

1/14

Figure 1

	SEQ ID NO:	Name	Sequences (5'-3')	Structure ^a	Binding ^b
RNA	4	TERC18	GGGUUGCGGAGGGUGGGC	Parallel	+
	5	12-nt TER	UAGGGUUAGGGU	Parallel	+
	6	10-nt TER	GGGUUAGGGU	Parallel	+
DNA	7	T95_2T	TTGGGTGGGTGGGTGGGT	Parallel	+
	8	Pu24T	TGA GGG TGG TGA GGG TGG GGA	Parallel	+
	9	CEB1	AGGGGGGAGGGAGGGTGG	Parallel	+
	10	CEB25	AAGGGTGGGTGTAAGTGTGGGTGGGT	Parallel	+
	11	93del	GGGGTGGGAGGAGGGT	Parallel	+
	12	HT1	TTGGGTAGGGTTAGGGTTAGGGA	Non-Parallel	-
	13	Htelo1	TAGGGTTAGGGTTAGGGTTAGGG	Non-Parallel	-
	14	Htelo2	TAGGGTTAGGGTTAGGGTTAGGGTT	Non-Parallel	-
	15	Htelo3	GGGTAGGGTTAGGGTTAGGGT	Non-Parallel	-
	16	Htelo4	AGGGCTAGGGCTAGGGCTAGGG	Non-Parallel	-
	17	DX	CGCGAATTCGCG	Duplex	-
	18	ST95	ACCCACCCACCCACCCAAAGATCCGA A AGGATCUTTGGGTGGGTGGGTGGGT	Stem-loop	-

^a Structures formation were monitored by NMR^b A negative binding is considered when the dissociation constant (K_d) is larger than 10 μ M.

2/14

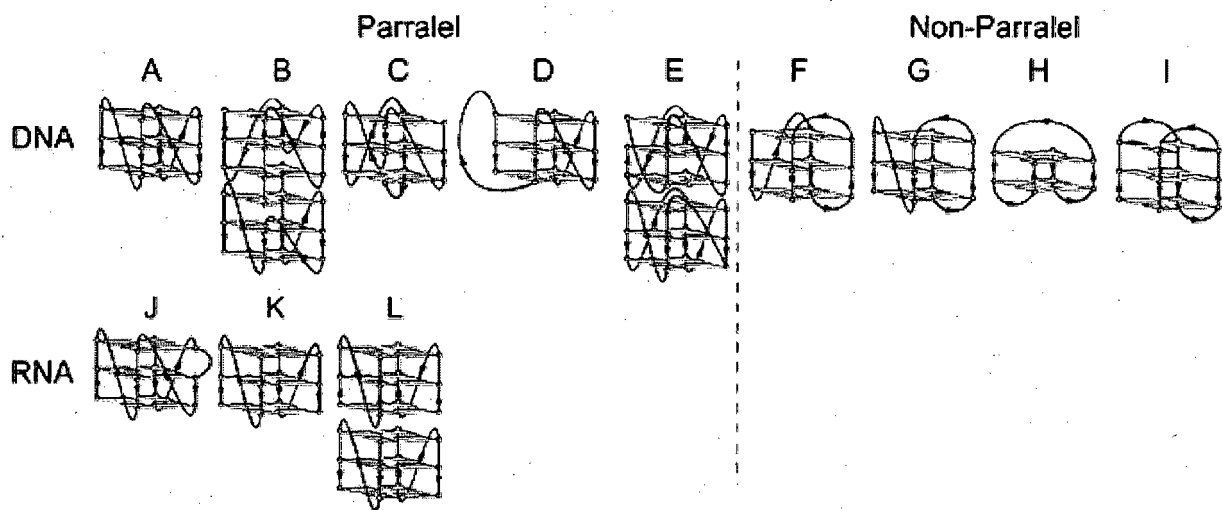
Figure 2

SEQ ID NO:	Name	Sequences (N_{term} - C_{term})	Binding ^a
19	Rhan55	SMHPGHLKGREIGMWYAKKQGQKNKEAERQERAVVHMDERREEQIVQLINSVQAK	+
20	Rhan29	HPGHLKGREIGMWYAKKQGQKNKEAERQE	+
21	Rhan23	HPGHLKGREIGMWYAKKQGQKNK	+
22	Rhan20	HPGHLKGREIGMWYAKKQGQ	+
23	Rhan18	HPGHLKGREIGMWYAKKQ	+
24	Rhan18sm	SMHPGHLKGREIGMWYAKKQ	+
1	Rhan16	HPGHLKGREIGMWYAK	+
25	Rhan14	HPGHLKGREIGMWY	-
26	Rhan12	HPGHLKGREIGM	-
27	Rhan5	HPGHL	-
28	Rhan9	KGREIGMWY	-
29	Rhan15'	KGREIGMWYAKKQGQ	-
30	Rhan20m1	HPGLHLKIRELMWYAKKQGQ	-
31	Rhan20m2	HPGHLKGREIGMAA $\bar{A}$ AKKQGQ	-

^a A negative binding is considered when the dissociation constant (K_d) is larger than 10 μ M

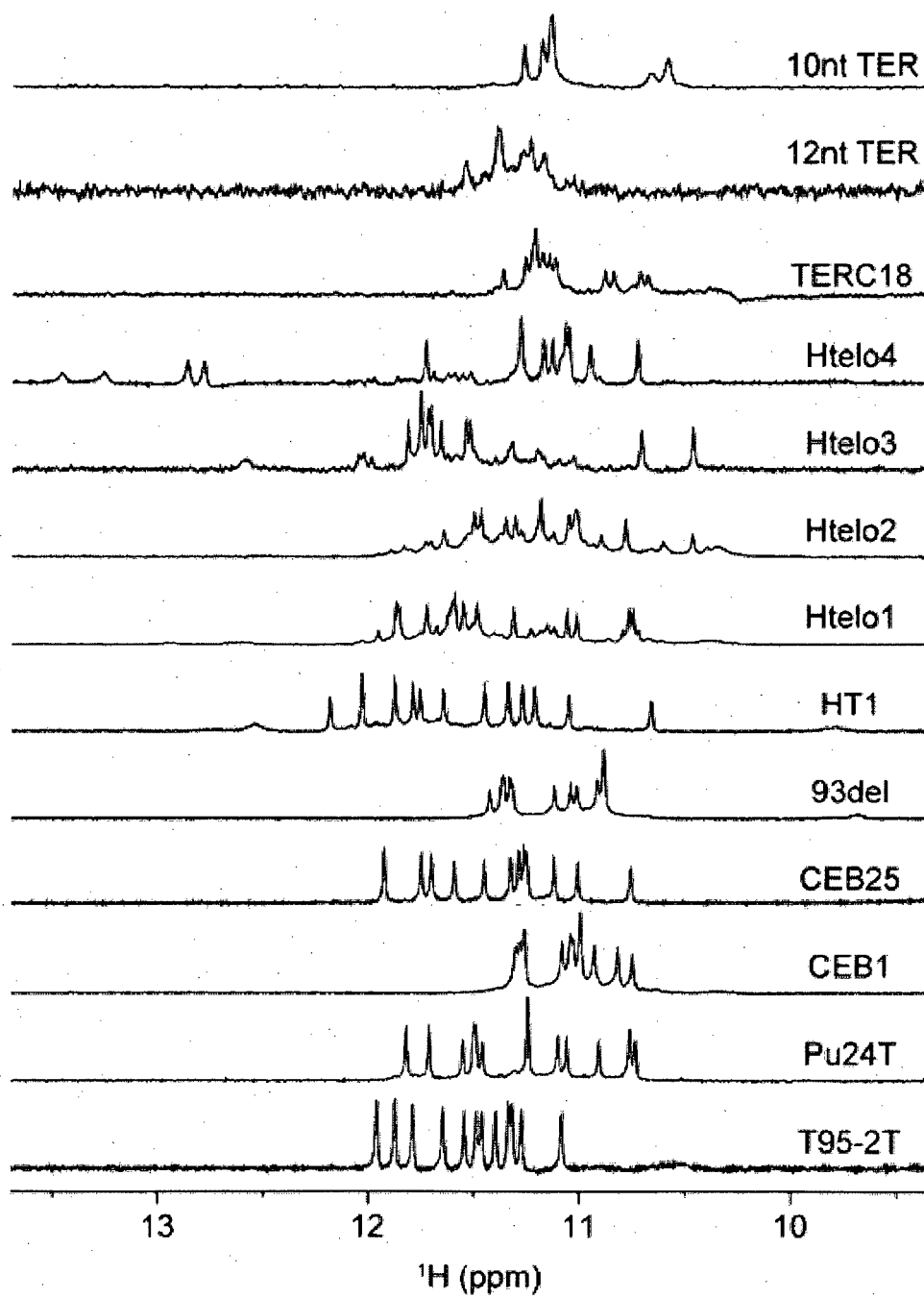
3/14

Figure 3



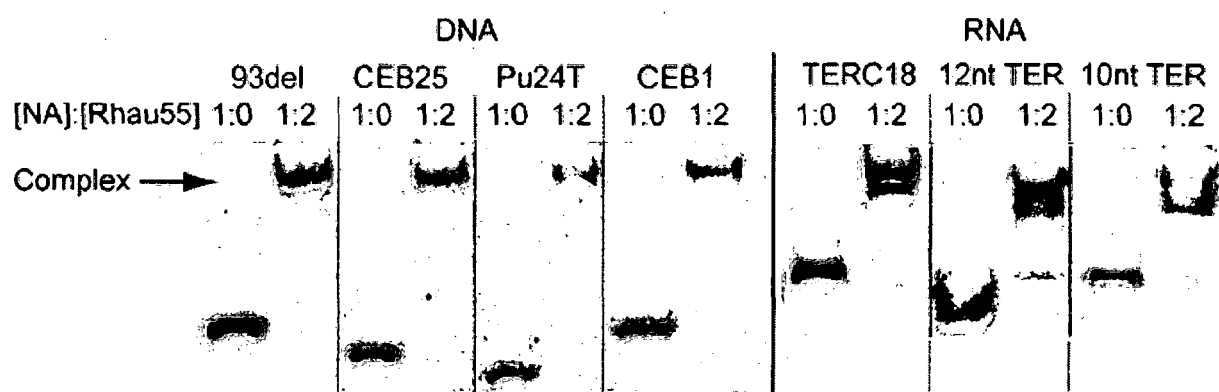
4/14

Figure 4



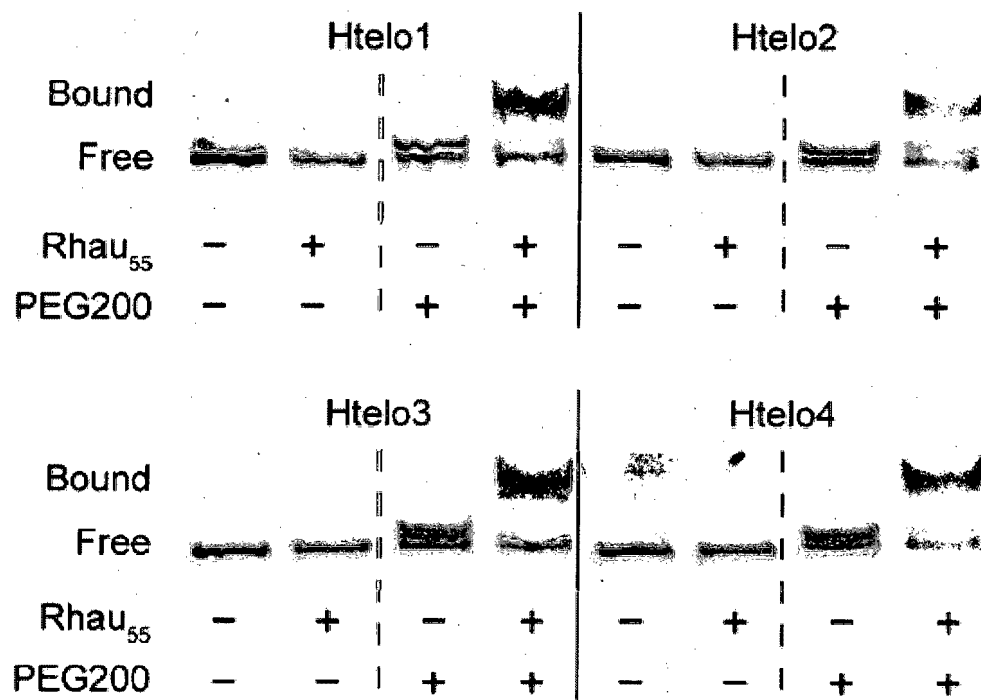
5/14

Figure 5



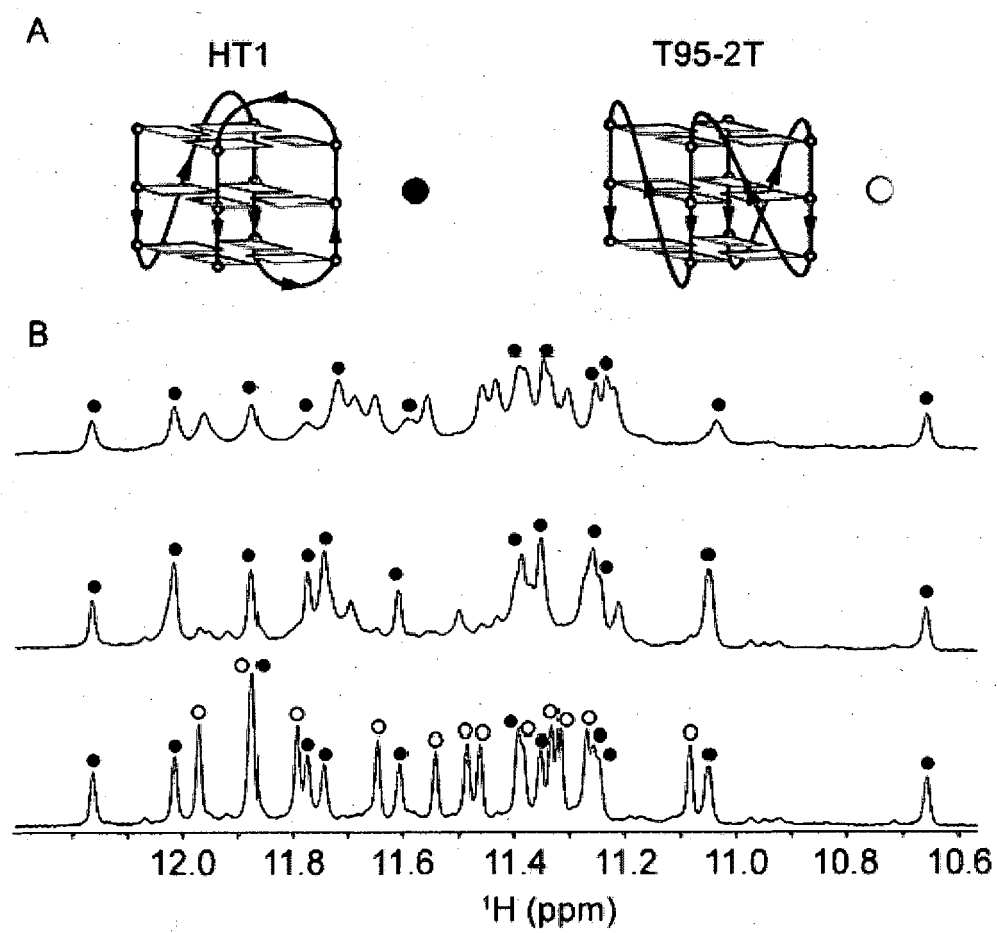
6/14

Figure 6



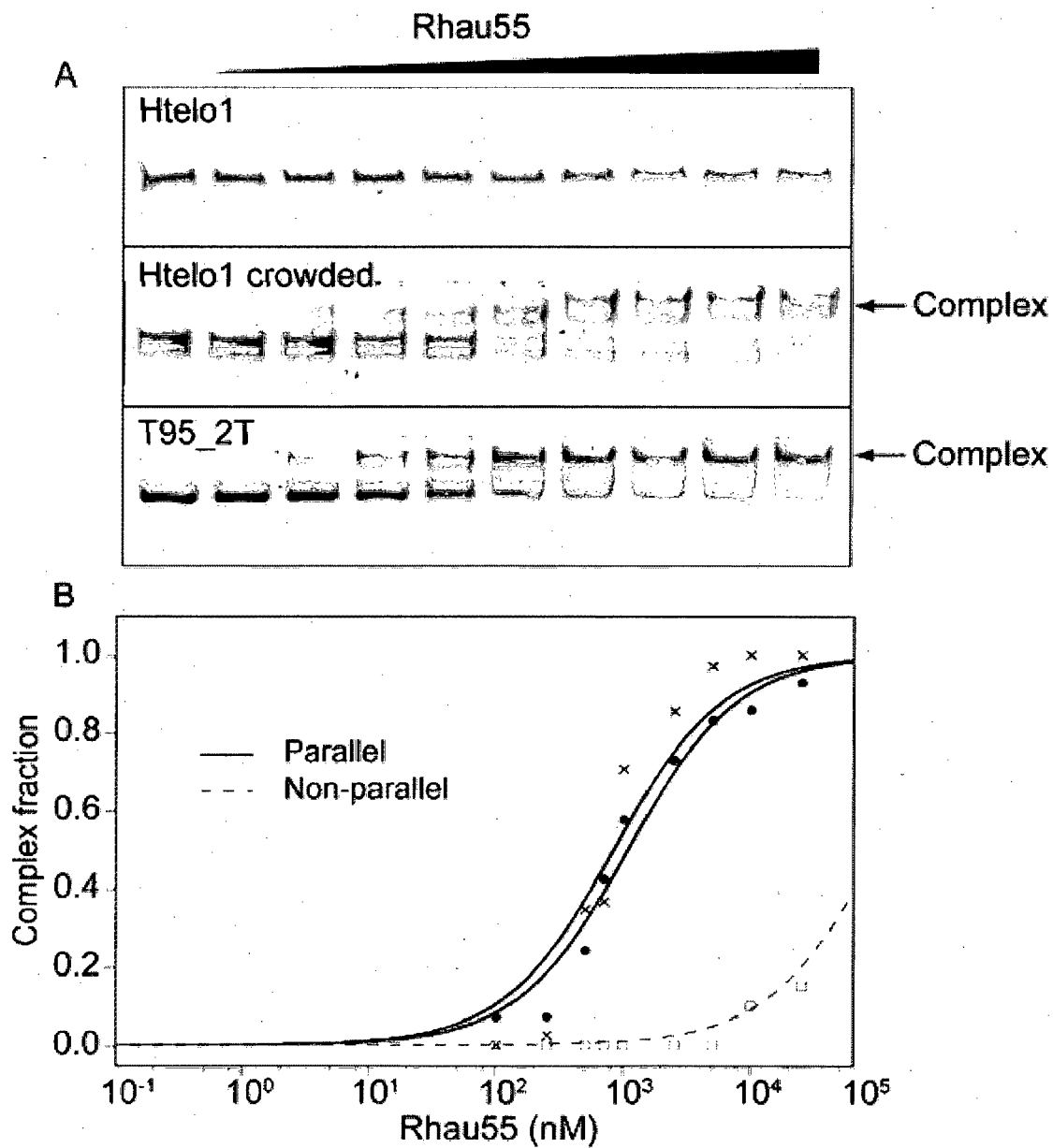
7/14

Figure 7



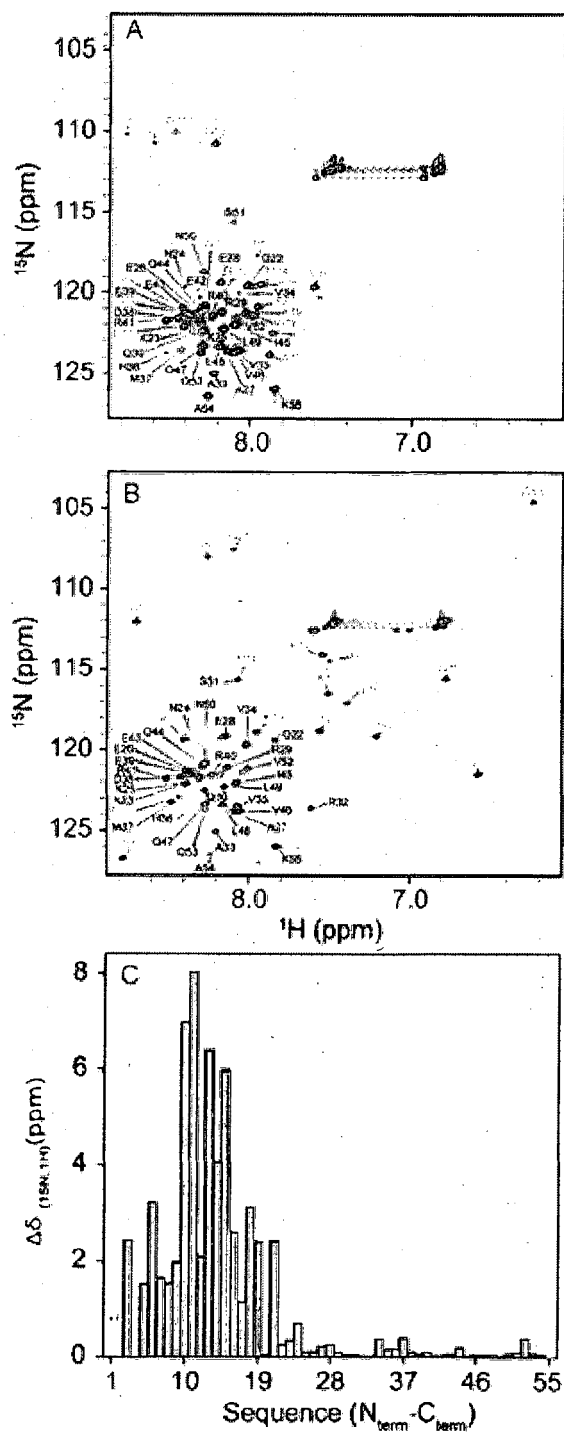
8/14

Figure 8



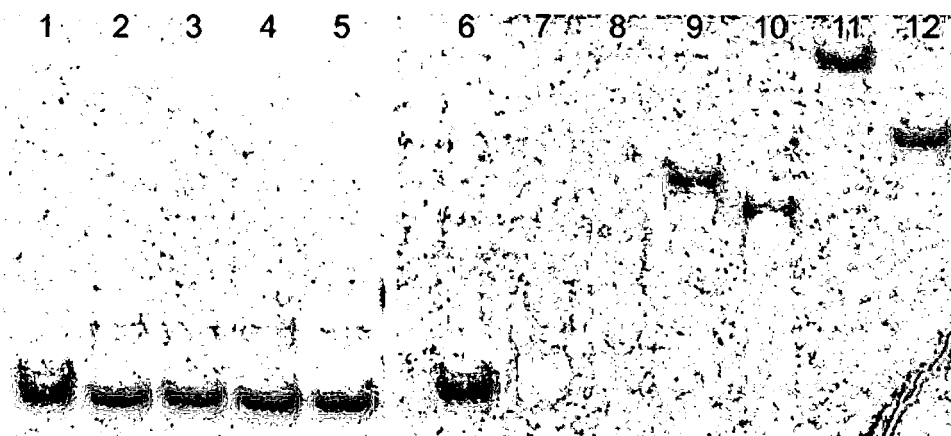
9/14

Figure 9



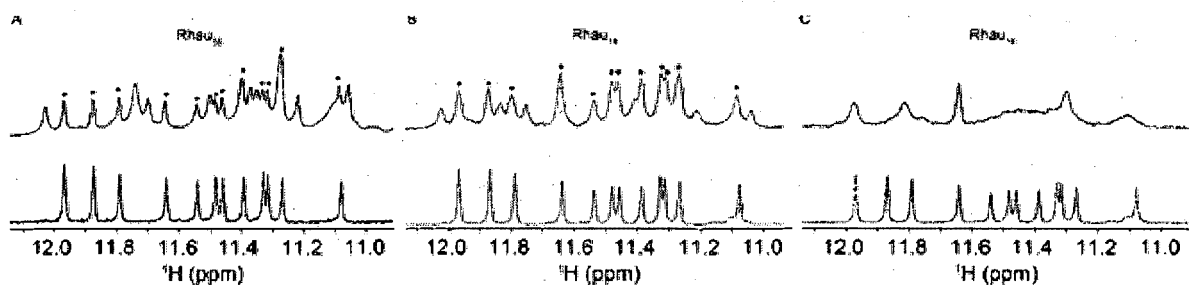
10/14

Figure 10



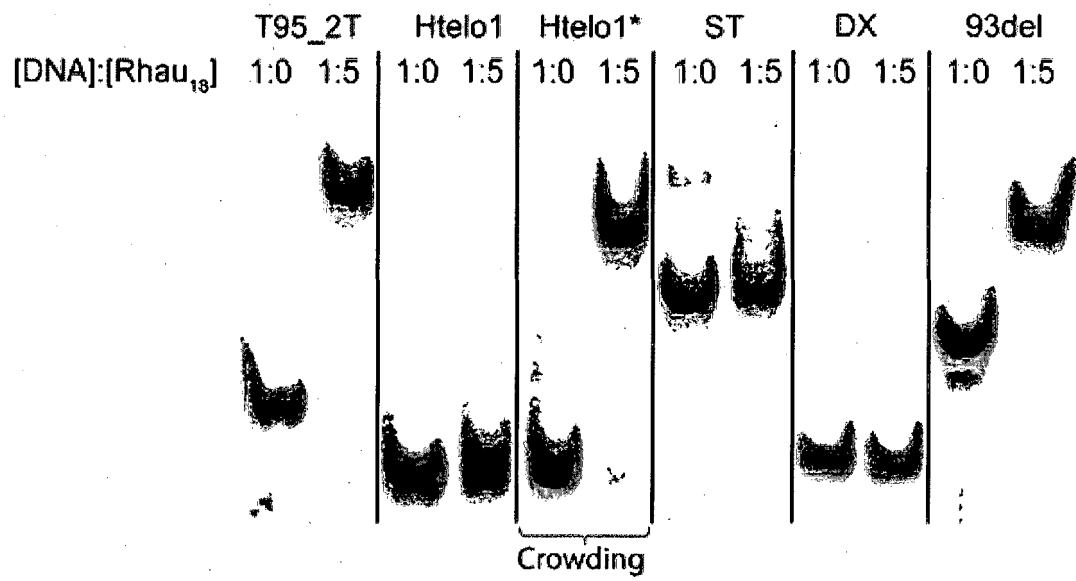
11/14

Figure 11



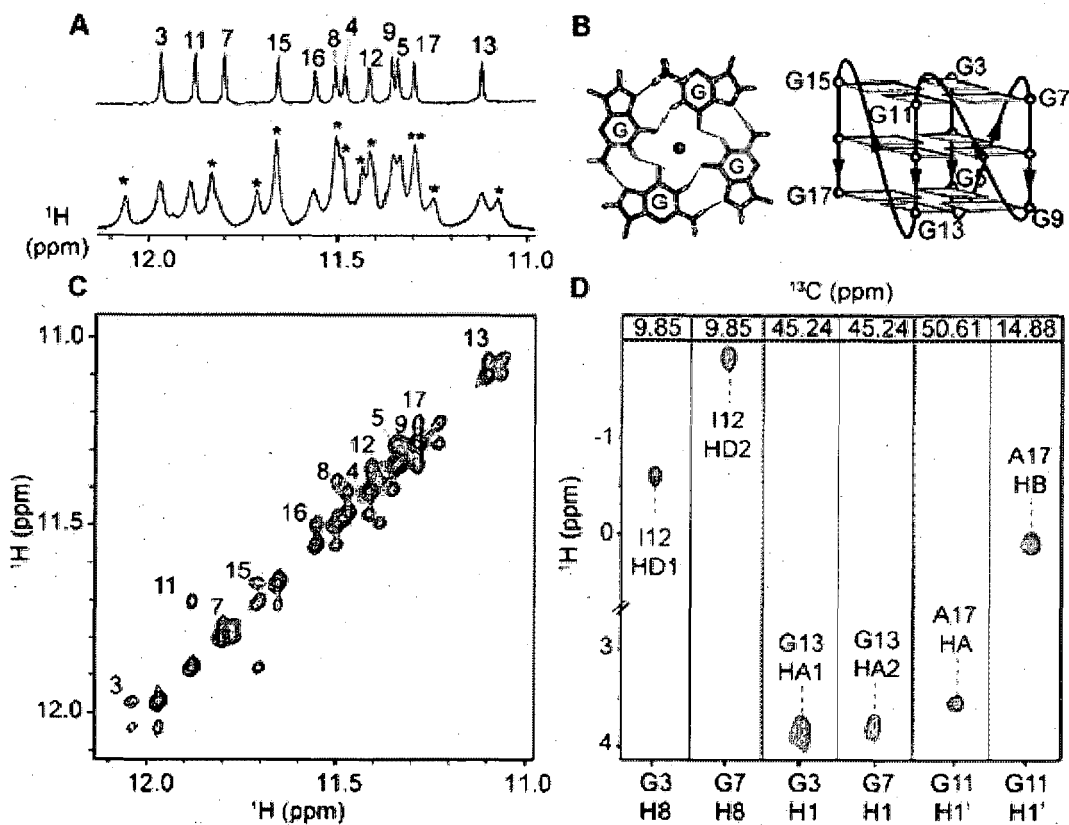
12/14

Figure 12



13/14

Figure 13



14/14

Figure 14

