Table S1. NMR and refinement statistics for complexes

	Peptide	RNA
NMR distance and dihedral constraints		
Distance restraints		
Total NOE	1162	1336
Intra-residue	294	436
Inter-residue	868	900
Sequential (|i-j| = 1)	406	548
Non-sequential (|i-j| > 1)	462	352
Hydrogen bonds		80
Peptide–RNA intermolecular	476	
Total dihedral angle restraints		84
RNA		
Sugar pucker		70
Backbone		14
Structure statistics		
Violations (mean and s.d.)		
Distance constraints (Å)	0.107 ± 0.00	
Dihedral angle constraints (°)	1.18 ± 0.06	
Max. dihedral angle violation (°)	5.0	
Max. distance constraint violation (Å)	0.51	
Deviations from idealized geometry		
Bond lengths (Å)	0.02 ± 0.00	
Bond angles (°)	1.84 ± 0.00	
Impropers (°)	1.87 ± 0.01	
Average pairwise r.m.s.d.* (Å)		
Peptide		
Heavy except residues 12	0.68 ± 0.20	
Backbone except residues 12	0.22 ± 0.06	
RNA		
All RNA heavy		0.59 ± 0.10
Complex		
Peptide except residues 12 and RNA	0.63 ± 0.09	

*Pairwise r.m.s.d. was calculated among 10 refined structures.

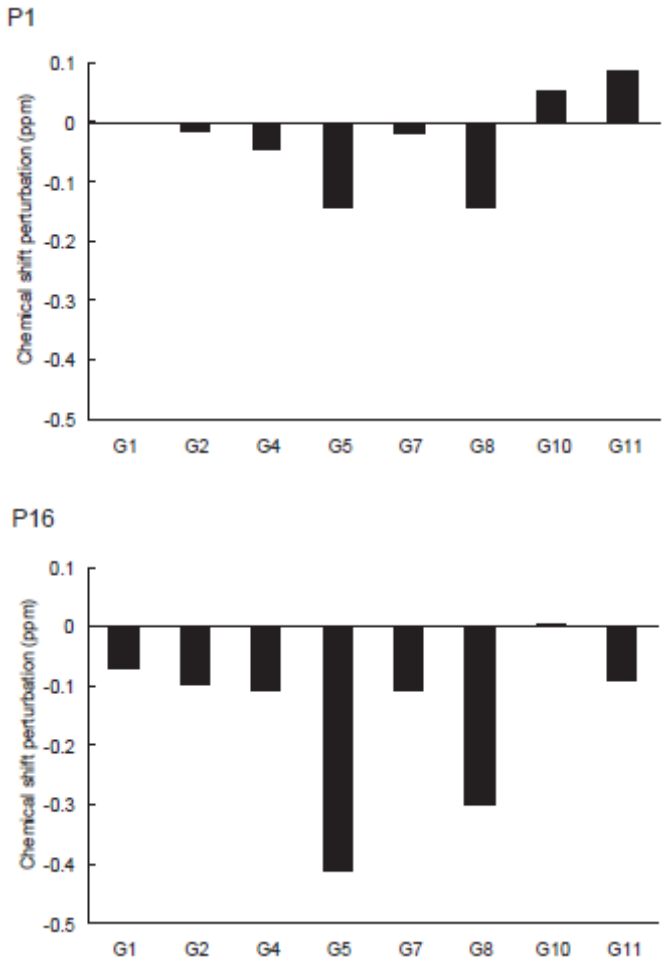

Figure S1. Chemical shift perturbation of R12 with the addition of either P1 or P16. Chemical shift perturbation observed for each imino proton of R12 on binding of either P1 (upper) or P16 (lower).

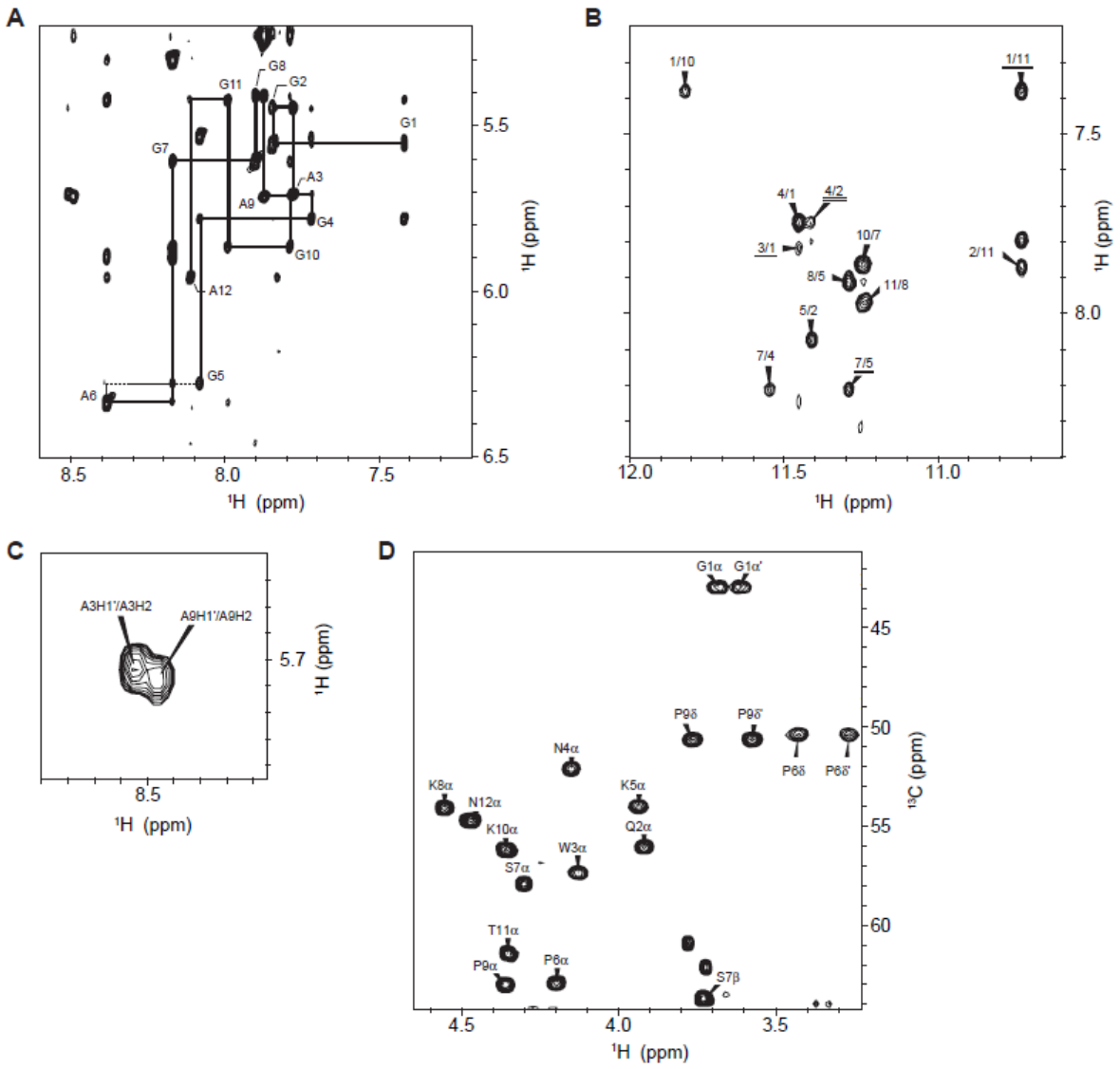

Figure S2. Analysis of NMR spectra of the R12:P16 complex. (**A**) The finger print region of the NOESY spectrum for R12. The H1' (i-1)-H8(i)-H1'(i) connectivities are traced, intraresidue cross peaks being denoted by residue numbers. (**B**) Imino-H8 NOESY cross peaks for R12. The cross peaks as to G:A base pairs are underlined, and those between the tetrad and hexad planes are double-underlined, respectively. (**C**) Intermolecular A3H2-A3H1' and A9H2-A9H1' NOESY cross peaks confirming the dimeric architecture of R12. (**D**) Hα-Cα and Proline Hδ-Cδ correlation peaks of P16 in the ^{1}H-^{13}C HSQC spectrum.