Supplementary Tables 1-2

Dataset	Chains	Single	Nts	in	Nts	in	Nts	in	Nts	in	%	Nts
	non-	nts	Pair		Triplet 4-tuple		le	5-tup	ole	with	a	
	redundant										neight	oor
Protein-RNA	288	188	674		39		16		5		80%	
AND-set												
Protein-RNA	95	26	312		27		8		0		93%	
OR-set												

Table S1: Frequencies of extruded nucleotides. The table presents the statistics of extruded consecutive nucleotides (nts) observed in the two dataset of protein-RNA complexes. Column 2 details the number of considered interacting protein-RNA chains. Columns 3-7 present the frequencies of different numbers of consecutive, extruded, protein interacting nucleotides that are not involved in RNA base pairing. Specifically, column 3 presents the number of single extruded nucleotides that are not part of an extruded pair. Column 4 presents the number of pairs that are not part of a triplet, column 5 presents the number of triplets that are not part of quadruplet, etc. The last column presents the percentage of protein interacting extruded nucleotides that have at least one RNA strand neighbor that interacts with the protein via its ring as well.

Pair	% π -stacked in	P-value	π -stacked in	P-value	% π -stacked in	P-value
	protein-RNA	in AND-	protein-RNA	in OR-	all RNA	
	AND-set	set	OR-set	set		
AA	36.21	0.34	50.00	0.18	50.22	0.00
AC	65.5	0	75	0.003	48.1	0.002
AG	45.00	0.18	75.00	0.02	49.55	0.00
AU	24.00	0.89	28.57	0.75	28.87	0.91
CA	16.67	1.00	26.67	0.82	31.67	0.78
CC	46.67	0.08	42.11	0.29	44.93	0.04
CG	41.67	0.36	33.33	0.67	33.96	0.58
CU	44.44	0.34	42.86	0.44	27.27	0.89
GA	27.27	0.80	12.50	0.97	22.73	1.00
GC	50.00	0.14	60.00	0.22	40.74	0.20
GG	37.50	0.53	25.00	0.81	51.61	0.00
GU	16.67	0.97	10.00	0.99	23.86	0.99
IC	0.00	1.00	0.00	1.00	0.00	1.00
UA	16.67	0.97	14.29	0.95	17.20	1.00
UC	42.11	0.27	40.00	0.46	24.36	0.99
UG	41.67	0.36	20.00	0.88	30.30	0.80
UU	11.36	1.00	5.00	1.00	19.88	1.00

Table S2: Sequence specificity of π -stacked nucleotides. The table presents the frequencies of consecutive nucleotide π -stacking for each type of dinucleotide pairs. The first column indicates the nucleotide identities. For each type of pair, column 2-3 present the percentages of π -stacked pairs and the hyper geometric p-value of the statistics significance in the protein-RNA AND-set dataset. Columns 4-5 and 6-7 provide the same details for the protein-RNA OR-set and all RNA datasets respectively.