

Supplementary Table S1. Binding energy and its components for ORF1p in complex with PolyU, PolyA and L1RNA

Energy Component (kCal)	PolyU	PolyA	L1RNA
ΔE_{vdW}	-363.82	-361.33	-378.25
ΔE_{elec}	-3201.45	-3289.11	-3250.78
ΔE_{pb}	3054.83	3144	3114.25
E_{npolar}	-258.11	-255.32	-260.31
$\Delta E_{\text{elec}} + \Delta E_{\text{pb}}$	-146.62	-145.11	-136.53
$\Delta E_{\text{vdW}} + E_{\text{npolar}} + E_{\text{disper}}$	-94.37	-84.72	-105.02
E_{disper}	527.56	531.91	533.54
ΔG_{gas}	-3565.28	-3650.44	-3629.04
ΔG_{solv}	3324.27	3420.68	3387.47
TOTAL (ΔG_{bind})	-241.01	-229.76	-241.56

Supplementary Table S2. List of ORF1p residues involved in contacts with RNA.

	PolyU	PolyA	L1RNA
CC	Glu136, Lys137, Lys140		Lys137, Arg141
RRM	Arg159, Hie216, Arg232, Arg235, Arg248, Thr250, Arg248', Leu249', Val251', Arg159'', His216'', Arg248'', Thr250''	Hie216, Arg235, Gly238, Arg248, Arg159', Leu231', Arg235', Arg248', Thr250'	Arg159, Hie216, Arg235, Arg248, Thr250, Arg159', Arg235', Arg248', Arg159''
RRM Loop	Arg206, Tyr207, Ser208, Ser209, Ala212, Thr213, Thr203', Gln205', Arg206', Thr203'', Tyr207'', Arg210'', Arg211''	Arg206, Tyr207, Ser209, Arg211, Gln205', Arg206', Arg210'', Arg211''	Arg206', Tyr207, Ser208, Ser208', Ser209', Arg210', Arg210'', Ala212'',
CTD	Arg261, Arg279, Pro278, Arg261', Arg279', Ser281', Tyr282', Lys285', Arg248'', Thr250'', Arg261'', Arg262'', Lys 300'', Gln301'', Asn322''	Arg262, Gly265, Gln277, Arg279, Ser287, Arg261', Arg279', Ser281', Tyr282', Lys285', Arg261'', Arg262'', Gln301'', Lys318'', Asn322'', Met323''	Leu258, Arg261, Arg262, Gly265, Pro278, Arg279, Tyr296, Arg261', Arg262', Ile280', Ser281', Tyr282', Ser287', Tyr296', Ile298', Arg261'', Gln301'', Arg304'', Asn322''

Supplementary Table S3. Stacking interactions of RNA nucleotides

	PolyU	PolyA	L1RNA
Bases involved in stacking interactions	UU: U9, U10 UU: U11, U12 UU: U14, U15 UUU: U18, U19, U20 UU: U21, U22 UU: U24, U25 UU: U26, U27 UU: U28, U29	AAAA: A2, A3, A4, A5 AA: A7, A8 AA: A10, A11 AA: A14, A15 AA: A16, A17 AAA: A18, A19, A20	UG: U4, G5, CAC: C6, A7, C8 UG: U11, G12 UG: U13, G14 ACA: A16, C17, A18 AA: A21, A22 AA: A23, A24 AA: A26, A27
Bases not in stacking interactions	U1, U2, U3, U4,U5, U6,U7,U8, U16, U17, U23,	A1, A6, A9, A12, A13, A21, A22, A24, A25, A26, A27, A29	A1, C2, C3, A9, U19, A25, A28, A29

Supplementary Table S4. H-bond interactions formed between ORF1p and polyU, polyA and L1RNA

Domain	Acceptor	Donor	Average Distance	Average Angle	% occupied
ORF1p-L1RNA					
Chain A					
CC	RC3O2	LYS137NZ	3.0477	156.3813	14.49
	RC3O3'	ARG141NH2	2.9438	157.5585	18.47
	RU4OP1	ARG141NH1	2.8692	162.4909	19.46
RRM	RA23O3'	ARG159NH1	3.0457	151.1567	25.02
	RA24OP2	ARG159NH2	2.8018	159.4062	33.72
	RA25OP1	ARG159NH1	2.8677	153.8342	21.53
	RA21OP2	TYR207OH	2.7364	162.4674	22.5
	RG20OP2	SER208N	2.9653	158.316	46.12
	RA23O2'	HIE216NE2	2.955	156.0266	41.69
	RA26OP2	ARG235NH1	2.8072	156.9597	21.71
	RA25OP2	ARG248NH1	2.8304	153.1822	38.45
	RA25OP2	THR250OG1	2.7217	163.6506	24.63
CTD	LEU258O	RA25N6	2.9331	157.7639	17.62
	ARG262O	RA25N6	3.0691	159.8322	44.84
	GLY265O	RA27N6	3.0652	153.74	34.53
	PRO278O	RA28N6	2.9746	153.8729	30.77
	RA26OP1	ARG261NH2	2.8571	150.9416	29.98
	RA24OP2	ARG262NH2	2.881	159.5111	20.13
	RA25OP1	ARG262NH2	2.8501	157.8495	23.93
	RA28OP1	ARG279NH1	2.8176	158.48	21.62
	RA29OP1	ARG279NH1	2.8357	151.8966	22.41
	RA29N7	TYR296OH	2.8558	161.1295	16.45
Chain B					
RRM	RC15OP2	ARG159`NH2	2.9054	156.5966	16.89
	RA10OP1	ARG206`NH1	2.8692	158.7042	15.39
	RA10N1	SER208`OG	2.903	157.2779	30.91
	SER209`O	RU11N3	3.0276	155.5941	34.91
	SER209`O	RG12N2	2.9415	148.964	69.76
	RG12O6	ARG210`NE	2.92	152.7713	51.51
	RA18OP2	ARG235`NH1	2.8977	157.6642	27.43
	RA16OP1	ARG248`NH1	2.8634	158.3098	17.69
CTD	RG14OP2	ARG261`NH1	2.8156	159.1321	29.94
	RC15OP1	ARG261`NH1	2.7952	154.4307	95.76
	RA16OP2	ARG261`NH2	2.9037	155.111	21.48
	RU13OP2	ARG262`NH2	2.8216	159.518	85.94

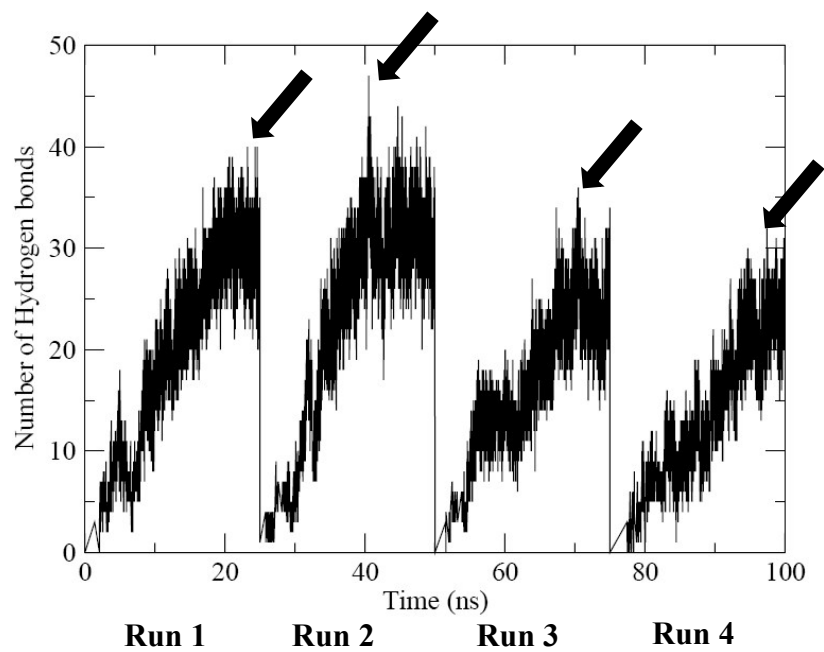
	RG14OP2	ARG262`NH2	2.8089	162.1619	48.42
	RA16O2'	SER281`OG	2.8722	160.6361	19.44
	RC17OP1	SER281`OG	2.6824	164.2244	38.5
	RA18N7	SER281`OG	2.8674	160.8802	17.34
	RA16OP2	TYR282`N	2.9627	149.5644	21.2
	RU19OP1	TYR296`OH	2.7515	165.8574	20.15
	TYR296`O	RG20N1	2.9072	160.4661	61.59
	RG20O6	ILE298`N	2.9725	156.4357	24
	ILE280`O	RC15O2'	2.782	155.7054	19.33
	SER287`OG	RA18N6	3.1572	151.4591	24.01
	Chain C				
RRM	RC8O2	ARG159``NH2	2.9036	153.9673	21.31
	RU4OP2	ARG210``NH2	2.9925	151.1986	37.19
	RG5OP1	ARG210``NE	2.9017	149.7324	90.19
	RC6O2	ALA212``N	3.038	159.2213	64.53
CTD	RA7OP1	ARG261``NH2	2.8386	160.5138	55.8
	RC8OP2	ARG261``NH1	2.8428	156.8251	34.64
	A1N7	GLN301``NE2	3.0014	154.5337	21.28
	GLN301``OE1	RA1N6	2.9723	151.4112	18.22
	RC3N3	GLN301``NE2	3.0935	160.1393	21.86
	RC3N3	ARG304``NH1	2.9836	157.8729	30.78
	RU4O4	ARG304``NH2	2.8916	153.3902	50.62
	RG5O6	ARG304``NH2	2.9176	146.0391	21.35
	ORF1p-PolyU				
	Chain A				
CC	GLU136OE2	RU1O2'	2.7152	162.8721	37.68
	RU2O2	LYS137NZ	2.8339	159.9846	34.02
	RU3O2P	LYS137NZ	2.8176	157.4198	32.58
RRM	RU23O2P	ARG159NH1	2.8245	156.7635	22.02286
	RU17O3'	ARG206NE	3.1077	146.0405	41.22286
	RU18O2P	ARG206NH2	2.8191	153.8926	85.73143
	RU19O2P	ARG206N	2.8053	156.8401	98.32571
	SER208OG	RU19N3	2.9639	152.8092	47.15429
	RU21O2P	TYR207OH	2.7303	160.352	76.80286
	RU18O2	SER208OG	2.7945	160.3332	51.20571
	RU19O2	SER208N	2.9481	158.1659	87.00571
	RU19O2	SER209N	3.1455	149.58	31.10571
	RU21O2P	SER209OG	2.6952	163.5843	25.08
	RU21O2	ALA212N	2.9996	156.8082	15.00857
	RU21O2	THR213OG1	2.8029	157.0456	19.13143
	RU22O3'	HIE216NE2	3.0039	152.8105	36.27714

	RU23O2P	HIE216NE2	3.0236	153.5663	17.57714
	RU27O2P	ARG232NH1	2.8615	158.1361	49.59143
	RU28O2P	ARG232NH1	2.8321	154.637	66.07143
	RU27O2P	ARG235NH2	2.8691	158.8198	42.03429
	RU29O2P	ARG235NH1	2.81	161.3784	15.83714
	RU23O3'	ARG248NH1	3.0082	153.1261	32.29429
	RU24O2P	ARG248NH2	2.8065	158.055	43.41429
	RU24O2P	THR250OG1	2.7387	161.2473	32.82571
CTD	PRO278O	RU29O3'	2.7344	159.5447	58.14571
	RU25O2P	ARG261NH1	2.8027	159.2595	85.18
	RU26O1P	ARG261NH1	2.8515	151.5289	79.98571
	RU29O2	ARG279NH1	2.8584	154.6315	66.65714
	ASP299OD1	RU3N3	2.9601	160.6259	19.24571
Chain B					
RRM	RU13O4	THR203`OG1	2.8002	154.7925	34.42857
	RU12O4	GLN205`N	3.0481	158.9996	22.71714
	RU12O2P	ARG206`NH2	2.864	157.2744	47.12
	RU14O2	ARG248`NH1	2.8712	157.9147	48.13714
	LEU249`O	RU15N3	2.9875	159.321	72.32
	RU15O2	VAL251`N	3.1068	150.8526	54.84
CTD	RU15O2P	ARG261`NH1	2.8527	151.7637	20.11714
	RU16O3'	ARG279`NH2	3.0706	156.6655	17.93143
	RU17O1P	ARG279`NH1	2.8059	157.6578	24.79143
	RU16O1P	SER281`OG	2.681	163.22	18.72571
	RU17O1P	SER281`OG	2.7324	164.1652	49.09143
	RU16O1P	TYR282`N	3.0163	155.9352	82.37143
	RU17O2P	LYS285`NZ	2.7908	159.2008	35.14571
	RU18O1P	LYS285`NZ	2.7795	158.0233	33.58286
Chain C					
CC	ASP151``OD1	RU10N3	2.9075	159.0425	36.11
	RU11O4	ARG155``NH1	2.9311	152.5001	18.73143
RRM	RU6O3'	ARG159``NH1	3.0736	152.3997	34.99429
	RU7O2P	ARG159``NH1	2.9106	157.8031	42.81429
	GLU169``O	RU27N3	2.9983	153.8385	29.73
	RU27O2'	ASN170``ND2	3.0513	158.1058	18.04286
	THR203``O	RU6N3	2.9735	162.8019	38.81
	RU26O4	GLN205``NE2	2.9329	157.3378	35.42571
	RU27O4	GLN205``NE2	2.9039	157.1326	18.10571
	RU5O2P	TYR207``OH	2.7911	162.1916	15.34857
	RU6O4	ARG210``N	2.8903	151.9667	17.34571
	RU6O4	ARG211``N	2.9661	156.0868	33.68

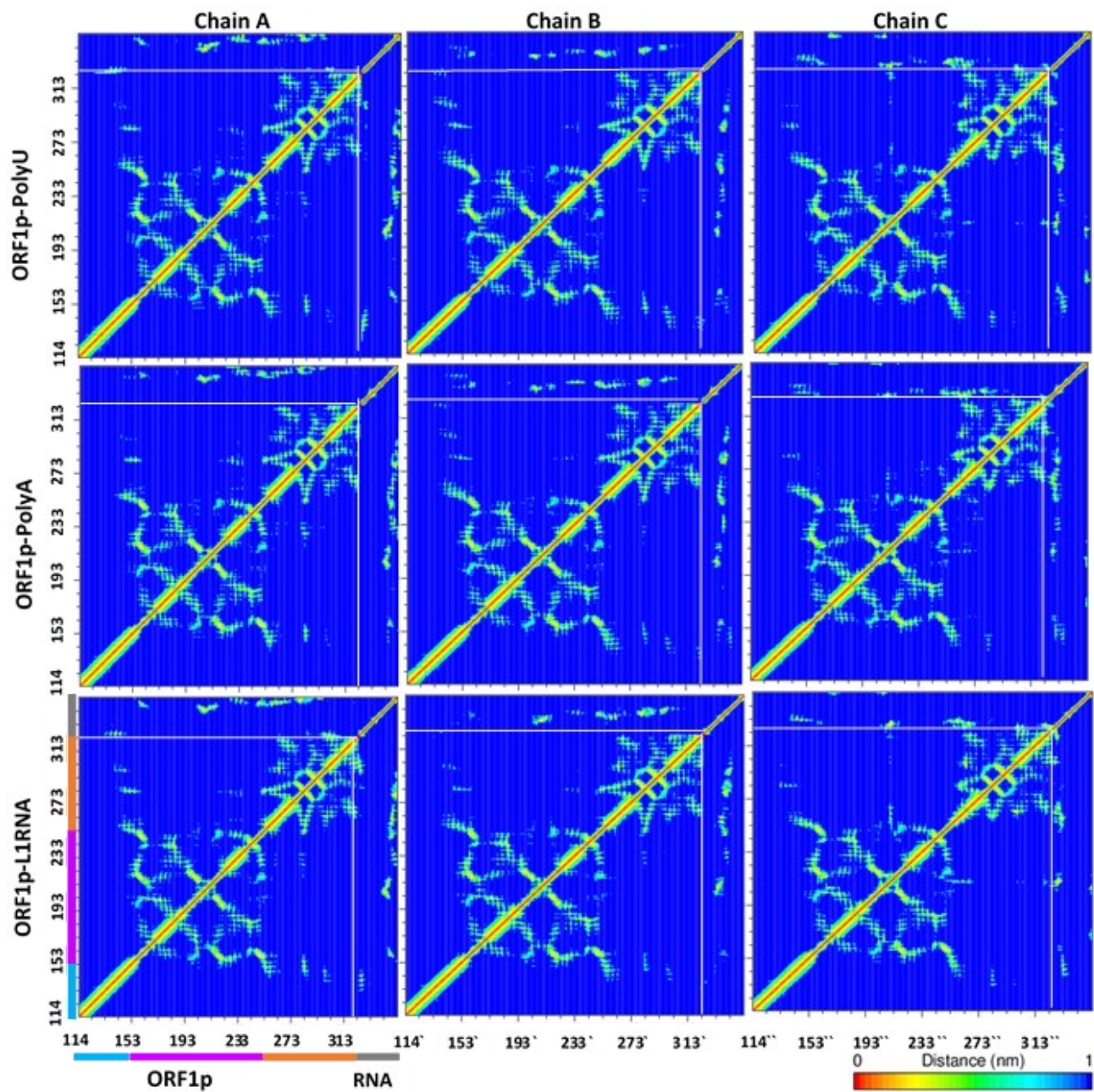
	RU6O2'	HIS216``NE2	2.9731	150.8876	16.95143
	RU7O4	ARG248``NH1	2.9024	158.0005	26.47714
	RU7O2	THR250``OG1	2.7753	160.4281	46.76857
CTD	RU8O2P	ARG261``NH1	2.8233	156.6969	71.48571
	RU9O2P	ARG261``NH1	2.8279	158.0209	78.23429
	RU5O4	ARG262``NE	2.8767	157.2641	43.26571
	GLU263``OE1	RU5N3	2.9571	162.5817	34.66
	RU3O2P	LYS300``NZ	2.8254	152.0865	15.36857
	RU3O2P	LYS300``NZ	2.8232	151.6734	15.3
	RU3O1P	GLN301``NE2	2.8538	160.9611	50.98286
	RU4O2'	ASN322``ND2	2.9819	156.5024	17.6
	ORF1p-PolyA				
Chain A					
RRM	RA23O1P	ARG159NH2	2.823	158.4223	26.25
	RA20O1P	ARG206NE	2.8438	155.8848	31.96
	RA20O2P	TYR207N	3.0209	161.6726	27.17
	RA21O2P	SER209OG	2.7238	163.2564	42.09
	RA21O2P	ARG211NH2	2.8339	158.9828	44.8
	RA22O2P	ARG211NH1	2.845	157.235	66.56
	RA23O1P	HIE216NE2	2.9124	155.4849	28.53
	RA25O2P	ARG235NH2	2.8514	157.1019	23.15
	GLY238O	RA26N6	0.5413	2.9493	54.13
	RA23O2'	ARG248NH1	2.9857	154.0875	15.3
	RA24O1P	ARG248NH1	2.899	157.0797	25.14
	CTD	RA25O1P	ARG248NH1	2.8187	155.6813
RA23O3'		ARG262NH2	2.9791	148.5868	17.07
RA24O1P		ARG262NH2	2.8924	156.2581	16.5
GLY265O		RA25N6	0.1942	3.1353	19.42
GLN277O		RA28N6	0.1603	2.9836	16.03
RA27O1P		ARG279NH2	2.9269	154.713	55.48
RA28O2P		ARG279NH2	2.8082	158.2713	79.53
RA28N7		SER287OG	2.7931	158.7031	16.74
Chain B					
RRM	RA14O1P	ARG159`NH2	2.8561	151.385	22.63
	RA14O1P	ARG159`NE	2.894	150.0197	18.04
	RA15O2P	ARG159`NH1	2.8512	155.4294	44.86
	RA10N7	GLN205`NE2	2.9896	159.9009	15.91
	RA12O2P	GLN205`N	2.9356	161.6606	30.68
	RA12O2P	ARG206`N	2.9626	159.1278	31.64
	LEU231`O	RA16N6	0.2046	3.0624	20.46
	RA16O1P	ARG235`NH1	2.9513	158.7658	27.4

	RA16O2P	ARG248`NH1	2.8081	155.9463	49.11
	RA15O2P	THR250`OG1	2.7187	164.6902	42.45
CTD	RA14N7	ARG261`NH1	3.0402	151.1058	18.92
	RA15O1P	ARG261`NH1	2.8201	151.4708	34.15
	RA17O1P	ARG279`NH2	2.8553	152.921	20
	RA17O1P	SER281`OG	2.7112	163.9647	24.92
	SER281`OG	RA18N6	0.662	3.0336	66.2
	RA17O2P	TYR282`N	2.9233	162.8818	94.67
	RA18O1P	LYS285`NZ	2.8276	159.2497	33.55
	RA19O1P	LYS285`NZ	2.8205	157.8609	16.48
	Chain C				
RRM	RA6O1P	ARG210``NE	2.9434	151.5862	45.67
	RA6O1P	ARG211``NE	2.9376	153.8264	18.64
	RA7O2P	ARG211`NH2	2.8686	158.4255	26.57
	RA7O1P	ARG211``NH1	2.8399	156.8347	25.34
CTD	RA8O2P	ARG261``NH1	2.8189	160.6875	41.28
	ARG262``O	RA6N6	0.1778	3.0866	17.78
	RA1N3	GLN301``NE2	3.0735	160.9513	66.65
	LYS318``O	RA5N6	0.2011	2.9558	20.11
	ASN322``O	RA1N6	0.2109	2.936	21.09
	RA4N3	ASN322``ND2	3.1096	159.186	25.88
	RA5O1P	ASN322``ND2	2.8591	162.0326	33.44
	MET323``O	RA1N6	0.1987	2.9631	19.87

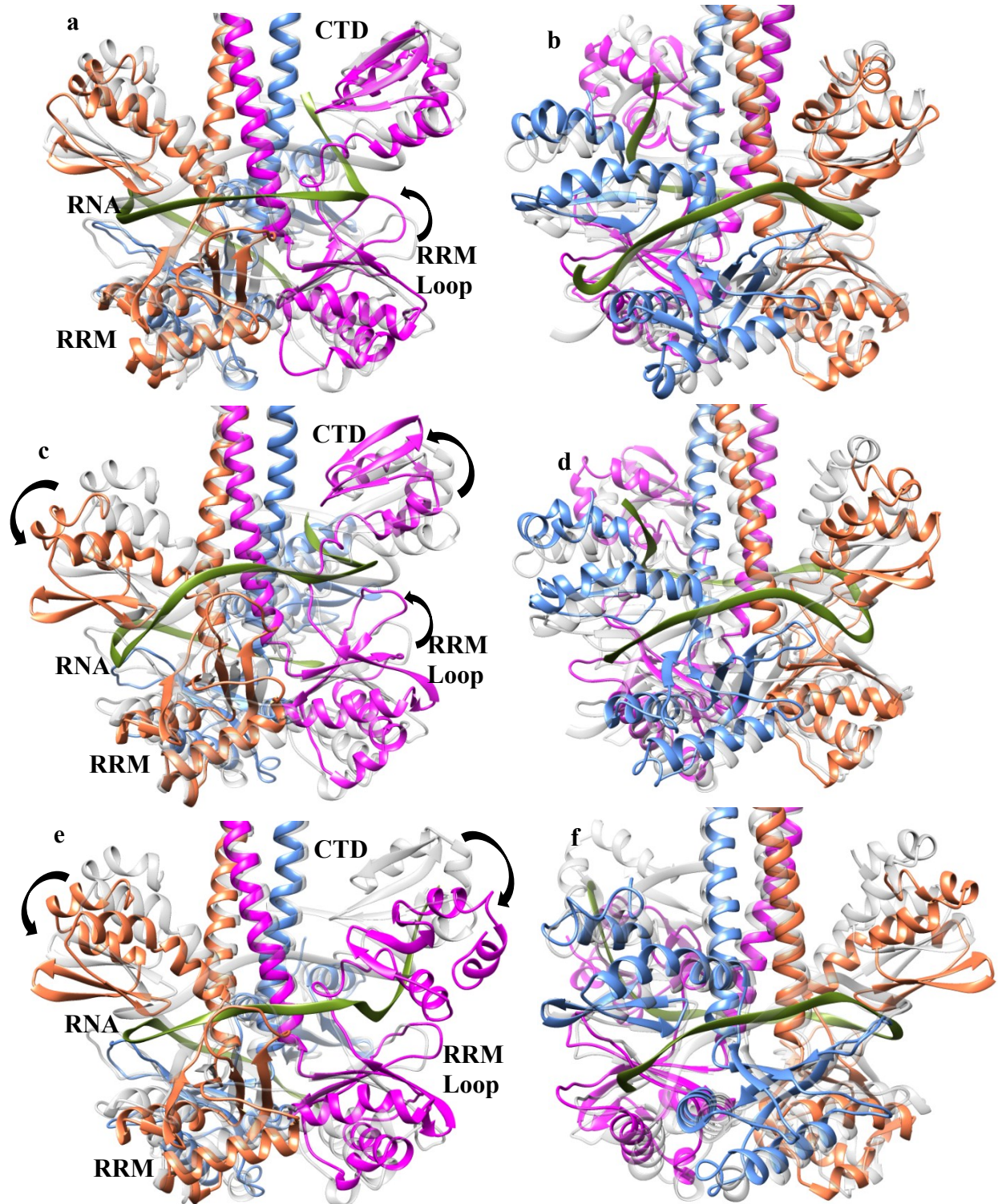
Supplementary Figure S1. Number of Hydrogen bonds formed between ORF1p and RNA fragments during 4 independent runs. The frames with maximum number of hydrogen bonds are indicated by arrows



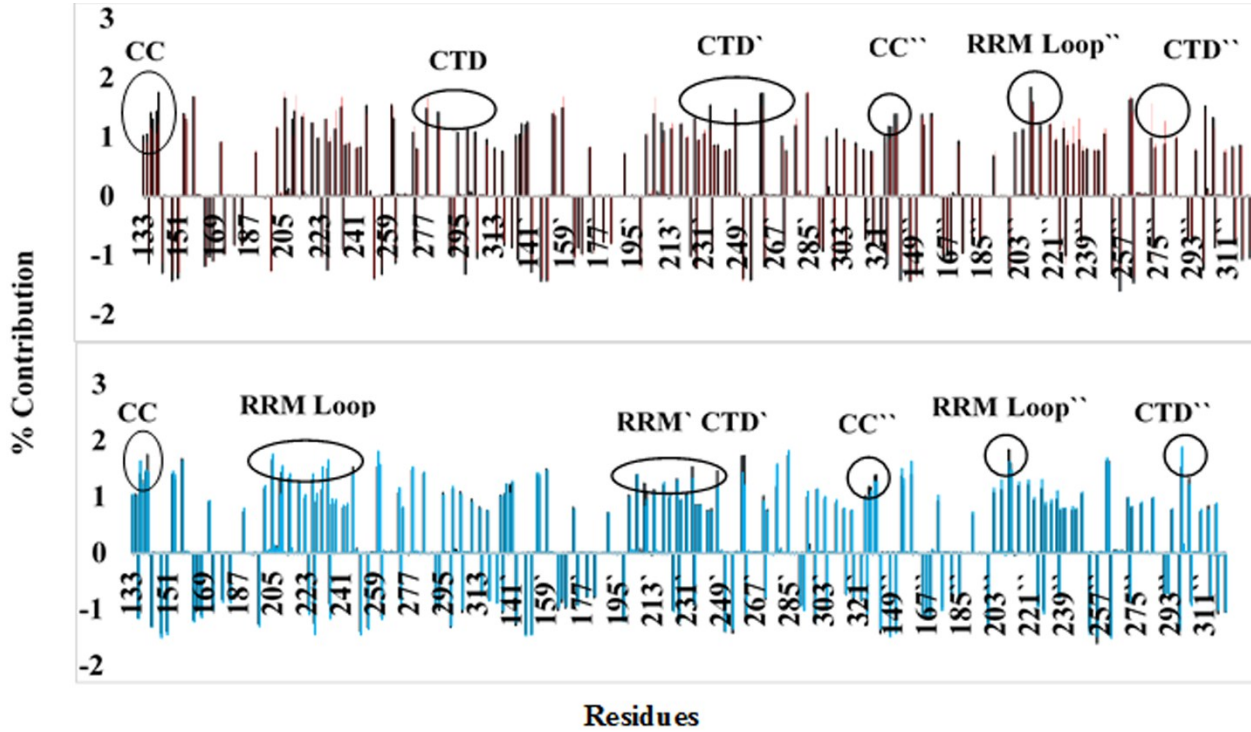
Supplementary Figure S2. The contact map of ORF1p-RNA complexes. The domains of ORF1p are colored as CC (cyan), RRM (Magenta), CTD (orange) and RNA (gray). The ORF1p residues are demarcated from RNA by white lines.



Supplementary Figure S3: The front and back views FEL minima structures of ORF-PolyU (a,b), ORF1-L1RNA (c,d) and ORF1p-PolyA (e,f) superimposed over the initial structure in grey. The movement/conformation of RRM loop and CTD are indicated by black color arrows. The upper part of trimeric coiled domain is cropped for the better visualization.



Supplementary Figure S4. The per-residue decomposition of ORF1-L1RNA (black), ORF1-polyU (Blue) and ORF1-polyA (red). The key differences are circled (black) and labeled respectively.



Supplementary Figure S5. Possible higher order assembly of ORF1p-RNA complexes. The linker RNA connecting two trimers is represented by dotted lines. The oligomerization can be extended on both sides by the assembly of trimers in a similar manner

