Minor Groove Orientation of the KWKK Peptide Tethered via the N-terminal Amine to the Acrolein-Derived 1,N^2-γ-Hydroxy-propanodeoxyguanosine Lesion with a Trimethylene Linkage[†]

Supporting Information

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Abbreviations: DPC, DNA-protein conjugate; γ-OH-PdG, γ-hydroxy-1,N^2-propanodeoxyguanosine; NOESY, nuclear Overhauser effect spectroscopy; COSY, correlation spectroscopy; DQF-COSY, double-quantum filtered COSY; NOE, nuclear Overhauser effect; rMD, restrained molecular dynamics

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SUPPORTING INFORMATION

Table S1. Chemical Shifts of the Nucleotide Protons.

Nucleotide	Chemical Shift (ppm)					
	H6/H8	H2/H5/CH_3	H1'	H2'	H2''	H3'
G^1	8.00		6.03	2.68	2.80	4.86
C^2	7.56	5.42	6.08	2.14	2.52	4.84
T^3	7.43	1.69	5.56	2.15	2.42	4.89
A^4	8.24	7.42	6.05	2.77	2.92	5.07
G^5	7.68		5.7	2.49	2.63	4.97
C^6	7.17	5.23	5.65	1.69	2.21	4.79
G^7	7.89		5.48	2.70	2.72	4.99
A^8	8.13	7.75	6.10	2.77	2.88	4.99
G^9	7.49		5.72	2.31	2.56	4.71
T^{10}	7.21	1.24	6.05	2.11	2.52	4.84
C^{11}	7.61	5.72	6.11	2.25	2.50	4.85
C^{12}	7.72	5.86	6.27	2.3	2.30	4.58
G^{13}	7.82		5.64	2.46	2.63	4.81
G^{14}	7.86		5.56	2.71	2.79	5.03
A^{15}	8.23	7.94	6.29	2.76	2.93	5.07
C^{16}	7.28	5.22	5.84	1.96	2.50	4.69
T^{17}	7.38	1.53	6.08	2.12	2.50	4.88
C^{18}	7.49	5.67	5.51	2.05	2.24	4.84
G^{19}	7.91		5.91	2.73	2.75	4.97
C^{20}	7.38	5.36	5.88	1.95	2.42	4.70
T^{21}	7.36	1.66	5.51	2.08	2.37	4.83
A^{22}	8.22	7.46	6.03	2.75	2.88	5.05
G^{23}	7.70		5.82	2.49	2.64	4.95
C^{24}	7.44	5.42	6.14	2.13	2.21	4.47

Table S2. Chemical Shifts of the Trimethylene Tether (X^{25}) and Amino Acid Protons.

Residue	Chemical Shift (ppm)							
	$H^{\alpha 1}$	$H^{\alpha 2}$	H^{β}	$H^{\gamma 1}$	$H^{\gamma 2}$			
X^{25}	2.55	2.72	1.35	1.97	2.24			
	H^{α}	$H^{\beta 1}$	$H^{\beta 2}$	H2	H4	H5	H6	H7
W^{27}	4.99	3.14	3.42	7.38	7.80	7.23	7.31	7.55
	H^{α}	$H^{\beta 1}$	$H^{\beta 2}$	$H^{\gamma 1}$	$H^{\gamma 2}$	H^{δ}	H^{ε}	
K^{26}	3.00	1.56	1.56	1.23	1.31	1.68	2.96	
K^{28}	4.43	1.80	1.90	1.47	1.50	1.72	3.01	
K^{29}	4.19	1.73	1.87	1.44	1.44	1.69	2.98	

Table S3. NOE Distance Restraints Used for the Structure Refinement.[1]

Residue I No.	Residue I Name	Atom I Name	Residue II No.	Residue II Name	Atom II Name	Lower Bound	Upper Bound
1	DG5	H3'	1	DG5	H8	2.43	5.84
1	DG5	H2'2	1	DG5	H8	3.08	4.18
1	DG5	H2'2	1	DG5	H3'	2.10	2.84
1	DG5	H2'1	1	DG5	H8	1.92	2.60
1	DG5	H2'1	1	DG5	H3'	2.36	2.91
2	DC	H6	1	DG5	H8	5.11	6.75
2	DC	H6	1	DG5	H2'2	2.21	2.99
2	DC	H5	1	DG5	H8	3.65	4.93
2	DC	H5	1	DG5	H2'2	2.39	3.23
2	DC	H2'1	2	DC	H6	1.93	2.61
3	DT	M7	2	DC	H6	3.41	4.61
3	DT	M7	2	DC	H5	3.54	4.80
4	DA	H8	3	DT	H6	3.89	5.27
4	DA	H8	3	DT	H2'1	2.90	4.34
6	DC	H6	5	DG	H8	4.66	5.74
6	DC	H6	5	DG	H3'	3.48	5.95
6	DC	H5	5	DG	H8	3.30	4.46
6	DC	H2'2	6	DC	H6	2.79	3.77
6	DC	H2'1	6	DC	H6	2.22	2.90
6	DC	H2'1	6	DC	H5	3.09	4.65
7	DG	H8	6	DC	H6	3.55	5.21
7	DG	H8	6	DC	H2'1	2.45	3.83
8	DA	H8	7	DG	H8	4.48	6.24
8	DA	H2'2	8	DA	H8	2.86	3.70

9	DG	H8	8	DA	H8	3.23	4.37
9	DG	H8	8	DA	H3'	4.16	5.62
9	DG	H8	8	DA	H2'2	2.36	3.2
9	DG	H3'	9	DG	H1'	3.73	4.79
9	DG	H3'	9	DG	H8	4.10	5.64
9	DG	H2'1	9	DG	H3'	1.95	2.63
10	DT	H6	9	DG	H8	4.45	5.75
10	DT	H6	9	DG	H3'	4.76	6.72
10	DT	H6	9	DG	H2'1	3.00	3.98
10	DT	M7	9	DG	H8	2.95	3.99
10	DT	M7	9	DG	H3'	3.52	4.76
10	DT	M7	9	DG	H2'1	3.16	4.28
10	DT	H3'	10	DT	H6	2.91	3.93
10	DT	H2'1	10	DT	H6	1.84	2.48
11	DC	H6	10	DT	H6	3.88	5.26
11	DC	H6	10	DT	H2'1	3.25	4.39
11	DC	H5	10	DT	H3'	3.81	4.71
11	DC	H5	10	DT	H2'1	2.48	3.36
11	DC	H2'1	11	DC	H6	1.83	2.47
12	DC3	H5	11	DC	H6	4.12	5.58
12	DC3	H3'	12	DC3	H6	2.20	2.98
12	DC3	H3'	12	DC3	H5	5.07	6.85
12	DC3	R2’	12	DC3	H3'	2.15	2.91
13	DG5	H3'	13	DG5	H8	2.85	5.08
13	DG5	H2'2	13	DG5	H8	2.99	4.05
13	DG5	H2'1	13	DG5	H8	1.85	2.51
14	DG	H8	13	DG5	H3'	4.57	5.86

14	DG	H8	13	DG5	H2'1	3.35	4.10
14	DG	H3'	14	DG	H8	2.59	3.51
15	DA	H8	14	DG	H8	3.88	6.32
16	DC	H1'	15	DA	H2	2.94	3.98
16	DC	H6	15	DA	H8	3.41	4.61
16	DC	H6	15	DA	H3'	3.95	4.97
16	DC	H6	15	DA	H2'2	2.24	3.02
16	DC	H6	15	DA	H2'1	3.08	4.08
16	DC	H6	16	DC	H1'	2.96	3.84
16	DC	H5	15	DA	H8	3.37	4.55
16	DC	H5	15	DA	H2'2	2.91	3.93
16	DC	H5	15	DA	H2'1	3.19	4.31
16	DC	H3'	16	DC	H1'	3.79	5.19
16	DC	H3'	16	DC	H6	3.27	4.27
16	DC	H2'2	16	DC	H6	2.48	4.67
16	DC	H2'1	16	DC	H1'	2.19	2.97
16	DC	H2'1	16	DC	H6	2.47	3.39
16	DC	H2'1	16	DC	H5	2.60	4.30
17	DT	M7	16	DC	H1'	4.36	5.90
17	DT	M7	16	DC	H6	2.63	3.55
17	DT	M7	16	DC	H5	3.09	4.17
17	DT	M7	16	DC	H3'	3.10	4.20
17	DT	M7	16	DC	H2'2	2.93	3.97
17	DT	H2'1	17	DT	M7	3.52	4.76
18	DC	H5	17	DT	M7	3.75	5.07
18	DC	H5	17	DT	H2'1	2.75	3.71
18	DC	H2'1	18	DC	H5	3.33	4.29

19	DG	H8	18	DC	H6	4.13	5.49
20	DC	H6	19	DG	H8	3.50	4.74
20	DC	H5	19	DG	H8	2.81	3.81
20	DC	H2'2	20	DC	H5	4.66	6.00
20	DC	H2'1	20	DC	H5	3.35	4.47
21	DT	M7	20	DC	H5	2.73	3.69
21	DT	M7	20	DC	H3'	3.38	4.58
21	DT	M7	20	DC	H2'2	3.27	4.43
21	DT	M7	20	DC	H2'1	3.26	4.40
21	DT	H3'	21	DT	H6	2.96	4.00
21	DT	H2'1	21	DT	M7	3.20	4.34
22	DA	H8	21	DT	H6	3.71	5.01
22	DA	H8	21	DT	H3'	5.03	6.81
22	DA	H8	21	DT	H2'1	2.58	3.47
24	DC3	H6	23	DG	H3'	3.22	5.13
24	DC3	H6	23	DG	H2'2	2.30	3.12
24	DC3	H3'	24	DC3	H6	2.70	3.64
25	X	HB	25	X	HA1	2.17	2.93
25	X	HG1	25	X	HA1	2.22	2.88
25	X	HG1	25	X	HB	2.01	2.73
25	X	HG2	25	X	HB	2.06	2.78
27	TRP	HD1	25	X	HB	3.73	4.91
27	TRP	HD1	25	X	HG1	2.97	4.15
27	TRP	HD1	27	TRP	HB3	2.12	2.88
27	TRP	HD1	27	TRP	HB2	2.89	3.91
27	TRP	HZ2	25	X	HB	4.22	5.70
27	TRP	HE3	27	TRP	HB3	3.13	4.07

27	TRP	HE3	27	TRP	HB2	2.41	3.25
28	LYS	HG	28	LYS	HB2	2.80	3.86
1	DG5	H1'	1	DG5	H8	3.46	4.68
1	DG5	H1'	2	DC	H5	4.37	6.21
3	DT	H1'	3	DT	H6	3.34	4.52
3	DT	H1'	3	DT	H3'	3.19	4.31
3	DT	H1'	3	DT	H2'2	1.79	2.43
3	DT	H1'	3	DT	H2'1	2.42	3.08
2	DC	H1'	3	DT	M7	3.76	5.08
2	DC	H3'	3	DT	M7	3.28	4.44
2	DC	H2'2	3	DT	M7	2.78	4.04
5	DG	H1'	5	DG	H8	3.09	4.17
5	DG	H1'	5	DG	H3'	3.06	4.14
5	DG	H1'	6	DC	H5	4.26	5.48
5	DG	H2'2	6	DC	H6	2.29	3.09
5	DG	H2'2	6	DC	H5	2.51	3.39
5	DG	H2'1	6	DC	H6	2.83	3.83
6	DC	H1'	6	DC	H2'1	2.59	3.17
7	DG	H1'	7	DG	H3'	2.91	3.93
7	DG	H1'	8	DA	H8	2.78	3.76
8	DA	H1'	8	DA	H8	3.05	4.03
8	DA	H1'	8	DA	H3'	2.93	3.97
8	DA	H1'	8	DA	H2'2	2.07	2.79
8	DA	H1'	25	X	HB	4.50	5.50
8	DA	H2	9	DG	H1'	3.45	4.57
8	DA	H2	25	X	HA1	3.08	4.18
8	DA	H2	25	X	HB	3.05	4.13

8	DA	H2	27	TRP	HZ2	3.00	4.00
8	DA	H2	27	TRP	HH2	5.00	6.00
8	DA	H2'1	9	DG	H8	2.74	3.70
10	DT	H1'	10	DT	H6	3.42	4.62
10	DT	H1'	11	DC	H5	3.30	4.46
9	DG	H2'2	10	DT	M7	2.49	3.85
11	DC	H1'	12	DC3	H6	3.63	6.13
11	DC	H1'	15	DA	H2	3.31	4.49
11	DC	H3'	12	DC3	H6	4.35	5.89
11	DC	H3'	12	DC3	H5	3.90	5.18
12	DC3	H1'	12	DC3	H6	3.53	4.60
12	DC3	H1'	12	DC3	H3'	3.59	5.46
12	DC3	R2’	12	DC3	H1'	1.93	2.61
13	DG5	H1'	13	DG5	H8	2.94	3.98
13	DG5	H1'	13	DG5	H2'2	1.85	2.49
13	DG5	H1'	14	DG	H8	3.52	4.32
14	DG	H1'	14	DG	H8	2.87	3.87
14	DG	H1'	14	DG	H3'	2.98	3.92
15	DA	H1'	15	DA	H8	2.98	4.02
15	DA	H1'	15	DA	H3'	3.01	4.07
15	DA	H1'	15	DA	H2'2	2.02	2.74
15	DA	H1'	15	DA	H2'1	2.36	3.20
15	DA	H1'	16	DC	H6	2.66	3.60
15	DA	H1'	16	DC	H5	4.51	6.11
17	DT	H6	17	DT	H3'	2.86	3.88
17	DT	H6	18	DC	H5	2.98	4.02
18	DC	H1'	18	DC	H6	3.57	4.83

18	DC	H1'	18	DC	H2'2	1.93	2.61
18	DC	H1'	27	TRP	HZ2	3.08	4.18
18	DC	H1'	27	TRP	HH2	3.07	4.15
18	DC	H3'	19	DG	H8	5.01	6.79
19	DG	H1'	19	DG	H3'	3.10	4.08
19	DG	H1'	20	DC	H5	3.80	5.14
19	DG	H1'	25	X	HB	3.96	5.36
20	DC	H1'	20	DC	H3'	3.73	4.71
20	DC	H1'	20	DC	H2'2	1.86	2.52
20	DC	H1'	20	DC	H2'1	2.24	3.02
20	DC	H1'	21	DT	M7	3.55	4.81
21	DT	H1'	21	DT	H6	3.01	4.07
21	DT	H1'	21	DT	H2'2	1.74	2.36
23	DG	H1'	23	DG	H3'	3.77	4.77
23	DG	H1'	23	DG	H2'2	1.93	2.61
23	DG	H1'	24	DC3	H6	2.99	4.05
23	DG	H1'	24	DC3	H5	4.34	5.88
23	DG	H8	24	DC3	H6	3.96	4.88
23	DG	H8	24	DC3	H5	3.45	4.67
24	DC3	H1'	24	DC3	H6	3.12	4.22
24	DC3	H1'	24	DC3	H3'	3.33	4.51
25	X	HA2	25	X	HB	1.94	2.62
19	DG	H4'	26	LYS	HB3	2.63	3.57
19	DG	H4'	26	LYS	HG	3.43	4.65
27	TRP	HA	27	TRP	HB3	2.57	3.20
27	TRP	HA	27	TRP	HB2	1.92	2.60
27	TRP	HA	27	TRP	HZ3	4.42	5.98

27	TRP	HA	27	TRP	HE3	2.21	2.99
9	DG	H4'	27	TRP	HD1	2.52	4.86
9	DG	H5'1	27	TRP	HE3	4.24	5.74
28	LYS	HA	28	LYS	HB2	2.15	2.91
28	LYS	HA	28	LYS	HB3	1.99	2.69
28	LYS	HA	28	LYS	HG	3.08	4.18
29	LYS	HA	29	LYS	HB3	2.52	4.14
29	LYS	HA	29	LYS	HG	3.65	4.53
2	DC	H2'2	2	DC	H6	2.87	3.67
3	DT	H3'	3	DT	H6	3.03	4.09
3	DT	H2'2	3	DT	H6	2.57	3.33
3	DT	H2'2	3	DT	H3'	2.12	2.88
4	DA	H8	3	DT	H2'2	2.55	3.45
5	DG	H3'	5	DG	H8	3.92	4.80
7	DG	H8	6	DC	H2'2	2.51	3.39
7	DG	H3'	7	DG	H8	3.69	4.71
14	DG	H8	13	DG5	H2'2	2.33	3.15
14	DG	H2'2	14	DG	H8	2.67	4.01
14	DG	H2'1	14	DG	H8	1.76	2.38
17	DT	H2'1	17	DT	H6	1.70	2.30
18	DC	H6	17	DT	H2'2	2.47	3.26
18	DC	H3'	18	DC	H6	3.82	5.03
18	DC	H2'2	18	DC	H6	2.67	3.51
18	DC	H2'1	18	DC	H6	1.90	2.58
19	DG	H8	18	DC	H2'2	2.4	3.26
22	DA	H8	21	DT	H2'2	2.78	4.40
23	DG	H3'	23	DG	H8	3.11	4.13

26	LYS	HA	25	X	HG1	2.00	2.70
26	LYS	HA	25	X	HG2	2.40	3.14
26	LYS	HB2	26	LYS	HA	2.43	3.11
26	LYS	HB3	26	LYS	HA	2.00	2.46
26	LYS	HG	26	LYS	HB3	2.11	2.85
1	DG5	H2'1	2	DC	H6	2.65	3.81
1	DG5	H3'	2	DC	H5	3.85	5.21
2	DC	H1'	3	DT	H6	3.56	4.82
4	DA	H3'	5	DG	H8	4.53	5.68
4	DA	H2'2	5	DG	H8	2.24	3.04
5	DG	H1'	5	DG	H2'2	1.96	2.66
5	DG	H1'	6	DC	H6	3.71	4.79
6	DC	H1'	6	DC	H6	3.20	4.32
6	DC	H1'	6	DC	H2'2	1.98	2.68
6	DC	H1'	7	DG	H8	4.74	6.42
7	DG	H1'	7	DG	H8	3.33	4.51
8	DA	H3'	8	DA	H2'2	2.58	3.30
8	DA	H1'	8	DA	H2'1	2.58	3.48
9	DG	H3'	9	DG	H2'2	2.31	3.15
9	DG	H1'	9	DG	H2'1	2.29	3.11
9	DG	H8	9	DG	H2'1	2.00	2.70
10	DT	M7	10	DT	H2'1	3.76	4.97
10	DT	H1'	11	DC	H6	3.47	5.32
11	DC	H1'	11	DC	H6	3.37	4.55
11	DC	H1'	11	DC	H3'	3.80	5.14
11	DC	H1'	11	DC	H2'1	2.29	2.99
12	DC3	R2’	12	DC3	H6	2.37	3.21

13	DG5	H3'	13	DG5	H2'2	2.86	3.56
13	DG5	H3'	13	DG5	H2'1	1.92	2.60
13	DG5	H1'	13	DG5	H2'1	2.60	3.52
14	DG	H1'	14	DG	H2'2	1.91	2.59
14	DG	H1'	14	DG	H2'1	2.88	3.74
16	DC	H3'	16	DC	H2'2	2.57	3.47
16	DC	H1'	17	DT	H6	4.01	5.57
17	DT	H3'	17	DT	H2'2	2.11	2.79
18	DC	H1'	19	DG	H8	3.22	4.36
20	DC	H3'	20	DC	H2'2	2.74	3.78
21	DT	H3'	21	DT	H2'2	2.27	3.16
21	DT	H6	21	DT	H2'1	1.75	2.37
22	DA	H3'	23	DG	H8	4.42	5.64
22	DA	H2'2	23	DG	H8	2.22	3.00
24	DC3	H1'	24	DC3	H2'2	1.76	2.38
24	DC3	H1'	24	DC3	H2'1	2.90	3.92
24	DC3	H3'	24	DC3	H2'1	1.98	2.68
8	DA	H2	25	X	HA2	2.80	3.90
8	DA	H2	25	X	HG1	4.06	5.32
25	X	HA1	25	X	HG2	2.42	5.04
19	DG	H4'	26	LYS	HB2	2.08	2.82
28	LYS	HA	28	LYS	HD	3.79	5.87
2	DC	H3'	2	DC	H6	2.87	3.68
3	DT	H6	2	DC	H6	3.97	5.37
5	DG	H2'2	5	DG	H8	2.82	3.68
5	DG	H2'1	5	DG	H8	1.85	2.49
6	DC	H5	5	DG	H2'1	2.83	3.83

11	DC	H2'1	11	DC	H5	3.14	4.14
12	DC3	H6	11	DC	H2'2	2.34	3.16
12	DC3	H6	11	DC	H2'1	2.42	3.28
12	DC3	H5	11	DC	H2'1	3.21	4.41
12	DC3	R2’	12	DC3	H5	3.95	5.51
23	DG	H8	22	DA	H8	3.73	5.05
23	DG	H2'2	23	DG	H8	2.49	3.37
23	DG	H2'1	23	DG	H8	1.91	2.59
1	DG5	H1'	1	DG5	H2'1	2.53	3.05
1	DG5	H1'	2	DC	H6	2.53	3.43
2	DC	H1'	2	DC	H6	3.08	4.16
2	DC	H2'1	3	DT	M7	2.76	3.74
4	DA	H1'	4	DA	H2'2	1.86	2.52
4	DA	H1'	5	DG	H8	3.35	4.53
4	DA	H8	5	DG	H8	3.59	4.85
4	DA	H2'1	5	DG	H8	3.29	4.05
5	DG	H3'	5	DG	H2'2	2.12	2.80
5	DG	H3'	5	DG	H2'1	2.11	2.85
8	DA	H8	8	DA	H3'	3.18	4.22
9	DG	H1'	9	DG	H2'2	1.86	2.52
9	DG	H8	9	DG	H2'2	3.03	3.93
10	DT	H6	10	DT	H2'2	2.63	3.55
10	DT	H1'	10	DT	H2'1	2.31	3.03
10	DT	M7	11	DC	H5	3.55	4.81
11	DC	H6	11	DC	H3'	2.37	3.21
11	DC	H1'	11	DC	H2'2	1.79	2.41
14	DG	H3'	14	DG	H2'2	2.33	3.15

14	DG	H3'	14	DG	H2'1	2.21	2.99
16	DC	H2'1	17	DT	M7	3.19	4.31
17	DT	H1'	17	DT	H3'	3.02	4.08
17	DT	H2'1	18	DC	H6	2.73	3.38
17	DT	H2'2	18	DC	H5	3.49	4.73
21	DT	H1'	22	DA	H8	3.84	6.08
22	DA	H1'	22	DA	H2'2	1.80	2.44
22	DA	H1'	23	DG	H8	3.93	5.31
22	DA	H3'	22	DA	H2'2	2.25	2.93
22	DA	H2'1	23	DG	H8	3.02	4.15
23	DG	H3'	23	DG	H2'2	2.46	3.08
23	DG	H3'	23	DG	H2'1	2.19	2.97
25	X	HA2	25	X	HG2	2.59	3.91
27	TRP	HA	27	TRP	HD1	3.25	4.19
28	LYS	HB3	28	LYS	HG	2.78	3.76
29	LYS	HA	29	LYS	HB2	2.49	3.47
3	DT	H6	2	DC	H3'	4.25	5.51
21	DT	H6	20	DC	H2'2	2.32	3.14
22	DA	H2'1	22	DA	H3'	1.96	2.64
24	DC3	H2'2	24	DC3	H6	2.60	3.52
26	LYS	HB3	25	X	HG1	3.01	4.07
1	DG5	H1'	1	DG5	H3'	2.97	4.03
1	DG5	H2'1	2	DC	H5	2.52	3.40
2	DC	H1'	2	DC	H3'	3.33	4.51
2	DC	H2'2	3	DT	H6	2.21	2.99
4	DA	H1'	4	DA	H8	2.84	3.84
4	DA	H1'	4	DA	H3'	3.58	4.44

5	DG	H1'	5	DG	H2'1	2.21	2.99
8	DA	H8	8	DA	H2'1	2.06	2.78
8	DA	H3'	8	DA	H2'1	2.11	2.85
9	DG	H1'	9	DG	H8	3.84	4.78
9	DG	H2'2	10	DT	H6	2.14	2.90
10	DT	H1'	10	DT	H3'	3.08	4.18
10	DT	H1'	10	DT	H2'2	1.77	2.39
17	DT	H1'	17	DT	H6	2.86	3.76
17	DT	H3'	18	DC	H6	3.66	4.80
20	DC	H6	20	DC	H2'2	2.91	3.79
22	DA	H1'	22	DA	H8	2.90	3.82
22	DA	H1'	22	DA	H3'	3.17	4.29
23	DG	H1'	23	DG	H8	3.59	4.85
23	DG	H2'1	24	DC3	H6	2.81	3.69
23	DG	H2'2	24	DC3	H5	3.48	4.70
25	X	HA2	25	X	HG1	2.16	2.92
26	LYS	HG	26	LYS	HE	3.62	4.50
8	DA	H1'	27	TRP	HD1	2.74	3.70
9	DG	H5'1	27	TRP	HZ3	5.00	6.00
28	LYS	HG	28	LYS	HD	2.53	3.59
28	LYS	HG	28	LYS	HE	3.62	4.88
3	DT	H6	2	DC	H2'1	2.27	2.93
3	DT	H2'1	3	DT	H6	2.13	2.87
4	DA	H3'	4	DA	H8	2.98	4.18
4	DA	H2'2	4	DA	H8	2.75	3.47
4	DA	H2'2	4	DA	H3'	2.35	3.17
4	DA	H2'1	4	DA	H8	1.99	2.53

4	DA	H2'1	4	DA	H3'	2.22	3.29
8	DA	H8	7	DG	H2'2	2.58	3.50
8	DA	H8	7	DG	H2'1	3.26	4.40
11	DC	H6	10	DT	H2'2	2.13	2.75
11	DC	H5	10	DT	H6	3.30	4.46
11	DC	H5	10	DT	H2'2	2.74	3.50
11	DC	H2'2	11	DC	H6	2.84	3.62
12	DC3	H5	11	DC	H2'2	3.39	4.59
15	DA	H3'	15	DA	H8	2.87	4.13
15	DA	H2'2	15	DA	H8	2.71	3.57
15	DA	H2'2	15	DA	H3'	2.09	2.83
15	DA	H2'1	15	DA	H8	2.20	2.96
15	DA	H2'1	15	DA	H3'	2.30	2.88
17	DT	H6	16	DC	H2'2	2.73	3.69
17	DT	H6	16	DC	H2'1	2.23	3.03
17	DT	H2'2	17	DT	H6	2.75	3.61
18	DC	H2'2	18	DC	H3'	2.05	2.77
18	DC	H2'1	18	DC	H3'	2.17	2.93
20	DC	H6	19	DG	H2'2	2.69	3.71
20	DC	H6	19	DG	H2'1	2.88	3.90
20	DC	H5	19	DG	H2'2	3.14	4.26
20	DC	H5	19	DG	H2'1	3.25	4.39
20	DC	H3'	20	DC	H6	3.15	3.85
20	DC	H2'1	20	DC	H6	2.17	3.15
20	DC	H2'1	20	DC	H3'	1.92	2.60
21	DT	H6	20	DC	H2'1	3.02	3.90
21	DT	M7	20	DC	H6	2.59	3.51

21	DT	H2'1	21	DT	H3'	1.86	2.52
24	DC3	H5	23	DG	H2'1	4.17	5.65
24	DC3	H2'1	24	DC3	H5	3.50	4.74
26	LYS	HG	26	LYS	HA	2.19	2.97
26	LYS	HD	26	LYS	HA	3.47	4.69
26	LYS	HD	26	LYS	HG	2.52	3.40
26	LYS	HE	26	LYS	HD	2.50	3.50
27	TRP	HZ2	25	X	HA2	3.17	4.29
27	TRP	HZ2	25	X	HA1	3.82	5.10
1	DG5	H1'	1	DG5	H2'2	1.86	2.52
2	DC	H1'	2	DC	H2'2	2.00	2.62
2	DC	H1'	2	DC	H2'1	2.42	3.28
2	DC	H5	2	DC	H2'2	4.28	5.62
2	DC	H5	2	DC	H2'1	3.26	4.30
2	DC	H3'	2	DC	H2'2	2.38	3.12
2	DC	H3'	2	DC	H2'1	2.24	2.92
3	DT	H3'	3	DT	H2'1	2.15	2.63
3	DT	H1'	4	DA	H8	2.81	3.73
4	DA	H1'	4	DA	H2'1	2.23	3.01
6	DC	H1'	6	DC	H3'	3.26	6.02
7	DG	H1'	7	DG	H2'2	2.58	3.50
7	DG	H1'	7	DG	H2'1	2.41	3.25
7	DG	H8	7	DG	H2'2	2.56	3.58
7	DG	H8	7	DG	H2'1	1.92	2.60
7	DG	H3'	7	DG	H2'2	2.09	2.75
7	DG	H3'	7	DG	H2'1	2.32	3.10
8	DA	H1'	9	DG	H8	2.83	3.52

8	DA	H1'	25	X	HA2	3.00	4.00
8	DA	H1'	25	X	HA1	3.38	4.96
9	DG	H1'	10	DT	H6	3.32	4.22
9	DG	H1'	27	TRP	HZ2	3.30	4.46
10	DT	H3'	10	DT	H2'2	2.07	2.81
10	DT	H3'	10	DT	H2'1	1.90	2.56
11	DC	H3'	11	DC	H2'2	2.14	2.90
11	DC	H3'	11	DC	H2'1	2.04	2.76
14	DG	H1'	15	DA	H8	3.47	4.69
14	DG	H2'2	15	DA	H8	2.00	2.70
14	DG	H2'1	15	DA	H8	2.25	3.05
16	DC	H1'	16	DC	H2'2	1.82	2.46
16	DC	H3'	16	DC	H2'1	1.96	2.66
17	DT	H1'	17	DT	H2'2	1.84	2.5
17	DT	H1'	17	DT	H2'1	2.22	3.00
17	DT	H1'	18	DC	H6	3.19	4.25
17	DT	H3'	17	DT	H2'1	1.80	2.44
18	DC	H1'	18	DC	H3'	3.52	4.76
18	DC	H1'	18	DC	H2'1	2.71	3.35
19	DG	H1'	19	DG	H2'2	2.37	3.21
19	DG	H1'	19	DG	H2'1	2.56	3.46
19	DG	H1'	20	DC	H6	3.07	4.15
19	DG	H8	19	DG	H2'2	2.76	3.50
19	DG	H8	19	DG	H2'1	1.98	2.86
19	DG	H3'	19	DG	H2'2	2.45	3.31
19	DG	H3'	19	DG	H2'1	2.13	3.06
20	DC	H1'	20	DC	H6	2.68	3.62

20	DC	H1'	21	DT	H6	3.59	4.85
21	DT	H1'	21	DT	H3'	3.72	5.04
21	DT	H1'	21	DT	H2'1	2.68	3.62
22	DA	H8	22	DA	H3'	2.95	3.91
22	DA	H8	22	DA	H2'2	3.17	4.14
22	DA	H8	22	DA	H2'1	1.90	2.50
22	DA	H1'	22	DA	H2'1	2.32	3.04
23	DG	H1'	23	DG	H2'1	2.33	3.01
24	DC3	H6	24	DC3	H2'1	1.73	2.35
25	X	HB	26	LYS	HA	3.00	4.00
26	LYS	HB2	26	LYS	HG	2.16	2.92
19	DG	H4'	26	LYS	HD	3.59	4.85
9	DG	H5'1	27	TRP	HD1	3.01	3.77
9	DG	H5'2	27	TRP	HD1	3.00	4.00
18	DC	H5'1	27	TRP	HH2	2.91	3.93
18	DC	H4'	27	TRP	HH2	3.14	4.26
29	LYS	HG	29	LYS	HE	3.62	5.12
29	LYS	HD	29	LYS	HE	2.50	3.50
27	TRP	HN	26	LYS	HG	2.50	3.50
27	TRP	HN	26	LYS	HB2	3.50	4.50
27	TRP	HN	26	LYS	HB3	3.50	4.50
27	TRP	HN	27	TRP	HB2	3.00	4.00
27	TRP	HN	27	TRP	HB3	2.50	3.50
27	TRP	HN	26	LYS	HA	2.00	3.00
27	TRP	HN	27	TRP	HA	2.50	3.50
27	TRP	HN	27	TRP	HD1	3.50	4.50
27	TRP	HN	27	TRP	HE3	4.00	5.00

28	LYS	HN	26	LYS	HG	4.00	5.00
28	LYS	HN	28	LYS	HG	3.00	4.00
28	LYS	HN	28	LYS	HD	3.50	4.50
28	LYS	HN	28	LYS	HB2	3.00	4.00
28	LYS	HN	28	LYS	HB3	3.00	4.00
28	LYS	HN	27	TRP	HB2	3.50	4.50
28	LYS	HN	27	TRP	HB3	3.50	4.50
28	LYS	HN	19	DG	H4'	4.00	5.00
28	LYS	HN	28	LYS	HA	2.50	3.50
28	LYS	HN	27	TRP	HA	2.00	3.00
28	LYS	HN	27	TRP	HE3	3.50	4.50
28	LYS	HN	29	LYS	HN	3.50	4.50
29	LYS	HN	29	LYS	HG	2.50	3.50
29	LYS	HN	28	LYS	HG	3.00	4.00
29	LYS	HN	29	LYS	HD	3.00	4.00
29	LYS	HN	29	LYS	HB2	2.50	3.50
29	LYS	HN	28	LYS	HG	3.00	4.00
29	LYS	HN	28	LYS	HB2	3.00	4.00
29	LYS	HN	29	LYS	HB3	3.00	4.00
29	LYS	HN	28	LYS	HB3	2.00	3.00
29	LYS	HN	29	LYS	HA	2.50	3.50
29	LYS	HN	28	LYS	HA	2.00	3.00

$^{1}X^{25}$ is the trimethylene tether; amino acid protons were named based upon the AMBER nomenclature; M7 is the thymine methyl; R2' is the deoxyribose geminal H2'(") protons.

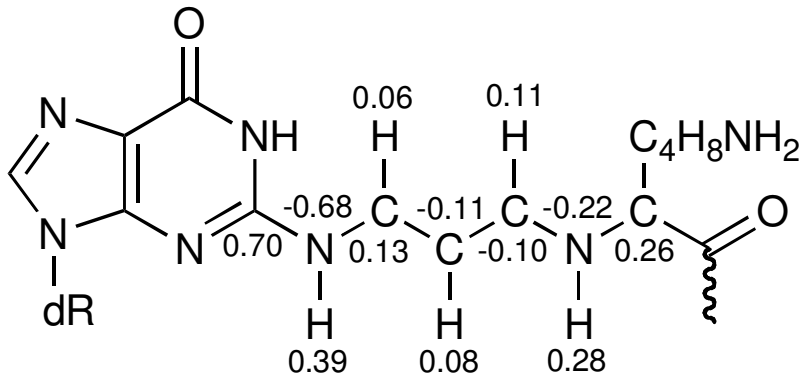
Table S4. Backbone Torsion Angles of the Refined Structure.[1]

Nucleotide	Alpha	Beta	Gamma	Delta	Epsilon	Zeta	Chi
G^{1}			52.6	141.1	-177.2	-95.7	-118.8
C^{2}	-69.0	-178.8	54.0	122.0	-171.2	-88.1	-120.0
T^{3}	-65.8	167.9	54.8	124.1	-176.6	-94.1	-109.8
A^{4}	-70.0	178.7	48.8	120.2	-177.9	-94.3	-118.9
G^{5}	-65.5	-179.0	48.7	118.5	-173.4	-99.1	-121.1
C^{6}	-70.4	177.3	55.0	113.2	-166.8	-85.9	-123.9
G^{7}	-67.9	170.9	52.5	134.9	-168.6	-130.4	-100.4
A^{8}	-64.9	176.1	54.1	144.5	178.9	-93.1	-101.2
G^{9}	-66.5	171.7	55.8	120.1	-174.6	-98.6	-134.6
T^{10}	-68.5	-173.8	50.7	123.7	-171.9	-98.4	-123.1
C^{11}	-73.1	175.7	56.9	111.0	-172.0	-83.5	-119.8
C^{12}	-68.1	166.6	50.1	88.4			-131.1
G^{13}			-174.4	151.0	-175.6	-91.7	-92.2
G^{14}	-69.5	162.5	57.5	97.0	-178.3	-90.8	-124.8
A^{15}	-63.0	173.4	59.6	139.9	-179.6	-89.7	-103.7
C^{16}	-63.9	163.5	62.8	104.0	-170.9	-85.0	-137.1
T^{17}	-66.3	178.4	52.1	116.1	-167.0	-86.0	-123.5
C^{18}	-69.8	166.9	55.0	115.6	-172.1	-107.5	-114.8
G^{19}	-69.3	-171.9	47.9	143.6	179.5	-90.9	-98.5
C^{20}	-67.3	170.4	58.8	103.9	-174.6	-88.4	-128.3
T^{21}	-65.3	170.0	56.3	113.6	-168.2	-84.9	-125.6
A^{22}	-70.3	172.5	50.2	99.0	-174.0	-92.3	-129.4
G^{23}	-65.9	179.8	51.2	133.2	-174.4	-90.1	-106.3
C^{24}	-65.9	166.8	56.5	108.2			-123.1

[1]alpha: O3'(i-1)-P-O5'-C5'; beta: P-O5'-C5'-C4'; gamma: O5'-C5'-C4'-C3'; delta: C5'-C4'-C3'-

O3'; epsilon: C4'-C3'-O3'-P(i+1); zeta: C3'-O3'-P(i+1)-O5'(i+1); chi for pyrimidines: O4'-C1'-N1-C2; chi for purines: O4'-C1'-N9-C4.

Figure S1. Partial charges for the trimethylene tether obtained from DFT calculations.



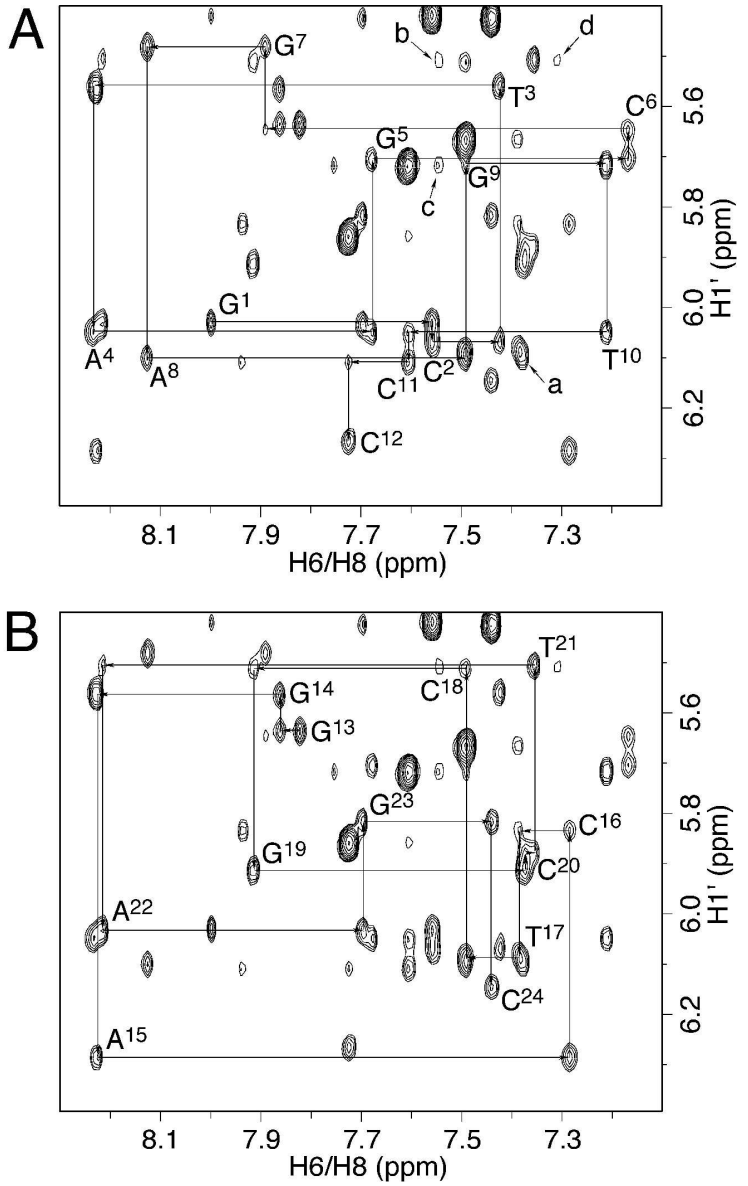


Figure S2. NOE connectivity of nucleobase H6/H8 protons to deoxyribose H1' protons. (A) KWKK-conjugated strand; (B) Complementary strand. The complete connectivity suggested the DNA-KWKK conjugate maintained an ordered right-handed helix. The C^6 H1'→ G^7 H8 NOE was weak, indicating a structural perturbation at the conjugated G^7 nucleobase. The additional cross-peaks were assigned as: a, W^{27} H2→A^8 H1'; b, W^{27} H7→C^{18} H1'; c, W^{27} H7→G^9 H1'; d, W^{27} H6→C^{18} H1'. The NOESY data were collected at 250 ms mixing time.

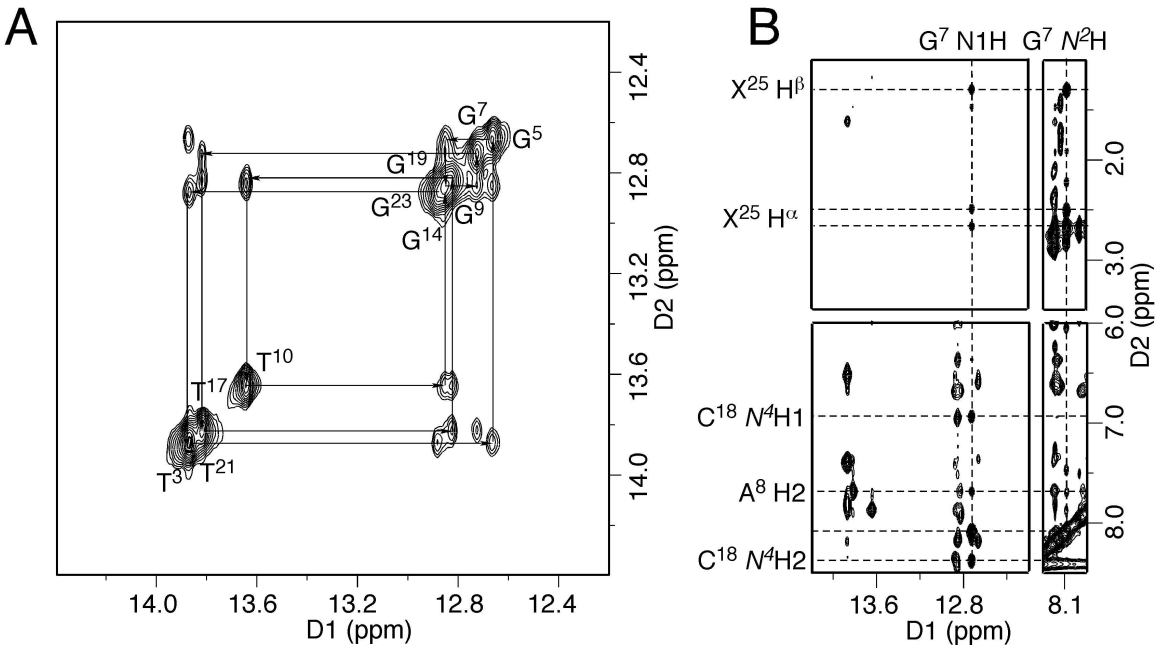
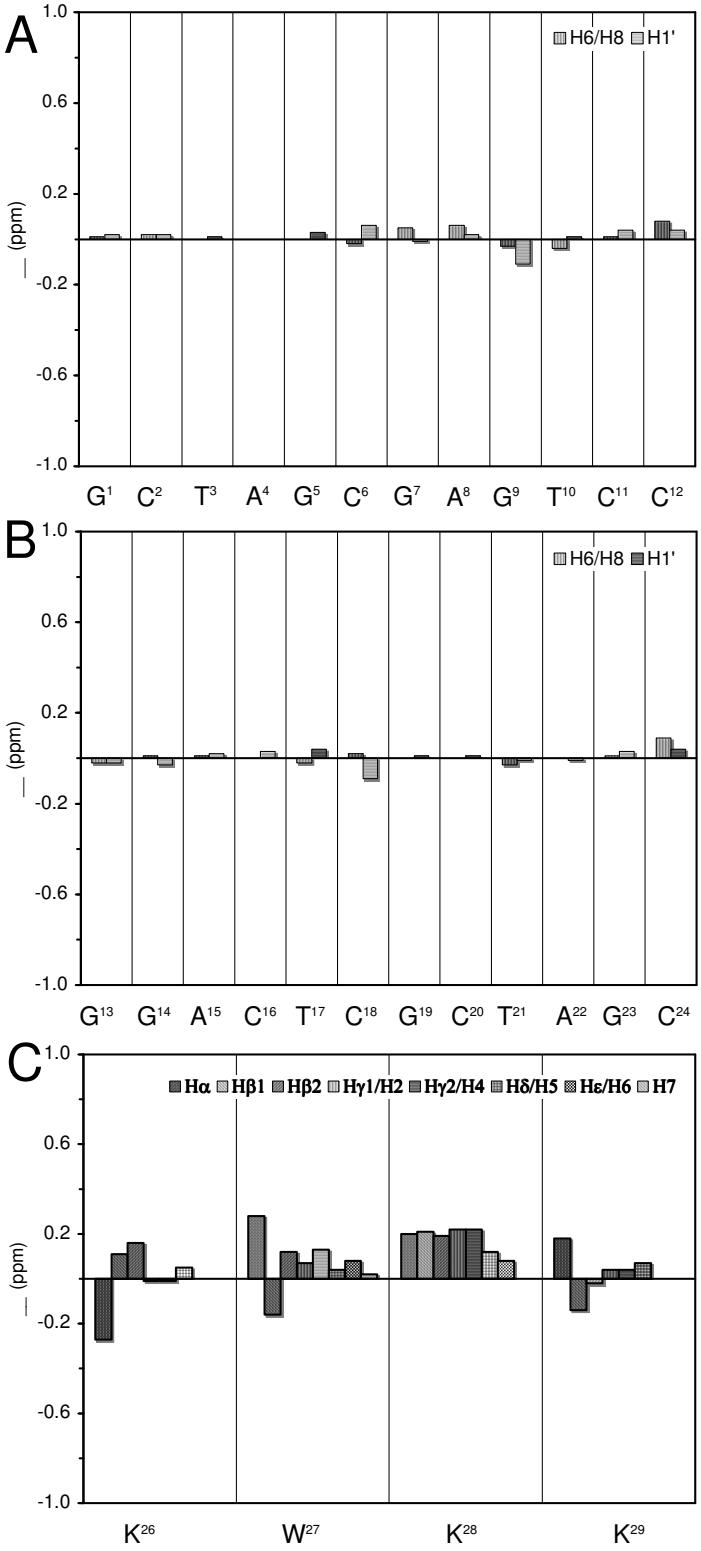


Figure S3. Assignment of nucleotide exchangeable protons. (A) NOE connectivity of the nucleobase imino protons. (B) NOEs observed for the imino and amino protons of the conjugated nucleotide G^7. The G^7 N^2H exocyclic amino proton was observed, indicating it was shielded from solvent. The NOESY data were collected at 250 ms mixing time.

Figure S4. Chemical shift perturbations of the DNA-peptide conjugate. (A) KWKK-conjugated strand; (B) Complementary strand; (C) Peptide.



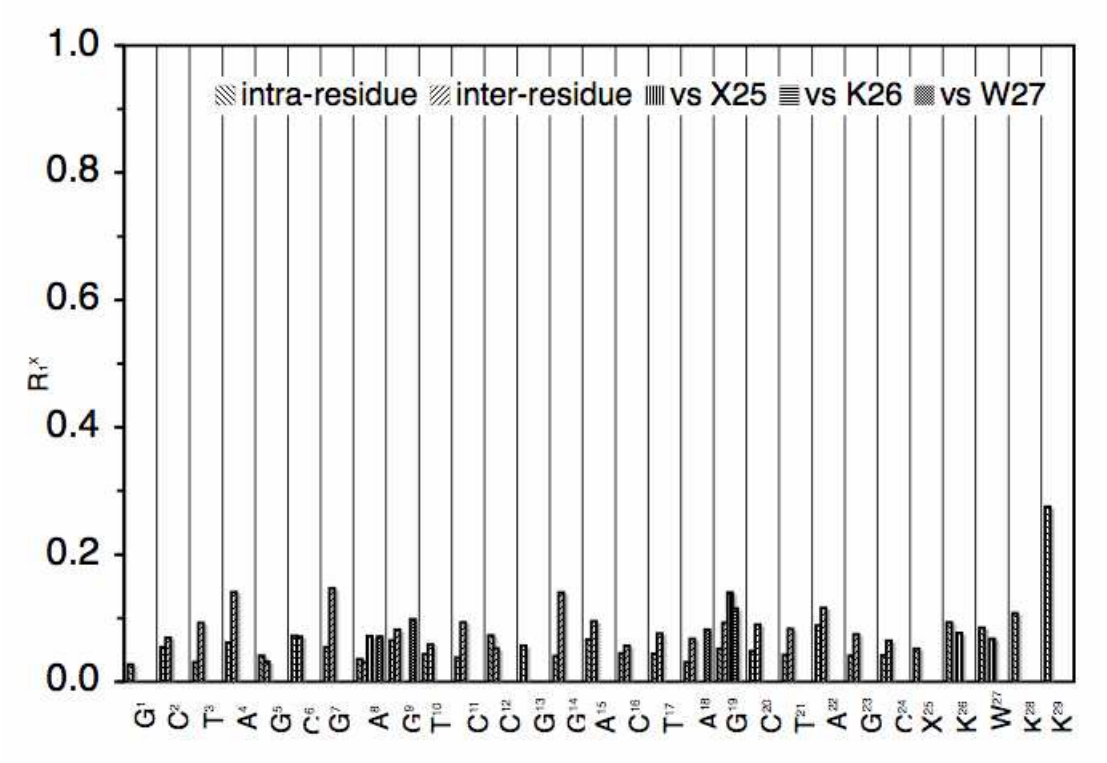


Figure S5. Sixth root CORMA residuals (R_1^x) of the DNA-KWKK conjugate.