Supplemental Table 1. Observed and predicted masses of 2006 interacting peptides analyzed using MS. MC corresponds to number of missed cleavages by trypsin.

Observed Mass	Predicted Mass	Position	#MC	Sequence
1390.55	1390.74	245-256	0	NYQLELALPAMK
2538.87	2538.40	271-292	3	TFVSLLICEHHLKKFPQGQK GK
1809.69	1809.95	293-307	0	VVFFANQIPVYEQQK
1162.43	1162.59	308-316	1	SVFSKYFER
2179.89	2180.19	395-418	0	LGGSSGPLPQVIGLTASVGV GDA
1390.55	1390.76	430-443	0	LCASLDASVIATVK
1853.72	1853.98	444-458	0	HNLEELEQVVYKPQK
2325.82	2325.31	462-480	4	KVESRISDKFKYIIAQLMR
1725.74	1725.97	467-480	2	ISDKFKYIIAQLMR
2470.01	2470.34	467-487	3	ISDKFKYIIAQLMRDTESLA K
1007.43	1007.57	473-480	0	YIIAQLMR
2252.79	2252.23	473-491	3	YIIAQLMRDTESLAKRICK
1329.50	1329.68	492-502	0	DLENLSQIQNR
1983.74	1984.02	503-518	1	EFGTQKYEQWIVTVQK
1220.51	1220.68	537-546	0	ALFLYTSHLR
1348.58	1348.77	537-547	1	ALFLYTSHLRK
1961.71	1961.98	560-575	2	MKDALDYLKDFFSNVR
1592.54	1592.76	576-589	0	AAGFDEIEQDLTQR
2125.72	2126.00	576-593	1	AAGFDEIEQDLTQRFEEK
1060.41	1060.56	594-602	0	LQELESVSR
1924.60	1925.06	636-652	2	TRALVDALKNWIEGNPK
1301.61	1301.79	653-664	0	LSFLKPGILTGR
1486.65	1486.91	653-666	1	LSFLKPGILTGRGK
1301.61	1301.73	724-734	3	MIQTRGRGRAR
1264.45	1264.63	768-777	0	LQTWDEAVFR
2621.02	2621.38	768-788	2	LQTWDEAVFREKILHIQTHE K
1118.47	1118.63	780-788	0	ILHIQTHEK
1028.38	1028.52	852-859	1	QFSSFEKR
947.47	946.56	881-888	0	TFEIPVIK
2252.79	2252.08	908-925	2	WKDFHFEKIPFDPAEMSK

sFig. 1. Sequence and predicted secondary structures of RNAs used for RIG-I assay. 3-css27 is a 27-nt RNA with three 5' phosphates and annealing two strands of 27 bases generated dsR27. Css27 is predicted by mfold to have minimally stable secondary structure. The sequence of HCV sgR and pIC are not shown. HCV sgR is an in vitro transcribed 9 kb long HCV subgenomic replicon RNA, pIC is poly(I:C) of heterogeneous length, pIC115 and pIC25 is poly(I:C) of 11-5 and 25-bp, respectively.

sFig. 2. Gel filtration profiles of the monomers and dimers of R-HR in complex with dsRNA of 24-bp. The black line represents the elution profile of R-HR while the grey line represents a sample with a 2:1 molar mix of R-HR with the ligand.

sFig. 3. Sample spreads for the particles used in the single particle reconstructions of R-HR, R-HR dimer with dsRNA, and R-HR dimer with 2006. Class averages and Fourier shell correlation for each set are shown at the bottom.

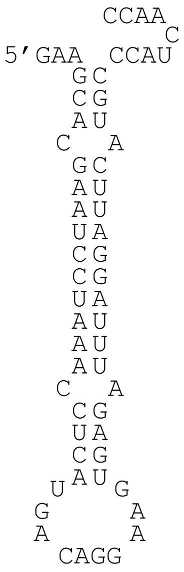
sFig. 4. Dimensions of the monomers of R-HR and the dimers with dsRNA of 24-bp and 2006. The rods indicate the dimension for which the measurements were made.

Supplemental Fig. 1

3P-css27: PPP-GGUGCAGAUGAACUUCAGGGUCAGCUU

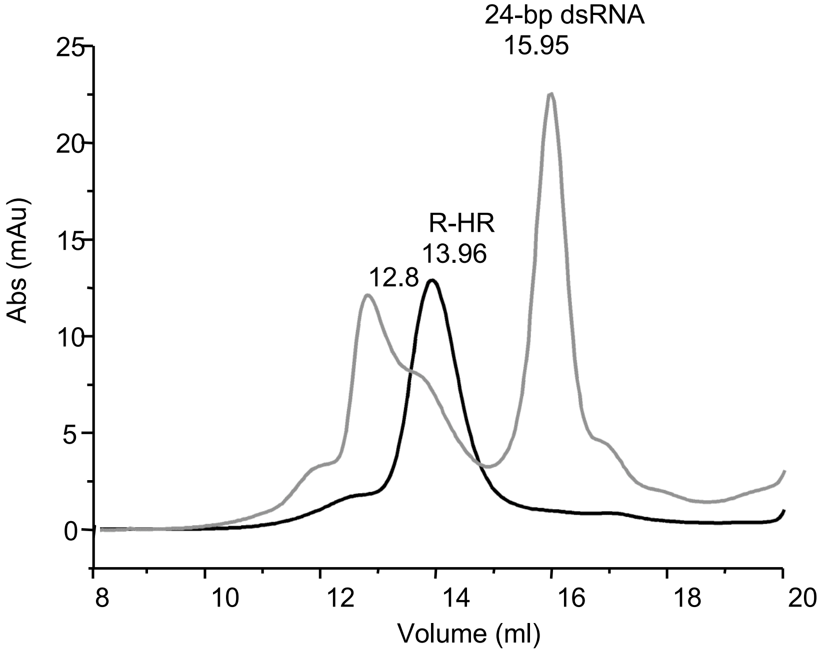
css27: GGUGCAGAUGAACUUCAGGGUCAGCUU

dsR27: AAGCUGACCCUGAAGUUCAUCUGCACC
UUCGACUGGGACUUCAAGUAGACGUGG

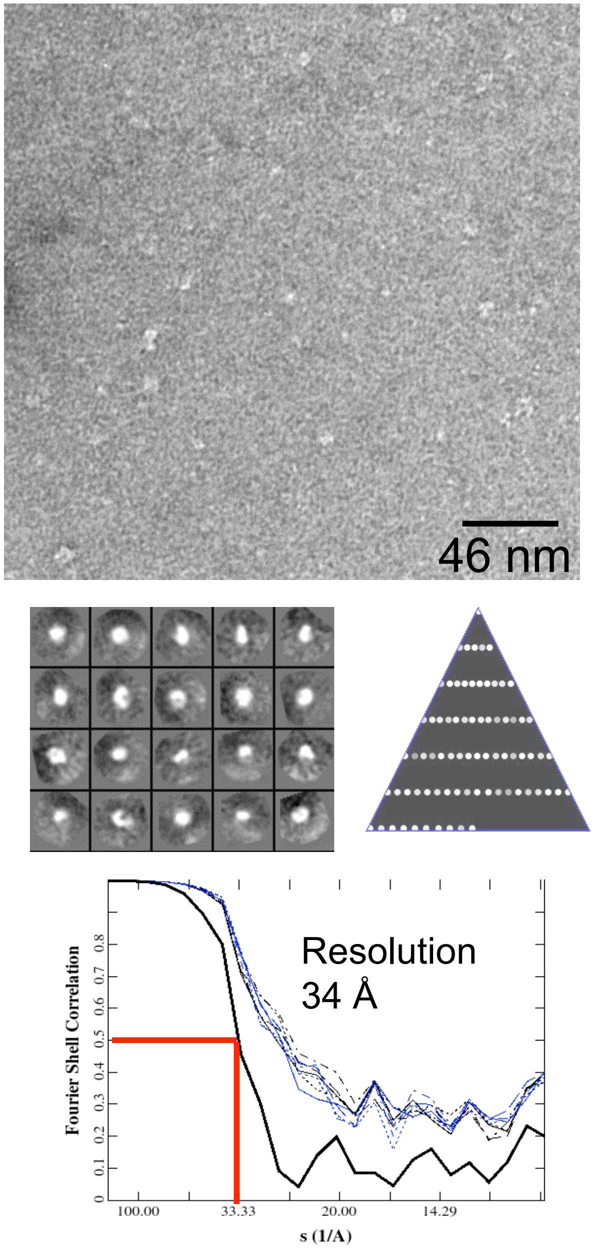


shRNA9

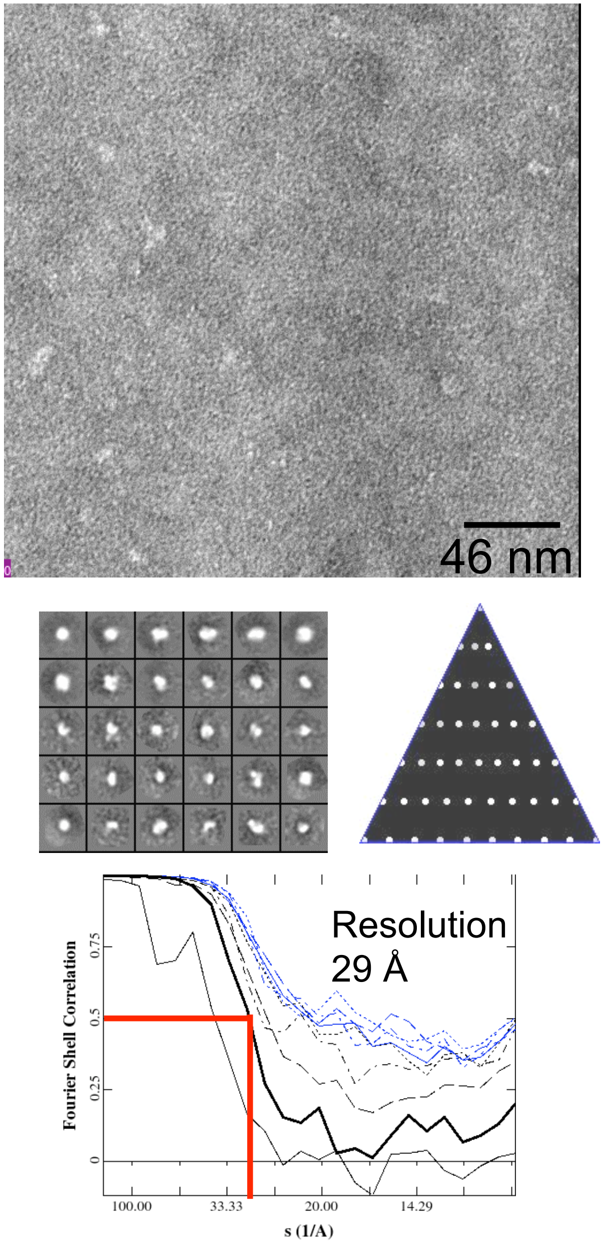
Supplemental Fig. 2



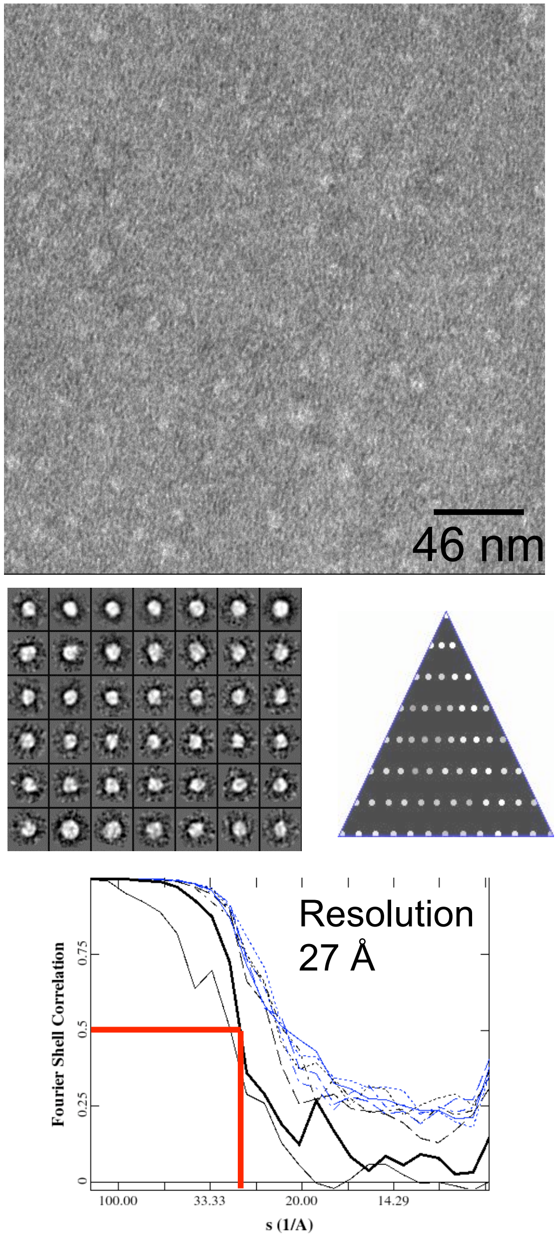
Supplemental Fig. 3



R-HR reconstruction

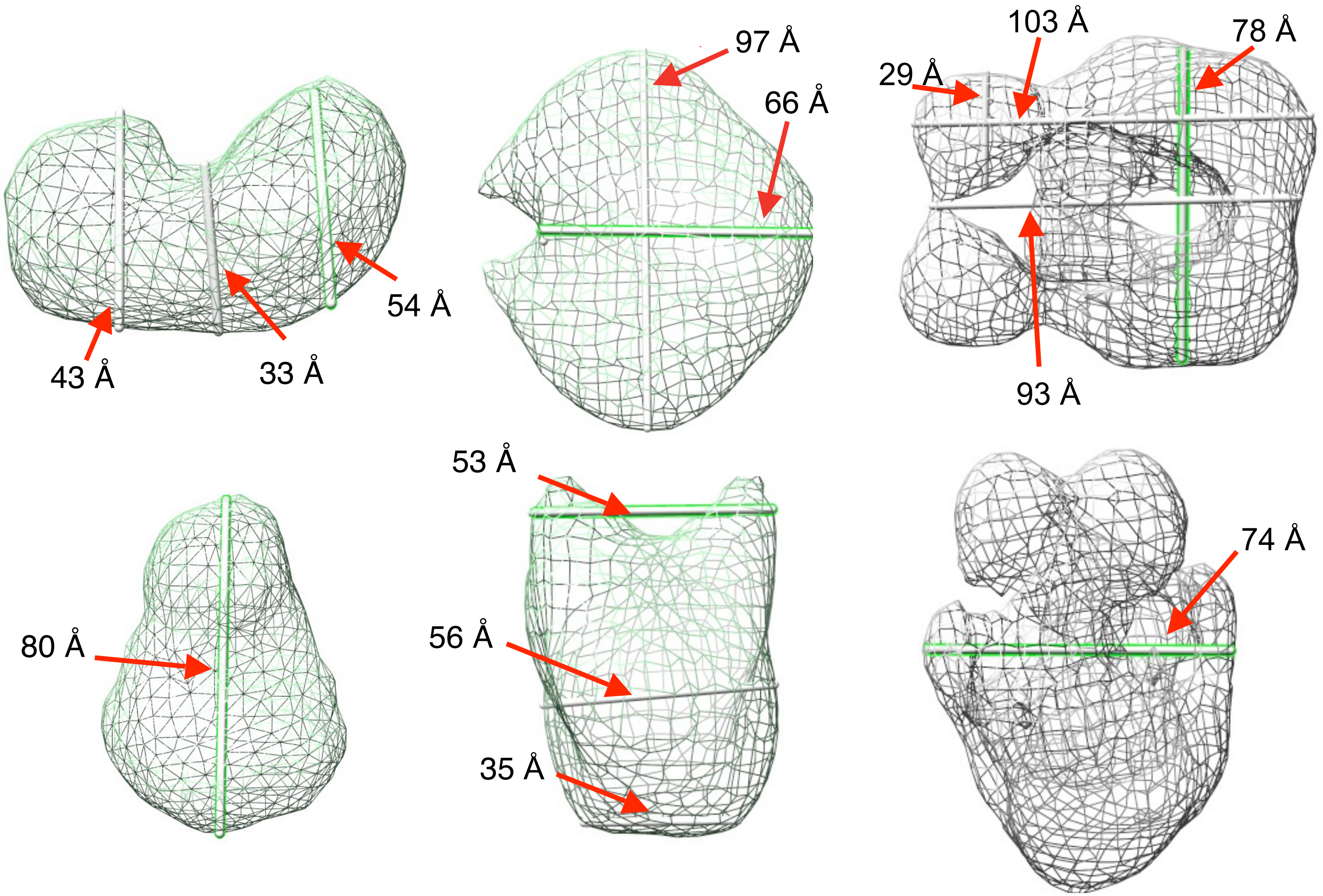


R-HR dimer complexed with a 24-bp dsRNA



R-HR dimer complex with 2006

Supplemental Fig. 4



R-HR monomer

R-HR dimer + 24 bp dsRNA)

R-HR dimer + 2006)