

Table S4. The 5% and 25% quantiles of the RMSD distributions for decoys with correct base pairing.

PDB ID	Len	Bps	BARNACLE		Mixture model		Uniform model	
			5%	25%	5%	25%	5%	25%
1ESY	19	6	2.99	3.28	3.46	4.17	8.39	8.63
1KKA	17	6	4.40	5.02	4.37	4.90	8.14	8.52
1L2X	27	8	5.43	6.88	6.69	7.66	9.58	9.99
1Q9A	27	6	4.80	5.42	5.63	6.65	9.69	10.40
1QWA	21	8	4.06	4.64	4.24	4.81	8.11	8.53
1XJR	46	15	10.41	11.01	-	-	-	-
1ZIH	12	4	1.72	2.16	2.16	2.89	6.07	6.56
28SP	28	8	3.23	3.76	7.17	7.91	10.31	10.50
2A43	26	7	4.72	6.08	6.96	7.72	10.96	11.19
2F88	34	13	3.82	4.41	5.34	5.70	-	-

Len: the number of nucleotides in the molecule; *Bps:* the number of Watson Crick and G-U wobble base pairs in the structure; *5%:* the 5% quantiles measured in Å; *25%:* the 25% quantiles measured in Å. A dash indicates that no structures with correct base paring (energy below 1.0Å) were obtained. Lowest (best) RMSD values are highlighted with bold face.