Table S1. Data Collection and Refinement Statistics, Related to Figure 1

	hAgo1-endoRNA	**hAgo1-let-7**
Data Collection		
Space group	$P2_1$	$P2_1$
Cell dimensions		
a, *b*, *c* (Å)	70.47, 98.63, 73.21	70.39, 97.73, 72.7
α, β, γ (°)	90.0, 110.96, 90.0	90.0, 110.89, 90.0
Wavelength (Å)	1.075	1.075
Resolution (Å)[a]	50.0-1.75 (1.8-1.75)	50.0-2.1 (2.16-2.1)
*R*merge (%)	5.5 (42.2)	4.1 (32.0)
$I/\sigma(I)$	12.63 (2.55)	16.9 (2.88)
Completeness (%)	98.08 (88.12)	94.41 (66.83)
Redundancy	3.1 (2.2)	3.0 (1.7)
Refinement		
Resolution (Å)	32.9-1.75	40.56-2.1
No. reflections	91605	50618
*R*work / *R*free (%)	17.2/20.2	17.4/21.7
No. atoms (non-hydrogen)	7179	7204
Protein	6475	6580
RNA	234	257
Water	470	367
<*B*-factors> (Å^2)		
Protein	30.0	37.77
RNA	45.7	41.1
Water	33.0	35.19
r.m.s. deviations		
Bond lengths (Å)	0.007	0.009
Bond angles (°)	1.070	1.164
MolProbity Statistics		
All atom clashscore	1.2	2.63
Poor rotamers (%)	0.42	0.28
Ramachandran Outliers (%)	0	0.25
Ramachandran Favored (%)	98.48	97.4
MolProbity score	0.84	1.17