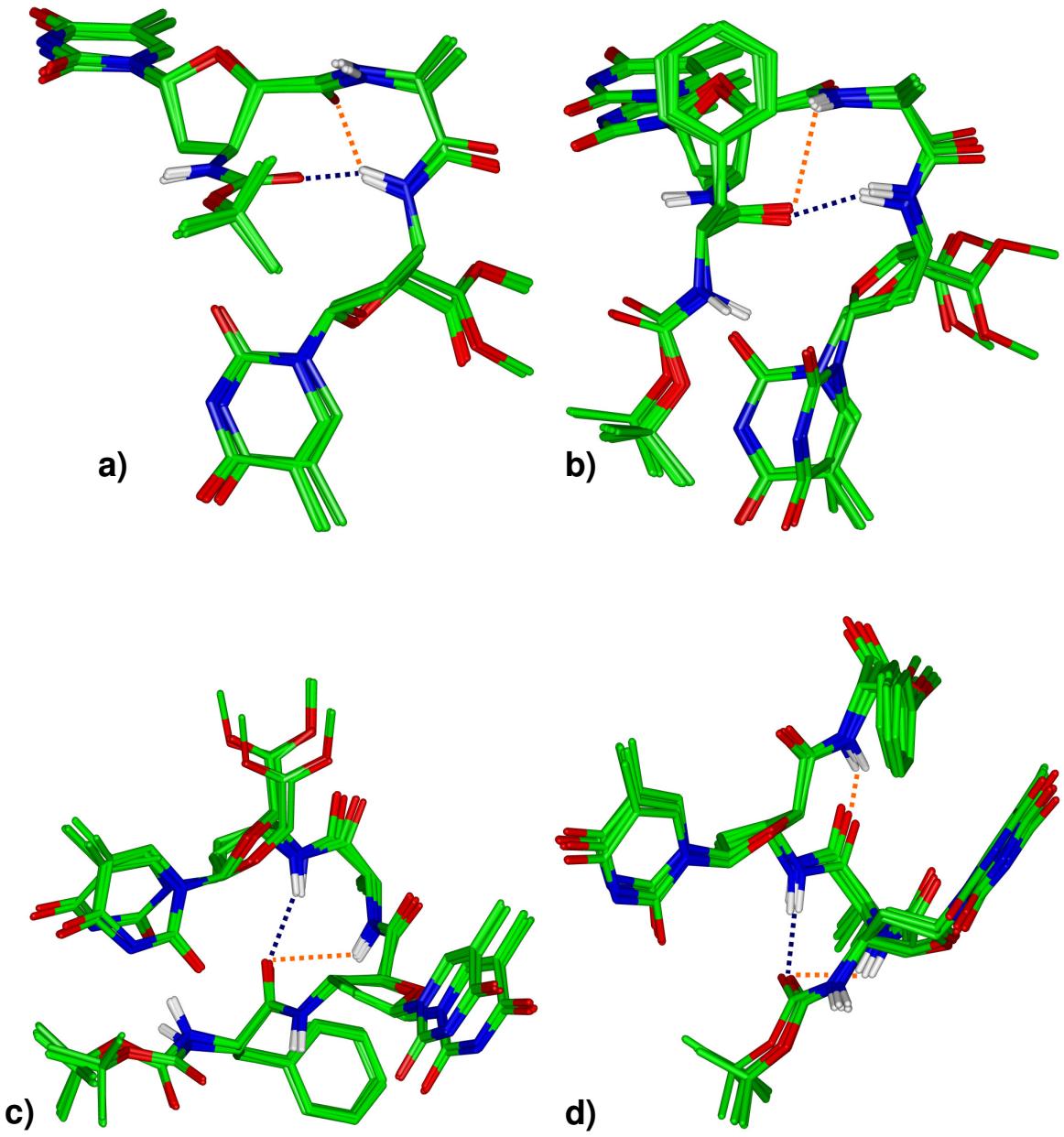
Supporting Figure-16: Expanded regions (a and b) from ROESY spectrum of **5** showing the characteristic ROEs that support 11/8 hydrogen-bonded helix. (c) Schematic representation of the characteristic ROEs (solid curves) and hydrogen bonding for **5** (11-mr and 8-mr hydrogen bonds are shown in dotted blue and orange curves, respectively), which depict an overall 11/8 helical fold.

MOLECULAR DYNAMICS

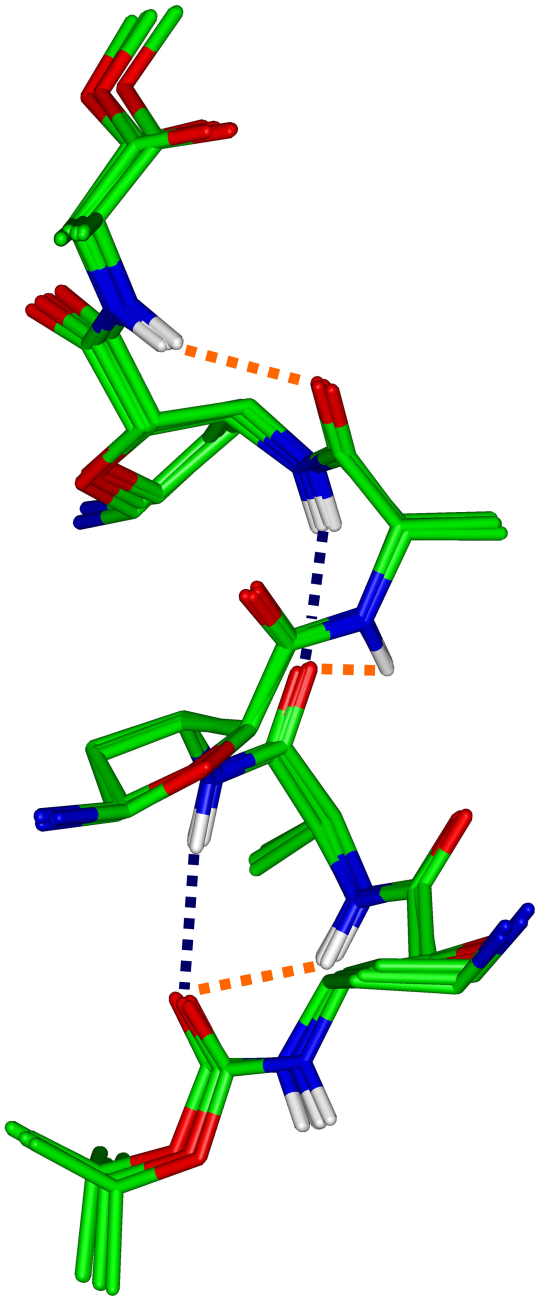
The cvff force field with default parameters was used throughout the simulations on insight II discover program (on Silicon Graphics-Fuel). Minimization's were done first with steepest decent, followed by conjugate gradient methods for a maximum of 100000 iterations each or RMS deviation of 0.001 kcal/mol, whichever was earlier. The energy-minimized structures were then subjected to MD simulations. A number of inter atomic distance and torsion angle constraints obtained from NMR data were used as restraints in the minimization as well as MD runs. The molecules were initially equilibrated for 50 ps and subsequently subjected to a 1000 ps dynamics with a step size of 1 fs, sampling the trajectory at equal intervals of 20 ps. In the trajectory, 100 samples were generated and were again energy minimized with above protocol. Among them 15 lower energy structures are aligned and shown below.

Minimum energy structures for compounds **2**–**5**, have all converged to structures displaying 11/8 helical fold. In these helical folds, the 11mr h-bonding distance is found to be shorter relative to the corresponding 8mr h-bond and the corresponding ∠NHO angles are found to be more linear for 11mr h-bonds than 8mr h-bonds. However, dynamics pathway has shown the presence of 8mr h-bonds as depicted in the supporting figures 20 and 21. The data show the variation of h-bonding distances and ∠NHO angles during the dynamics trajectory for the observed 11mr and 8mr h-bonds.

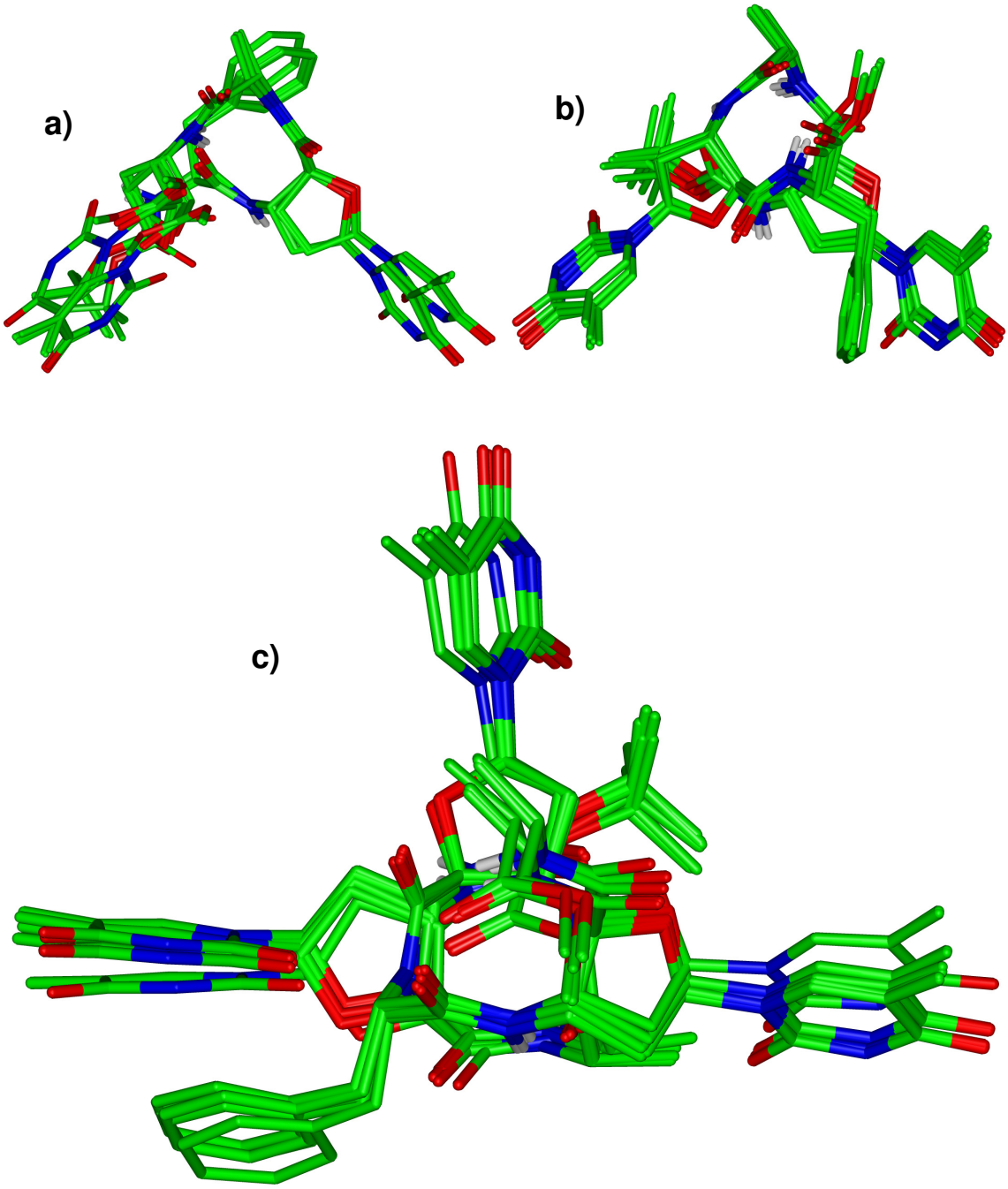
Molecular Dynamics Figures



Supporting Figure-17: Overlay of minimum energy structures obtained from Molecular Dynamics studies showing (a) side view for trimer **2**; (b) and (c) side views for tetramer **3**; and (d) side view for tetramer **4**. (11-mr and 8-mr hydrogen bonds are shown in dotted blue and orange lines, respectively).

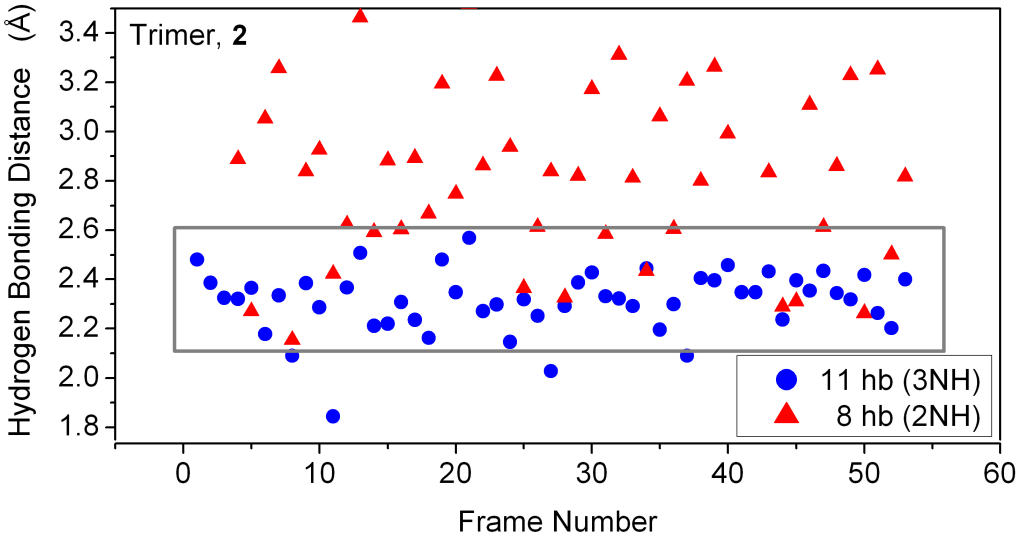


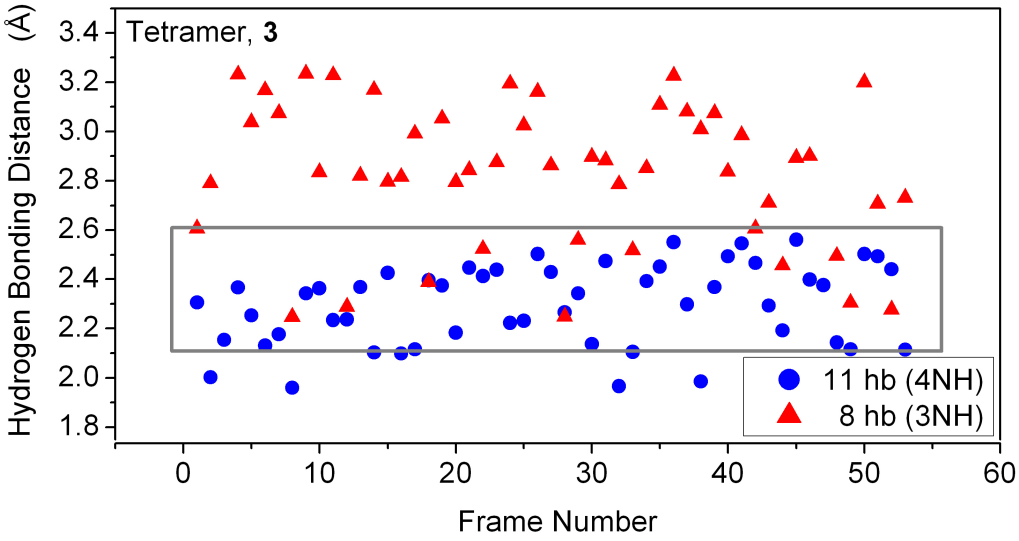
Supporting Figure-18: Overlay of minimum energy structures obtained from Molecular Dynamics studies showing side view for hexamer **5** (11-mr and 8-mr hydrogen bonds are shown in dotted blue and orange lines, respectively). Thymidine bases of NDA residues and side-chains of L-amino acids are removed for a better view.

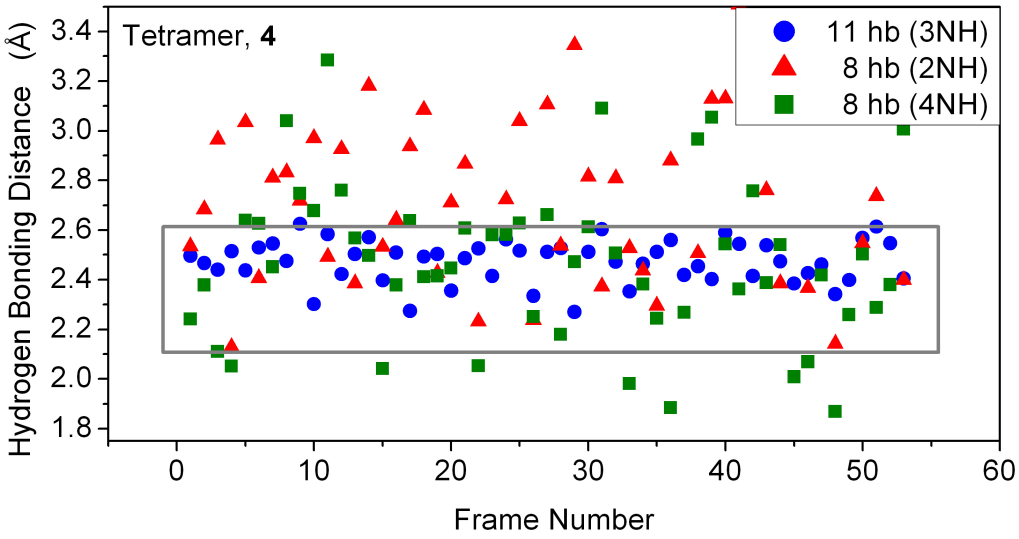


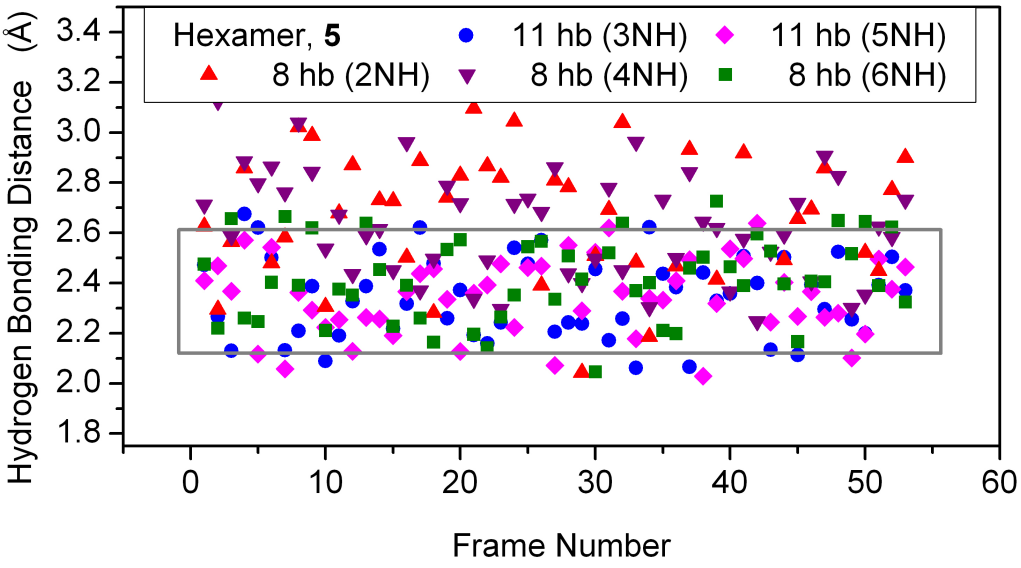
Supporting Figure-19: Overlay of minimum energy structures obtained from Molecular Dynamics studies showing the top view along the helical axis (C→N) for (a) tetramer **3**; (b) tetramer **4** and (c) hexamer **5**. A regular positioning of the nucleobases (at ~90° angular distance of each consecutive base from the previous one) around the helical axis can be noticed.

Supporting Figure-20: MD Trajectory Diagrams for compounds **2–5** with respect to the hydrogen bonding distances in the possible bifurcated 11-mr and 8-mr h-bondings (hb). It can be easily seen in **4** and **5** that the 11-mr hb and C-terminal 8-mr hb have shorter bond lengths compared to the 8-mr hb in 11/8 bifurcated bonds.

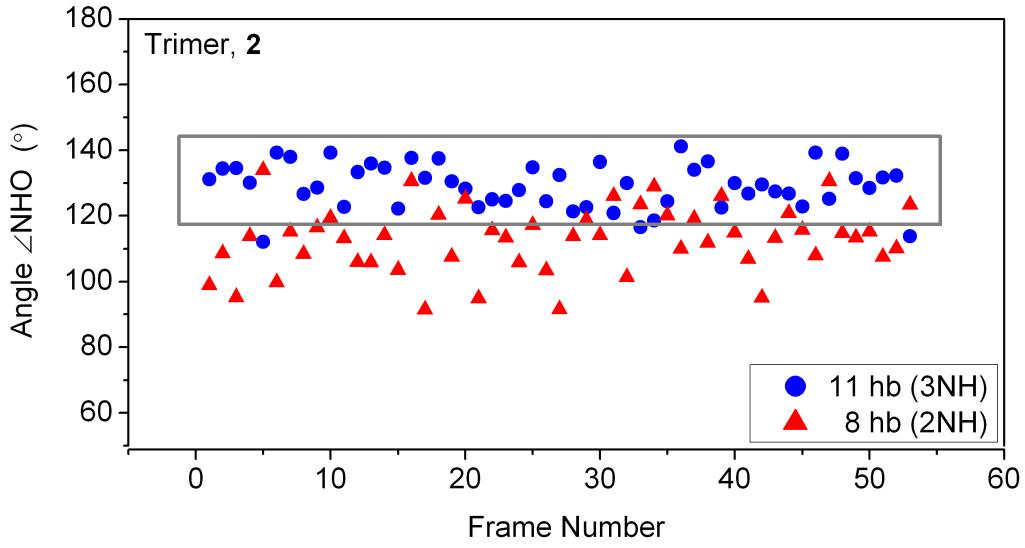


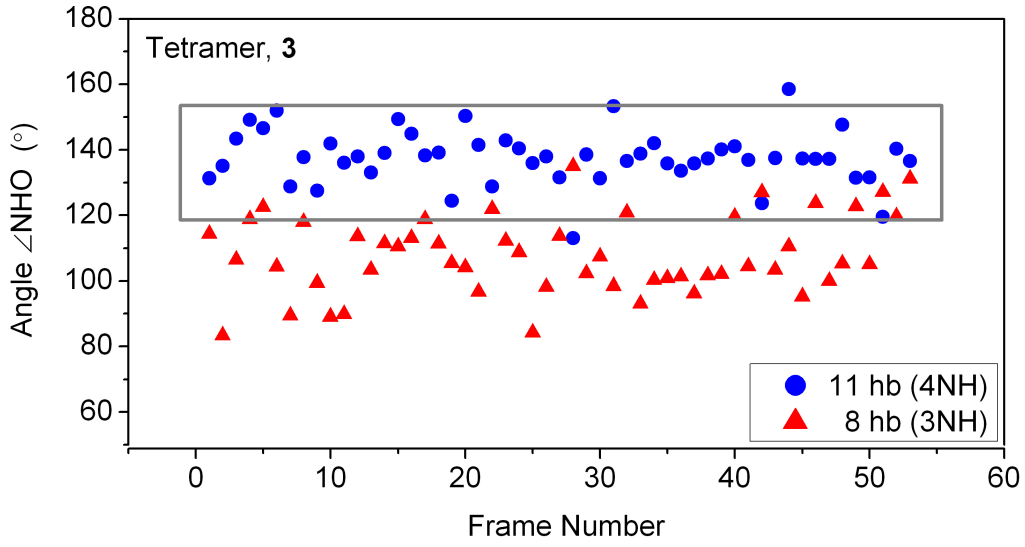


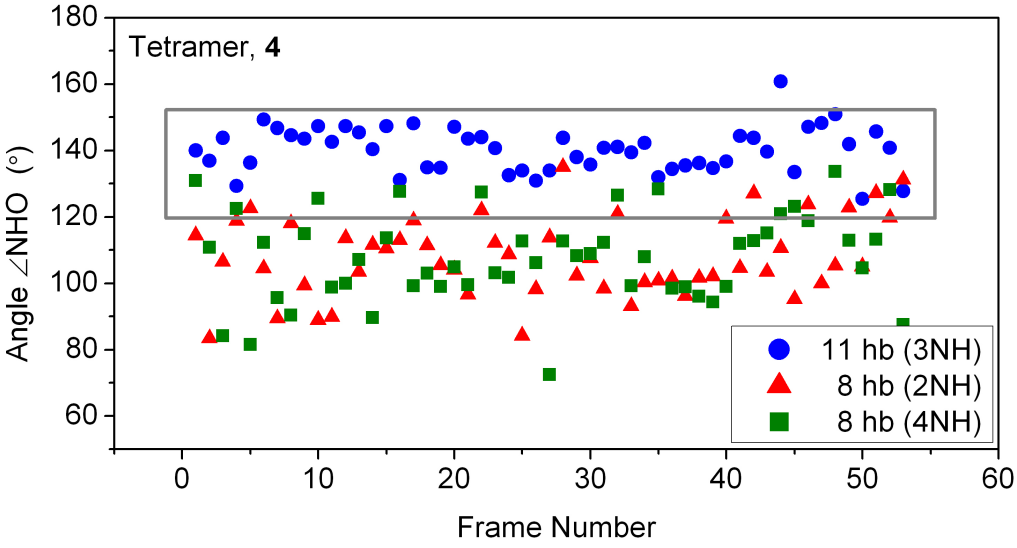

Tetramer, 4
11 hb (3NH)
8 hb (2NH)
8 hb (4NH)
Hydrogen Bonding Distance (Å)
3.4
3.2
3.0
2.8
2.6
2.4
2.2
2.0
1.8
0
10
20
30
40
50
60
Frame Number

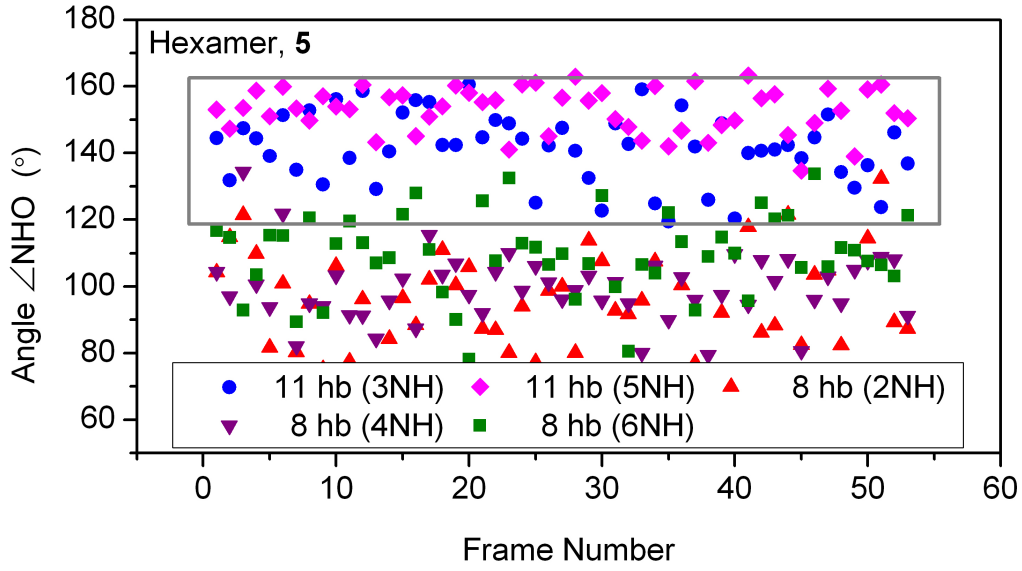

Hexamer, 5
11 hb (3NH)
11 hb (5NH)
8 hb (2NH)
8 hb (4NH)
8 hb (6NH)
Hydrogen Bonding Distance (Å)
3.4
3.2
3.0
2.8
2.6
2.4
2.2
2.0
1.8
0
10
20
30
40
50
60
Frame Number

Supporting Figure-21: MD Trajectory Diagrams for compounds **2–5** with respect to the hydrogen bonding angles (∠NHO) measured for the possible 11-mr and 8-mr h-bonds. It can be seen that ∠NHO angles for 11-mr hb are relatively linear than those of 8-mr hb in bifurcated 11/8-mr hb rings.

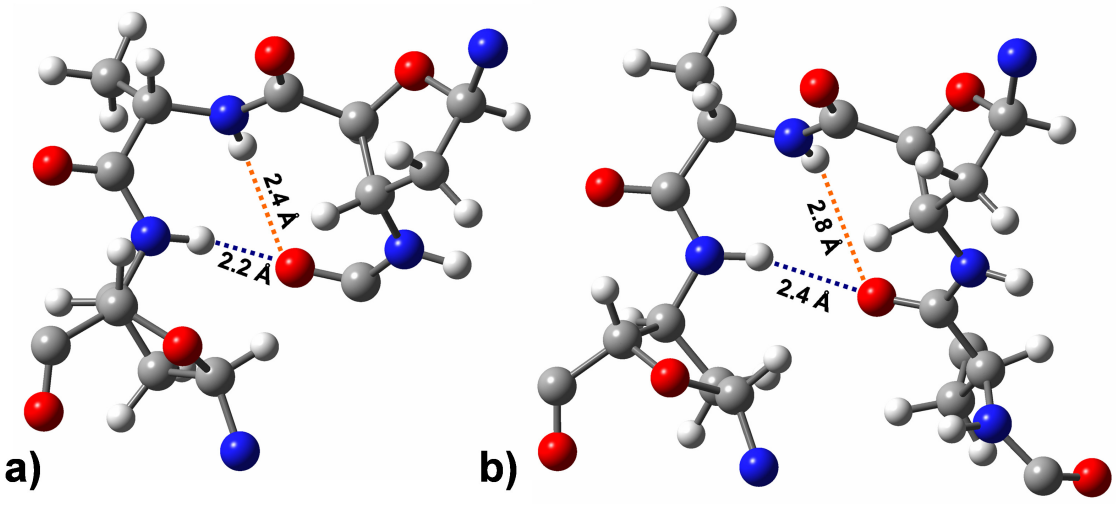





Tetramer, 4
Angle ∠NHO (°)
Frame Number
11 hb (3NH)
8 hb (2NH)
8 hb (4NH)


Hexamer, 5
Angle ∠NHO (°)
Frame Number
11 hb (3NH)
11 hb (5NH)
8 hb (2NH)
8 hb (4NH)
8 hb (6NH)

DFT CALCULATIONS



Supporting Figure-22: Minimum energy structures obtained from DFT calculations on (a) trimer **2** and (b) tetramer **3** show the formation of bifurcated 11/8 bifurcated h-bonded turns (11-mr and 8-mr hydrogen bonds are shown in dotted blue and orange lines, respectively). It is evident from these studies that the 8-mr h-bond distances in 11/8 bifurcated h-bonds are relatively longer than the corresponding 11-mr h-bond distances. The conformations are consistent with the ROE based structures.

Reference 18 cited in the manuscript: M. J. Frisch, G. W. Trucks, H. B. Schlegel, G. E. Scuseria, M. A. Robb, J. R. Cheeseman, J. A. Montgomery, Jr., T. Vreven, K. N. Kudin, J. C. Burant, J. M. Millam, S. S. Iyengar, J. Tomasi, V. Barone, B. Mennucci, M. Cossi, G. Scalmani, N. Rega, G. A. Petersson, H. Nakatsuji, M. Hada, M. Ehara, K. Toyota, R. Fukuda, J. Hasegawa, M. Ishida, T. Nakajima, Y. Honda, O. Kitao, H. Nakai, M. Klene, X. Li, J. E. Knox, H. P. Hratchian, J. B. Cross, V. Bakken, C. Adamo, J. Jaramillo, R. Gomperts, R. E. Stratmann, O. Yazyev, A. J. Austin, R. Cammi, C. Pomelli, J. W. Ochterski, P. Y. Ayala, K. Morokuma, G. A. Voth, P. Salvador, J. J. Dannenberg, V. G. Zakrzewski, S. Dapprich, A. D. Daniels, M. C. Strain, O. Farkas, D. K. Malick, A. D. Rabuck, K. Raghavachari, J. B. Foresman, J. V. Ortiz, Q. Cui, A. G. Baboul, S. Clifford, J. Cioslowski, B. B. Stefanov, G. Liu, A. Liashenko, P. Piskorz, I. Komaromi, R. L. Martin, D. J. Fox, T. Keith, M. A. Al-Laham, C. Y. Peng, A. Nanayakkara, M. Challacombe, P. M. W. Gill, B. Johnson, W. Chen, M. W. Wong, C. Gonzalez and J. A. Pople, ***Gaussian, Inc., Wallingford CT, 2004***.

Supporting Table-08: Comparison of the least five minimum energy structures obtained for **2** from DFT calculations.

Structure	RMSD (Å) (with protection groups and thymidine bases removed)	Zero point energies ($kcal.mol^{-1}$)	Hydrogen bond distances (Å)	
			11 hb (3NH)	8 hb (2NH)
Higher energy structure IV	0.70	4.1	2.3	2.7
Higher energy structure III	0.77	2.3	2.2	2.5
Higher energy structure II	0.66	1.4	2.2	2.6
Higher energy structure I	0.60	0.6	2.3	2.5
Stationary point	0.00	0.0	2.2	2.4

Supporting Table-09: Comparison of the least six minimum energy structures obtained for **3** from DFT calculations.

Structure	RMSD (Å) (with protection groups and thymidine bases removed)	Zero point energies ($kcal.mol^{-1}$)	Hydrogen bond distances (Å)	
			11 hb (4NH)	8 hb (3NH)
Higher energy structure V	1.95	3.3	2.3	2.6
Higher energy structure IV	1.93	2.4	2.3	2.7
Higher energy structure III	1.62	1.2	2.1	2.9
Higher energy structure II	0.13	0.6	2.3	2.9
Higher energy structure I	0.08	0.2	2.4	2.9
Stationary point	0.00	0.0	2.4	2.8

ATOMIC COORDINATE FILES

Below given are the atomic coordinates (in .pdb format) of one of the minimum energy structures obtained for compounds **2–4** in restrained molecular dynamics studies.

Atomic coordinates for trimer **2**

```
ATOM      1  C1  FRAG    1       1.464   3.606   1.638  0.00  0.00           C
ATOM      2  C2  FRAG    1       1.102   2.131   1.844  0.00  0.00           C
ATOM      3  C3  FRAG    1       0.611   2.097   3.320  0.00  0.00           C
ATOM      4  O4  FRAG    1       0.629   3.451   3.813  0.00  0.00           O
ATOM      5  C5  FRAG    1       0.611   4.331   2.685  0.00  0.00           C
ATOM      6  N6  FRAG    1       1.103   5.692   3.050  0.00  0.00           N
ATOM      7  C7  FRAG    1       0.371   6.823   2.711  0.00  0.00           C
ATOM      8  N8  FRAG    1       0.823   8.067   3.037  0.00  0.00           N
ATOM      9  C9  FRAG    1       1.982   8.314   3.709  0.00  0.00           C
ATOM     10  C10 FRAG    1       2.833   7.080   4.140  0.00  0.00           C
ATOM     11  C11 FRAG    1       2.382   5.845   3.801  0.00  0.00           C
ATOM     12  O12 FRAG    1      -0.703   6.768   2.111  0.00  0.00           O
ATOM     13  O13 FRAG    1       2.315   9.474   3.952  0.00  0.00           O
ATOM     14  C14 FRAG    1       4.143   7.272   4.876  0.00  0.00           C
ATOM     15  N15 FRAG    1       0.040   1.715   0.893  0.00  0.00           N
ATOM     16  C16 FRAG    1       1.436   1.170   4.225  0.00  0.00           C
ATOM     17  O17 FRAG    1       2.701   1.689   4.482  0.00  0.00           O
ATOM     18  C18 FRAG    1       3.590   0.918   5.319  0.00  0.00           C
ATOM     19  O19 FRAG    1       0.993   0.098   4.648  0.00  0.00           O
ATOM     20  H1  FRAG    1      -0.779   2.298   0.655  1.00  0.00           H
ATOM     21  H2  FRAG    1       1.295   3.979   0.612  0.00  0.00           H
ATOM     22  H3  FRAG    1       2.542   3.747   1.846  0.00  0.00           H
ATOM     23  H4  FRAG    1       2.018   1.524   1.686  0.00  0.00           H
ATOM     24  H5  FRAG    1      -0.445   1.765   3.371  0.00  0.00           H
ATOM     25  H6  FRAG    1      -0.434   4.350   2.310  0.00  0.00           H
ATOM     26  H7  FRAG    1       0.251   8.870   2.760  0.00  0.00           H
ATOM     27  H8  FRAG    1       2.950   4.952   4.073  0.00  0.00           H
ATOM     28  H9  FRAG    1       4.983   7.390   4.167  0.00  0.00           H
ATOM     29 0H1  FRAG    1       4.126   8.175   5.515  0.00  0.00           H
ATOM     30 1H1  FRAG    1       4.386   6.420   5.538  0.00  0.00           H
ATOM     31 2H1  FRAG    1       3.168   0.765   6.330  0.00  0.00           H
ATOM     32 3H1  FRAG    1       4.554   1.444   5.439  0.00  0.00           H
ATOM     33 4H1  FRAG    1       3.807  -0.074   4.879  0.00  0.00           H
ATOM     34  C1  FRAG    1C     -4.634   4.422   1.866  0.00  0.00           C
ATOM     35  C2  FRAG    1C     -3.408   4.049   1.024  0.00  0.00           C
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ATOM     36  C3  FRAG    1C     -3.950   2.892   0.132  0.00  0.00           C
ATOM     37  O4  FRAG    1C     -5.356   2.748   0.401  0.00  0.00           O
ATOM     38  C5  FRAG    1C     -5.817   3.960   1.006  0.00  0.00           C
ATOM     39  N6  FRAG    1C     -7.077   3.767   1.782  0.00  0.00           N
ATOM     40  C7  FRAG    1C     -8.037   4.771   1.816  0.00  0.00           C
ATOM     41  N8  FRAG    1C     -9.187   4.608   2.531  0.00  0.00           N
ATOM     42  C9  FRAG    1C     -9.492   3.496   3.257  0.00  0.00           C
ATOM     43  C10 FRAG    1C     -8.448   2.337   3.259  0.00  0.00           C
ATOM     44  C11 FRAG    1C     -7.302   2.509   2.551  0.00  0.00           C
ATOM     45  O12 FRAG    1C     -7.900   5.839   1.217  0.00  0.00           O
ATOM     46  O13 FRAG    1C    -10.554   3.441   3.876  0.00  0.00           O
ATOM     47  C14 FRAG    1C     -8.698   1.083   4.070  0.00  0.00           C
ATOM     48  N15 FRAG    1C     -2.933   5.232   0.259  0.00  0.00           N
ATOM     49  C16 FRAG    1C     -3.229   1.553   0.369  0.00  0.00           C
ATOM     50  O19 FRAG    1C     -3.374   0.946   1.433  0.00  0.00           O
ATOM     51  C20 FRAG    1C     -1.801   5.229  -0.450  0.00  0.00           C
ATOM     52  O21 FRAG    1C     -1.601   6.478  -1.034  0.00  0.00           O
ATOM     53  C22 FRAG    1C     -0.475   6.806  -1.913  0.00  0.00           C
ATOM     54  C23 FRAG    1C     -0.699   8.275  -2.324  0.00  0.00           C
ATOM     55  C24 FRAG    1C     -0.471   5.940  -3.196  0.00  0.00           C
ATOM     56  C25 FRAG    1C      0.882   6.716  -1.175  0.00  0.00           C
ATOM     57  O26 FRAG    1C     -1.057   4.251  -0.572  0.00  0.00           O
ATOM     58  H1  FRAG    1C     -4.700   5.493   2.141  0.00  0.00           H
ATOM     59  H2  FRAG    1C     -4.605   3.857   2.818  0.00  0.00           H
ATOM     60  H3  FRAG    1C     -2.598   3.712   1.703  0.00  0.00           H
ATOM     61  H4  FRAG    1C     -3.850   3.179  -0.929  0.00  0.00           H
ATOM     62  H5  FRAG    1C     -5.962   4.680   0.175  0.00  0.00           H
ATOM     63  H6  FRAG    1C     -9.864   5.377   2.526  0.00  0.00           H
ATOM     64  H7  FRAG    1C     -6.536   1.731   2.538  0.00  0.00           H
ATOM     65  H8  FRAG    1C     -8.204   0.192   3.638  0.00  0.00           H
ATOM     66  H9  FRAG    1C     -8.324   1.198   5.104  0.00  0.00           H
ATOM     67  H10 FRAG    1C     -9.776   0.846   4.137  0.00  0.00           H
ATOM     68  H11 FRAG    1C     -3.423   6.132   0.276  0.00  0.00           H
ATOM     69 2H1  FRAG    1C     -1.663   8.410  -2.849  0.00  0.00           H
ATOM     70 3H1  FRAG    1C      0.093   8.652  -2.998  0.00  0.00           H
ATOM     71 4H1  FRAG    1C     -0.723   8.946  -1.444  0.00  0.00           H
ATOM     72 5H1  FRAG    1C     -1.442   5.987  -3.723  0.00  0.00           H
ATOM     73 6H1  FRAG    1C      0.308   6.259  -3.914  0.00  0.00           H
ATOM     74 7H1  FRAG    1C     -0.281   4.874  -2.974  0.00  0.00           H
ATOM     75 8H1  FRAG    1C      1.124   5.679  -0.888  0.00  0.00           H
ATOM     76 9H1  FRAG    1C      0.881   7.314  -0.245  0.00  0.00           H
ATOM     77  H20 FRAG    1C      1.722   7.077  -1.797  0.00  0.00           H
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ATOM     78  N   ALA     1B     -2.394   1.150  -0.603  1.00  0.00           N
ATOM     79  CA  ALA     1B     -1.373   0.086  -0.384  1.00  0.00           C
ATOM     80  C   ALA     1B     -0.108   0.450   0.463  1.00  0.00           C
ATOM     81  O   ALA     1B      0.700  -0.438   0.752  1.00  0.00           O
ATOM     82  CB  ALA     1B     -0.982  -0.466  -1.769  1.00  0.00           C
ATOM     83  H   ALA     1B     -2.363   1.765  -1.423  1.00  0.00           H
ATOM     84  HA  ALA     1B     -1.856  -0.728   0.178  1.00  0.00           H
ATOM     85 2HB  ALA     1B     -0.472   0.293  -2.392  1.00  0.00           H
ATOM     86 3HB  ALA     1B     -0.295  -1.328  -1.682  1.00  0.00           H
ATOM     87 1HB  ALA     1B     -1.861  -0.825  -2.337  1.00  0.00           H
END
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Atomic coordinates for tetramer **3**

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ATOM      1  C1  FRAG    1      -3.626   2.035   0.074  0.00  0.00           C
ATOM      2  C2  FRAG    1      -4.798   2.053   1.067  0.00  0.00           C
ATOM      3  C3  FRAG    1      -4.283   1.129   2.209  0.00  0.00           C
ATOM      4  O4  FRAG    1      -2.875   0.889   1.988  0.00  0.00           O
ATOM      5  C5  FRAG    1      -2.398   1.764   0.958  0.00  0.00           C
ATOM      6  N6  FRAG    1      -1.233   1.173   0.237  0.00  0.00           N
ATOM      7  C7  FRAG    1      -0.049   1.890   0.104  0.00  0.00           C
ATOM      8  N8  FRAG    1       1.013   1.357  -0.562  0.00  0.00           N
ATOM      9  C9  FRAG    1       1.026   0.120  -1.131  0.00  0.00           C
ATOM     10  C10 FRAG    1      -0.264  -0.745  -0.982  0.00  0.00           C
ATOM     11  C11 FRAG    1      -1.323  -0.204  -0.327  0.00  0.00           C
ATOM     12  O12 FRAG    1       0.105   3.019   0.571  0.00  0.00           O
ATOM     13  O13 FRAG    1       2.029  -0.268  -1.729  0.00  0.00           O
ATOM     14  C14 FRAG    1      -0.331  -2.128  -1.595  0.00  0.00           C
ATOM     15  N15 FRAG    1      -5.057   3.443   1.519  0.00  0.00           N
ATOM     16  C16 FRAG    1      -5.040  -0.207   2.300  0.00  0.00           C
ATOM     17  O17 FRAG    1      -4.736  -1.050   1.235  0.00  0.00           O
ATOM     18  C18 FRAG    1      -5.373  -2.345   1.194  0.00  0.00           C
ATOM     19  O19 FRAG    1      -5.821  -0.460   3.222  0.00  0.00           O
ATOM     20  H1  FRAG    1      -4.338   4.169   1.588  1.00  0.00           H
ATOM     21  H2  FRAG    1      -3.521   2.956  -0.530  0.00  0.00           H
ATOM     22  H3  FRAG    1      -3.782   1.209  -0.646  0.00  0.00           H
ATOM     23  H4  FRAG    1      -5.705   1.655   0.569  0.00  0.00           H
ATOM     24  H5  FRAG    1      -4.383   1.629   3.193  0.00  0.00           H
ATOM     25  H6  FRAG    1      -2.117   2.715   1.452  0.00  0.00           H
ATOM     26  H7  FRAG    1       1.859   1.930  -0.643  0.00  0.00           H
ATOM     27  H8  FRAG    1      -2.249  -0.769  -0.207  0.00  0.00           H
ATOM     28  H9  FRAG    1       0.658  -2.621  -1.605  0.00  0.00           H
ATOM     29 0H1  FRAG    1      -1.016  -2.802  -1.046  0.00  0.00           H
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ATOM	30	1H1	FRAG	1	−0.684	−2.082	−2.642	0.00	0.00	H
ATOM	31	2H1	FRAG	1	−5.041	−2.906	0.302	0.00	0.00	H
ATOM	32	3H1	FRAG	1	−6.475	−2.256	1.139	0.00	0.00	H
ATOM	33	4H1	FRAG	1	−5.117	−2.954	2.082	0.00	0.00	H
ATOM	34	N	ALA	1D	−4.951	5.976	3.010	1.00	0.00	N
ATOM	35	CA	ALA	1D	−6.239	5.294	2.686	1.00	0.00	C
ATOM	36	C	ALA	1D	−6.179	3.829	2.141	1.00	0.00	C
ATOM	37	O	ALA	1D	−7.140	3.073	2.304	1.00	0.00	O
ATOM	38	CB	ALA	1D	−7.027	6.209	1.730	1.00	0.00	C
ATOM	39	H	ALA	1D	−4.517	6.647	2.366	1.00	0.00	H
ATOM	40	HA	ALA	1D	−6.810	5.222	3.621	1.00	0.00	H
ATOM	41	2HB	ALA	1D	−8.037	5.807	1.525	1.00	0.00	H
ATOM	42	3HB	ALA	1D	−7.172	7.222	2.151	1.00	0.00	H
ATOM	43	1HB	ALA	1D	−6.520	6.327	0.753	1.00	0.00	H
ATOM	44	N	ALA	1C	−0.364	5.690	−1.105	1.00	0.00	N
ATOM	45	CA	ALA	1C	−0.890	6.644	−0.094	1.00	0.00	C
ATOM	46	CN1	ALA	1C	0.914	5.663	−1.492	1.00	0.00	C
ATOM	47	ON1	ALA	1C	1.780	6.454	−1.106	1.00	0.00	O
ATOM	48	ON13	ALA	1C	1.118	4.615	−2.388	1.00	0.00	O
ATOM	49	CN13	ALA	1C	2.402	4.331	−3.037	1.00	0.00	C
ATOM	50	C4	ALA	1C	3.505	3.966	−2.013	1.00	0.00	C
ATOM	51	C5	ALA	1C	2.144	3.098	−3.927	1.00	0.00	C
ATOM	52	C6	ALA	1C	2.855	5.496	−3.950	1.00	0.00	C
ATOM	53	C	ALA	1C	−1.599	5.829	1.026	1.00	0.00	C
ATOM	54	O	ALA	1C	−2.645	5.218	0.785	1.00	0.00	O
ATOM	55	CB	ALA	1C	−1.831	7.669	−0.793	1.00	0.00	C
ATOM	56	C1	ALA	1C	−2.455	8.726	0.140	1.00	0.00	C
ATOM	57	C2	ALA	1C	−1.709	9.831	0.564	1.00	0.00	C
ATOM	58	C3	ALA	1C	−2.260	10.750	1.455	1.00	0.00	C
ATOM	59	C7	ALA	1C	−3.558	10.571	1.927	1.00	0.00	C
ATOM	60	C8	ALA	1C	−4.309	9.477	1.507	1.00	0.00	C
ATOM	61	C9	ALA	1C	−3.762	8.559	0.615	1.00	0.00	C
ATOM	62	1H4	ALA	1C	4.443	3.646	−2.505	1.00	0.00	H
ATOM	63	2H4	ALA	1C	3.764	4.821	−1.363	1.00	0.00	H
ATOM	64	3H4	ALA	1C	3.189	3.144	−1.346	1.00	0.00	H
ATOM	65	1H5	ALA	1C	3.048	2.778	−4.481	1.00	0.00	H
ATOM	66	2H5	ALA	1C	1.805	2.228	−3.334	1.00	0.00	H
ATOM	67	3H5	ALA	1C	1.356	3.292	−4.677	1.00	0.00	H
ATOM	68	1H6	ALA	1C	3.765	5.248	−4.527	1.00	0.00	H
ATOM	69	2H6	ALA	1C	2.069	5.772	−4.678	1.00	0.00	H
ATOM	70	3H6	ALA	1C	3.085	6.409	−3.370	1.00	0.00	H
ATOM	71	H	ALA	1C	−0.944	4.944	−1.504	1.00	0.00	H

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ATOM     72  HA  ALA     1C     -0.058   7.229   0.353  1.00  0.00           H
ATOM     73 1HB  ALA     1C     -2.632   7.131  -1.339  1.00  0.00           H
ATOM     74 2HB  ALA     1C     -1.269   8.192  -1.592  1.00  0.00           H
ATOM     75  H2  ALA     1C     -0.696   9.974   0.215  1.00  0.00           H
ATOM     76  H3  ALA     1C     -1.678  11.599   1.784  1.00  0.00           H
ATOM     77  H7  ALA     1C     -3.982  11.282   2.621  1.00  0.00           H
ATOM     78  H8  ALA     1C     -5.314   9.337   1.878  1.00  0.00           H
ATOM     79  H9  ALA     1C     -4.351   7.706   0.309  1.00  0.00           H
ATOM     80  C1  FRAG    1B     -0.697   5.021   4.568  0.00  0.00           C
ATOM     81  C2  FRAG    1B     -1.709   5.275   3.443  0.00  0.00           C
ATOM     82  C3  FRAG    1B     -2.762   6.220   4.096  0.00  0.00           C
ATOM     83  O4  FRAG    1B     -2.341   6.453   5.455  0.00  0.00           O
ATOM     84  C5  FRAG    1B     -0.941   6.154   5.572  0.00  0.00           C
ATOM     85  N6  FRAG    1B     -0.561   5.793   6.971  0.00  0.00           N
ATOM     86  C7  FRAG    1B      0.677   6.167   7.479  0.00  0.00           C
ATOM     87  N8  FRAG    1B      1.037   5.831   8.750  0.00  0.00           N
ATOM     88  C9  FRAG    1B      0.255   5.120   9.610  0.00  0.00           C
ATOM     89  C10 FRAG    1B     -1.146   4.670   9.092  0.00  0.00           C
ATOM     90  C11 FRAG    1B     -1.495   5.002   7.823  0.00  0.00           C
ATOM     91  O12 FRAG    1B      1.500   6.805   6.818  0.00  0.00           O
ATOM     92  O13 FRAG    1B      0.666   4.859  10.740  0.00  0.00           O
ATOM     93  C14 FRAG    1B     -2.060   3.846   9.976  0.00  0.00           C
ATOM     94  N15 FRAG    1B     -1.056   5.881   2.255  0.00  0.00           N
ATOM     95  C16 FRAG    1B     -4.186   5.626   4.058  0.00  0.00           C
ATOM     96  O19 FRAG    1B     -4.552   4.821   4.919  0.00  0.00           O
ATOM     97  H1  FRAG    1B     -0.181   6.411   2.321  1.00  0.00           H
ATOM     98  H2  FRAG    1B      0.358   4.973   4.238  0.00  0.00           H
ATOM     99  H3  FRAG    1B     -0.919   4.039   5.030  0.00  0.00           H
ATOM    100  H4  FRAG    1B     -2.149   4.294   3.165  0.00  0.00           H
ATOM    101  H5  FRAG    1B     -2.768   7.212   3.597  0.00  0.00           H
ATOM    102  H6  FRAG    1B     -0.388   7.056   5.237  0.00  0.00           H
ATOM    103  H7  FRAG    1B      1.961   6.129   9.079  0.00  0.00           H
ATOM    104  H8  FRAG    1B     -2.459   4.692   7.413  0.00  0.00           H
ATOM    105  H9  FRAG    1B     -1.927   4.091  11.046  0.00  0.00           H
ATOM    106 0H1  FRAG    1B     -3.130   4.006   9.745  0.00  0.00           H
ATOM    107 1H1  FRAG    1B     -1.856   2.766   9.861  0.00  0.00           H
END
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Atomic coordinates for tetramer **4**

ATOM	1	N	ALA	1	1.812	-3.940	4.089	1.00	0.00	N
ATOM	2	CA	ALA	1	2.600	-5.006	4.763	1.00	0.00	C
ATOM	3	C	ALA	1	1.990	-5.254	6.161	1.00	0.00	C
ATOM	4	OC	ALA	1	2.113	-4.148	7.001	1.00	0.00	O
ATOM	5	CC1	ALA	1	1.550	-4.240	8.327	1.00	0.00	C
ATOM	6	O	ALA	1	1.463	-6.330	6.461	1.00	0.00	O
ATOM	7	CB	ALA	1	4.114	-4.643	4.839	1.00	0.00	C
ATOM	8	C1	ALA	1	4.871	-4.638	3.495	1.00	0.00	C
ATOM	9	C2	ALA	1	4.924	-3.474	2.719	1.00	0.00	C
ATOM	10	C3	ALA	1	5.598	-3.468	1.501	1.00	0.00	C
ATOM	11	C7	ALA	1	6.231	-4.624	1.052	1.00	0.00	C
ATOM	12	C8	ALA	1	6.184	-5.788	1.815	1.00	0.00	C
ATOM	13	C9	ALA	1	5.506	-5.796	3.032	1.00	0.00	C
ATOM	14	H	ALA	1	1.559	-3.063	4.560	1.00	0.00	H
ATOM	15	HA	ALA	1	2.507	-5.963	4.211	1.00	0.00	H
ATOM	16	1HC1	ALA	1	0.458	-4.415	8.295	1.00	0.00	H
ATOM	17	2HC1	ALA	1	2.017	-5.054	8.913	1.00	0.00	H
ATOM	18	3HC1	ALA	1	1.717	-3.297	8.879	1.00	0.00	H
ATOM	19	1HB	ALA	1	4.620	-5.353	5.523	1.00	0.00	H
ATOM	20	2HB	ALA	1	4.242	-3.664	5.341	1.00	0.00	H
ATOM	21	H2	ALA	1	4.432	-2.572	3.054	1.00	0.00	H
ATOM	22	H3	ALA	1	5.634	-2.567	0.907	1.00	0.00	H
ATOM	23	H7	ALA	1	6.756	-4.618	0.108	1.00	0.00	H
ATOM	24	H8	ALA	1	6.673	-6.684	1.463	1.00	0.00	H
ATOM	25	H9	ALA	1	5.474	-6.708	3.612	1.00	0.00	H
ATOM	26	C1	FRAG	1D	-1.277	-2.543	1.223	0.00	0.00	C
ATOM	27	C2	FRAG	1D	-0.561	-2.364	2.566	0.00	0.00	C
ATOM	28	C3	FRAG	1D	0.923	-2.667	2.210	0.00	0.00	C
ATOM	29	O4	FRAG	1D	1.047	-2.649	0.772	0.00	0.00	O
ATOM	30	C5	FRAG	1D	-0.199	-2.275	0.161	0.00	0.00	C
ATOM	31	N6	FRAG	1D	-0.433	-3.010	-1.118	0.00	0.00	N
ATOM	32	C7	FRAG	1D	-1.094	-2.389	-2.171	0.00	0.00	C
ATOM	33	N8	FRAG	1D	-1.315	-3.052	-3.342	0.00	0.00	N
ATOM	34	C9	FRAG	1D	-0.931	-4.337	-3.583	0.00	0.00	C
ATOM	35	C10	FRAG	1D	-0.189	-5.087	-2.434	0.00	0.00	C
ATOM	36	C11	FRAG	1D	0.020	-4.423	-1.269	0.00	0.00	C
ATOM	37	O12	FRAG	1D	-1.511	-1.232	-2.100	0.00	0.00	O
ATOM	38	O13	FRAG	1D	-1.178	-4.855	-4.672	0.00	0.00	O
ATOM	39	C14	FRAG	1D	0.238	-6.529	-2.612	0.00	0.00	C
ATOM	40	N15	FRAG	1D	-0.733	-0.990	3.107	0.00	0.00	N
ATOM	41	C16	FRAG	1D	1.461	-3.990	2.795	0.00	0.00	C

ATOM	42	O19	FRAG	1D	1.600	-4.993	2.089	0.00	0.00	O
ATOM	43	H1	FRAG	1D	-0.774	-0.153	2.515	1.00	0.00	H
ATOM	44	H2	FRAG	1D	-2.167	-1.898	1.092	0.00	0.00	H
ATOM	45	H3	FRAG	1D	-1.639	-3.588	1.152	0.00	0.00	H
ATOM	46	H4	FRAG	1D	-0.966	-3.096	3.294	0.00	0.00	H
ATOM	47	H5	FRAG	1D	1.589	-1.865	2.589	0.00	0.00	H
ATOM	48	H6	FRAG	1D	-0.141	-1.185	-0.031	0.00	0.00	H
ATOM	49	H7	FRAG	1D	-1.806	-2.551	-4.088	0.00	0.00	H
ATOM	50	H8	FRAG	1D	0.519	-4.917	-0.433	0.00	0.00	H
ATOM	51	H9	FRAG	1D	0.494	-6.755	-3.664	0.00	0.00	H
ATOM	52	0H1	FRAG	1D	1.129	-6.785	-2.008	0.00	0.00	H
ATOM	53	1H1	FRAG	1D	-0.570	-7.222	-2.317	0.00	0.00	H
ATOM	54	C1	FRAG	1C	3.819	0.269	0.947	0.00	0.00	C
ATOM	55	C2	FRAG	1C	2.461	0.898	1.268	0.00	0.00	C
ATOM	56	C3	FRAG	1C	2.735	1.763	2.533	0.00	0.00	C
ATOM	57	O4	FRAG	1C	4.162	1.774	2.749	0.00	0.00	O
ATOM	58	C5	FRAG	1C	4.851	1.171	1.639	0.00	0.00	C
ATOM	59	N6	FRAG	1C	6.072	0.423	2.071	0.00	0.00	N
ATOM	60	C7	FRAG	1C	7.124	0.236	1.182	0.00	0.00	C
ATOM	61	N8	FRAG	1C	8.220	-0.490	1.544	0.00	0.00	N
ATOM	62	C9	FRAG	1C	8.382	-1.087	2.758	0.00	0.00	C
ATOM	63	C10	FRAG	1C	7.234	-0.910	3.798	0.00	0.00	C
ATOM	64	C11	FRAG	1C	6.145	-0.190	3.429	0.00	0.00	C
ATOM	65	O12	FRAG	1C	7.115	0.699	0.040	0.00	0.00	O
ATOM	66	O13	FRAG	1C	9.402	-1.736	2.991	0.00	0.00	O
ATOM	67	C14	FRAG	1C	7.322	-1.580	5.154	0.00	0.00	C
ATOM	68	N15	FRAG	1C	1.911	1.685	0.138	0.00	0.00	N
ATOM	69	C16	FRAG	1C	1.992	1.224	3.776	0.00	0.00	C
ATOM	70	O19	FRAG	1C	2.553	0.461	4.568	0.00	0.00	O
ATOM	71	C20	FRAG	1C	0.597	1.893	-0.007	0.00	0.00	C
ATOM	72	O21	FRAG	1C	0.358	2.713	-1.107	0.00	0.00	O
ATOM	73	C22	FRAG	1C	-0.972	3.199	-1.490	0.00	0.00	C
ATOM	74	C23	FRAG	1C	-0.737	4.089	-2.728	0.00	0.00	C
ATOM	75	C24	FRAG	1C	-1.612	4.073	-0.383	0.00	0.00	C
ATOM	76	C25	FRAG	1C	-1.912	2.042	-1.902	0.00	0.00	C
ATOM	77	O26	FRAG	1C	-0.268	1.435	0.749	0.00	0.00	O
ATOM	78	H1	FRAG	1C	4.023	0.149	-0.134	0.00	0.00	H
ATOM	79	H2	FRAG	1C	3.843	-0.751	1.377	0.00	0.00	H
ATOM	80	H3	FRAG	1C	1.764	0.064	1.480	0.00	0.00	H
ATOM	81	H4	FRAG	1C	2.427	2.816	2.373	0.00	0.00	H
ATOM	82	H5	FRAG	1C	5.130	1.993	0.949	0.00	0.00	H
ATOM	83	H6	FRAG	1C	8.967	-0.605	0.852	0.00	0.00	H

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ATOM     84  H7  FRAG    1C      5.309  -0.063   4.120  0.00  0.00           H
ATOM     85  H8  FRAG    1C      6.944  -2.618   5.107  0.00  0.00           H
ATOM     86  H9  FRAG    1C      8.364  -1.628   5.521  0.00  0.00           H
ATOM     87  H10 FRAG    1C      6.736  -1.051   5.929  0.00  0.00           H
ATOM     88  H11 FRAG    1C      2.502   2.129  -0.573  0.00  0.00           H
ATOM     89 2H1  FRAG    1C     -0.060   4.934  -2.501  0.00  0.00           H
ATOM     90 3H1  FRAG    1C     -1.676   4.523  -3.122  0.00  0.00           H
ATOM     91 4H1  FRAG    1C     -0.269   3.524  -3.555  0.00  0.00           H
ATOM     92 5H1  FRAG    1C     -1.841   3.486   0.525  0.00  0.00           H
ATOM     93 6H1  FRAG    1C     -0.940   4.893  -0.072  0.00  0.00           H
ATOM     94 7H1  FRAG    1C     -2.563   4.534  -0.712  0.00  0.00           H
ATOM     95 8H1  FRAG    1C     -2.884   2.406  -2.285  0.00  0.00           H
ATOM     96 9H1  FRAG    1C     -2.136   1.369  -1.054  0.00  0.00           H
ATOM     97  H20 FRAG    1C     -1.462   1.415  -2.694  0.00  0.00           H
ATOM     98  N   ALA     1B      0.691   1.553   3.869  1.00  0.00           N
ATOM     99  CA  ALA     1B     -0.264   0.824   4.751  1.00  0.00           C
ATOM    100  C   ALA     1B     -0.462  -0.683   4.389  1.00  0.00           C
ATOM    101  O   ALA     1B     -0.299  -1.544   5.259  1.00  0.00           O
ATOM    102  CB  ALA     1B     -1.594   1.601   4.788  1.00  0.00           C
ATOM    103  H   ALA     1B      0.358   2.175   3.124  1.00  0.00           H
ATOM    104  HA  ALA     1B      0.143   0.848   5.775  1.00  0.00           H
ATOM    105 2HB  ALA     1B     -2.079   1.650   3.794  1.00  0.00           H
ATOM    106 3HB  ALA     1B     -2.317   1.131   5.480  1.00  0.00           H
ATOM    107 1HB  ALA     1B     -1.454   2.642   5.137  1.00  0.00           H
END
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