

Supplementary Material

Evaluation of the stereochemical quality of predicted RNA 3D models in the RNA-Puzzles submissions

F. Carrascoza^{1,†}, M. Antczak^{1,2,†}, Z. Miao^{3,4}, E. Westhof⁵, M. Szachniuk^{1,2,*}

¹ Institute of Computing Science and European Centre for Bioinformatics and Genomics, Poznan University of Technology, 60-965 Poznan, Poland

² Institute of Bioorganic Chemistry, Polish Academy of Sciences, 61-704 Poznan, Poland

³ European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Wellcome Genome Campus, CB10 1SD, UK

⁴ Translational Research Institute of Brain and Brain-Like Intelligence and Department of Anesthesiology, Shanghai Fourth People's Hospital Affiliated to Tongji University School of Medicine, Shanghai 200081, China

⁵ Architecture et Réactivité de l'ARN, Université de Strasbourg, Institut de biologie moléculaire et cellulaire CNRS, 12 allée Konrad Roentgen, 67084 Strasbourg, France

[†]joint first authors

*To whom correspondence should be addressed: mszachniuk@cs.put.poznan.pl

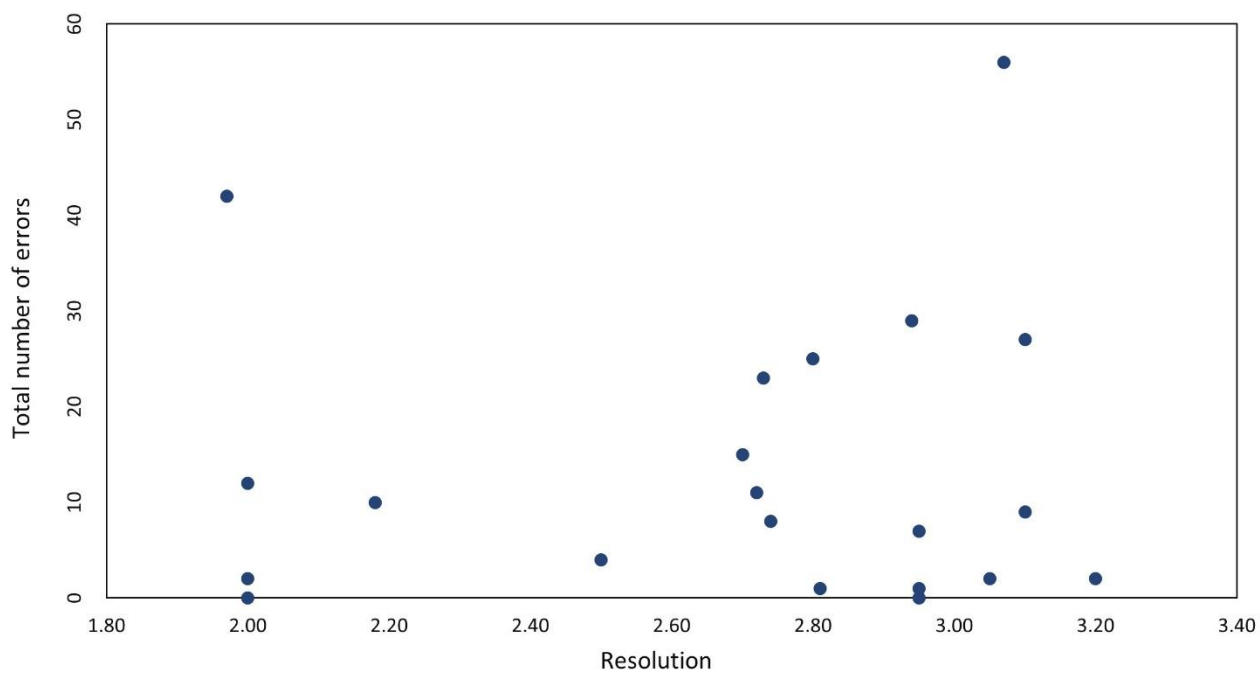


Figure S1. Resolution of reference structures versus number of errors reported by MAXIT.

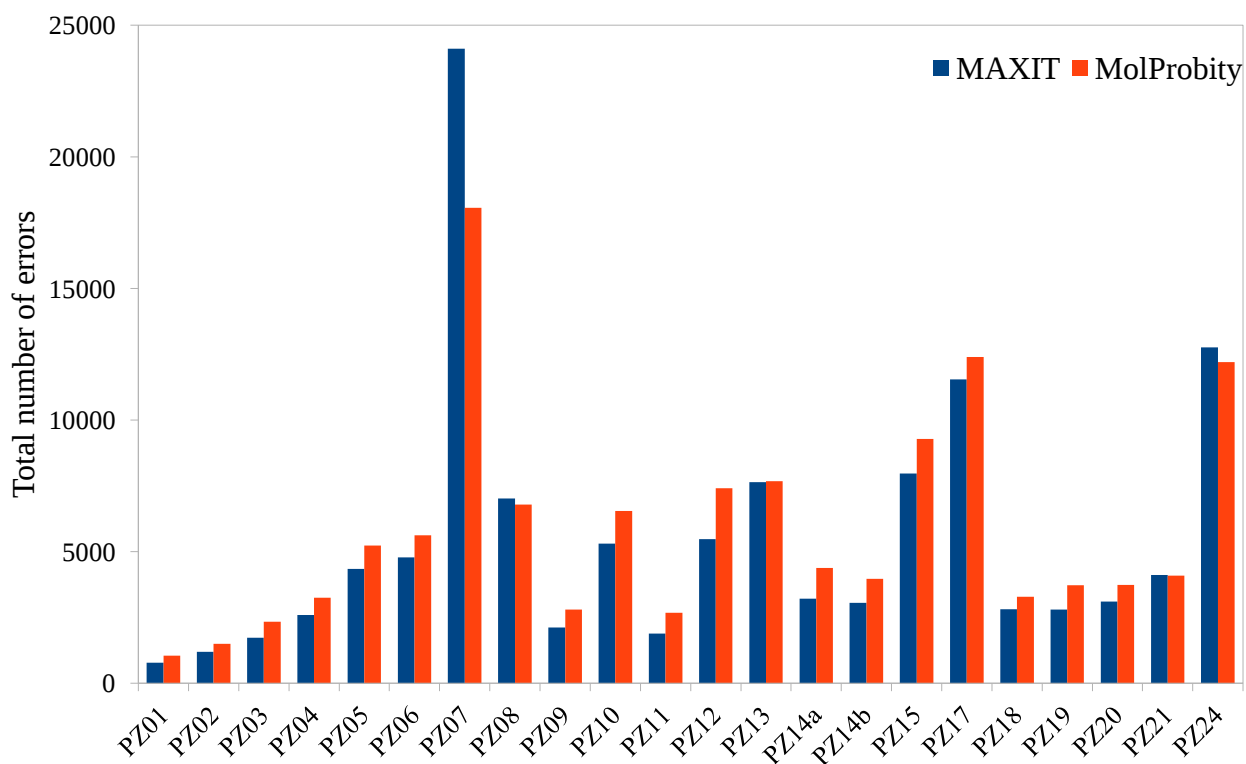


Figure S2. The total number of errors identified by MAXIT and MolProbity in all predicted models, divided by RNA-Puzzles challenges.

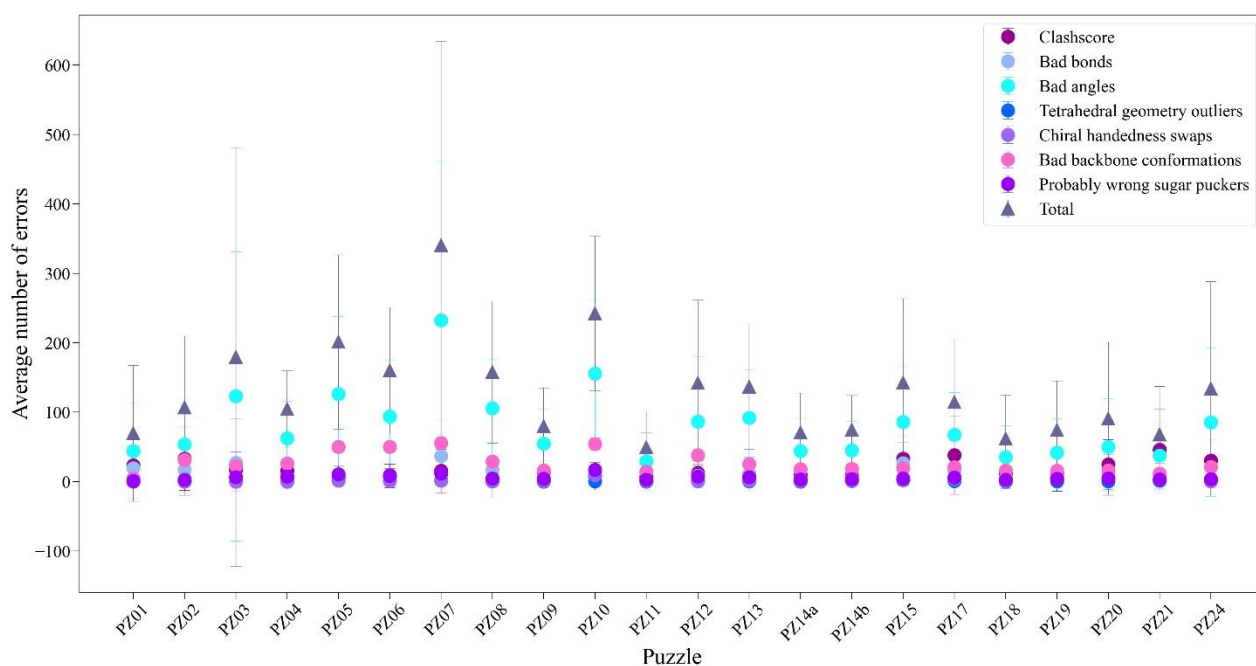


Figure S3. The average number of errors identified for each puzzle by MolProbity software.

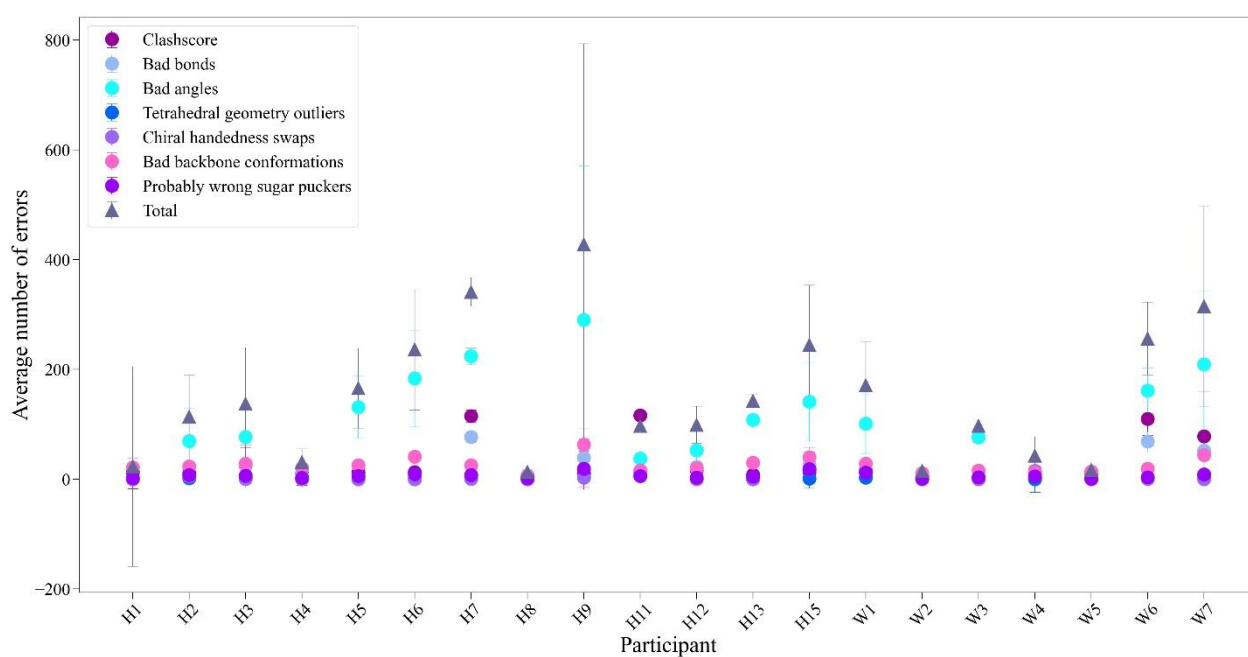


Figure S4. The average number of errors identified for each participant by MolProbity software.

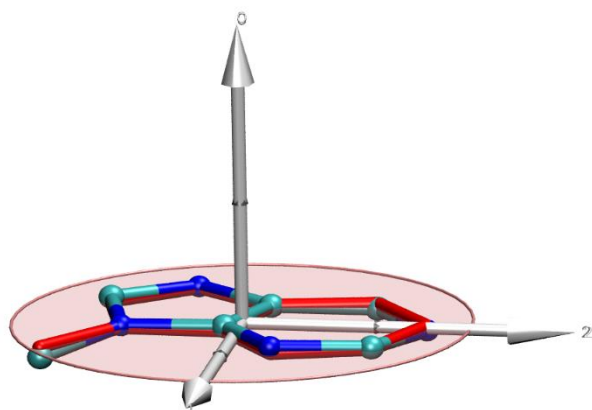


Figure S5. Planarity deviation for residue A28 in the PZ04 reference structure. Adenine from the target structure is depicted in ball-and-sticks representation with carbons in green and nitrogen in blue. Idealized structure is highlighted in red sticks. The reference plane appears in a red-transparent circle in its best fit from all atoms but hydrogen. Principle axes of inertia are shown with white arrows. The plane deviation presented in the figure equals $0.074\text{\AA}$. Although this value is not high, MAXIT indicates it as an error. MAXIT reports an error in this category whenever the deviations computed over all the atoms for the plane is higher than $6 \times 0.02\text{\AA}$ or at least one atom distance exceeds $0.02\text{\AA}$. In the presented example, the deviation of a single atom exceeds the threshold.

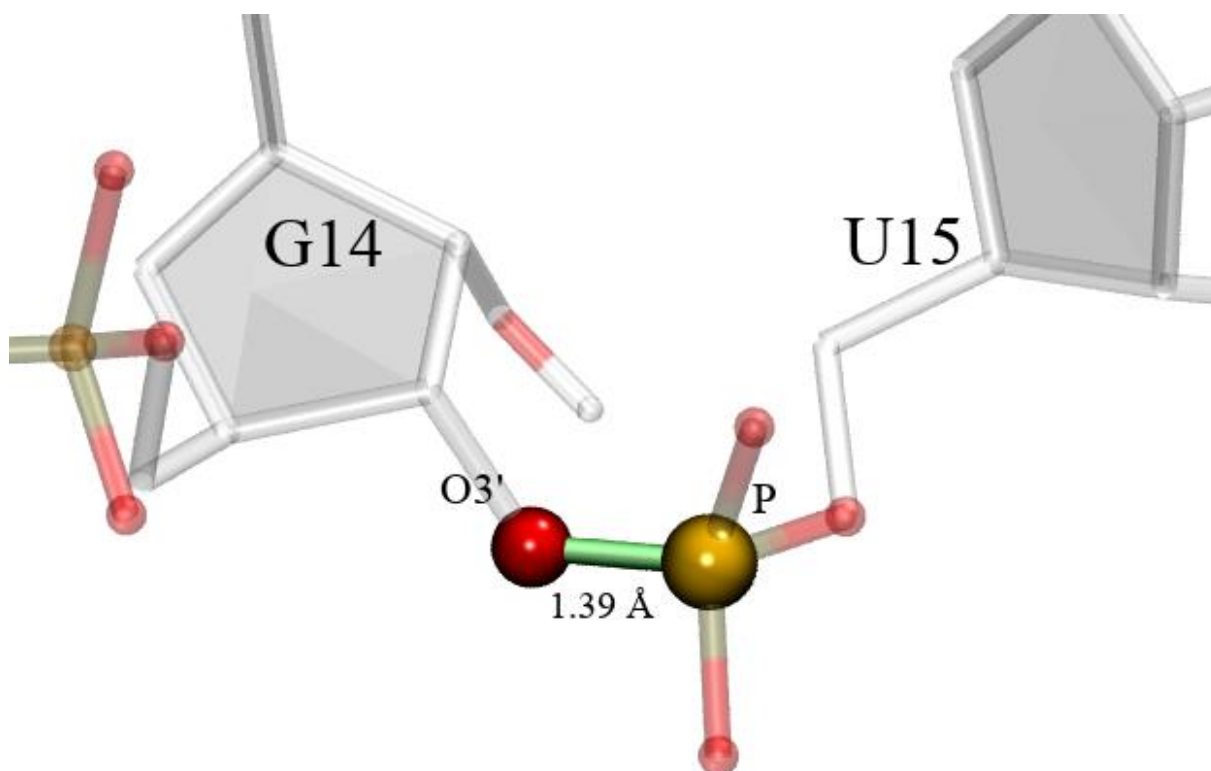


Figure S6. Polymer linkage abnormality found between Guanidine 14 and Uracil 15 (in the H7 model submitted to PZ24). The distance $1.39\text{\AA}$ was measured by MAXIT (when it should be around $1.6\text{\AA}$ with a sigma around 0.01).

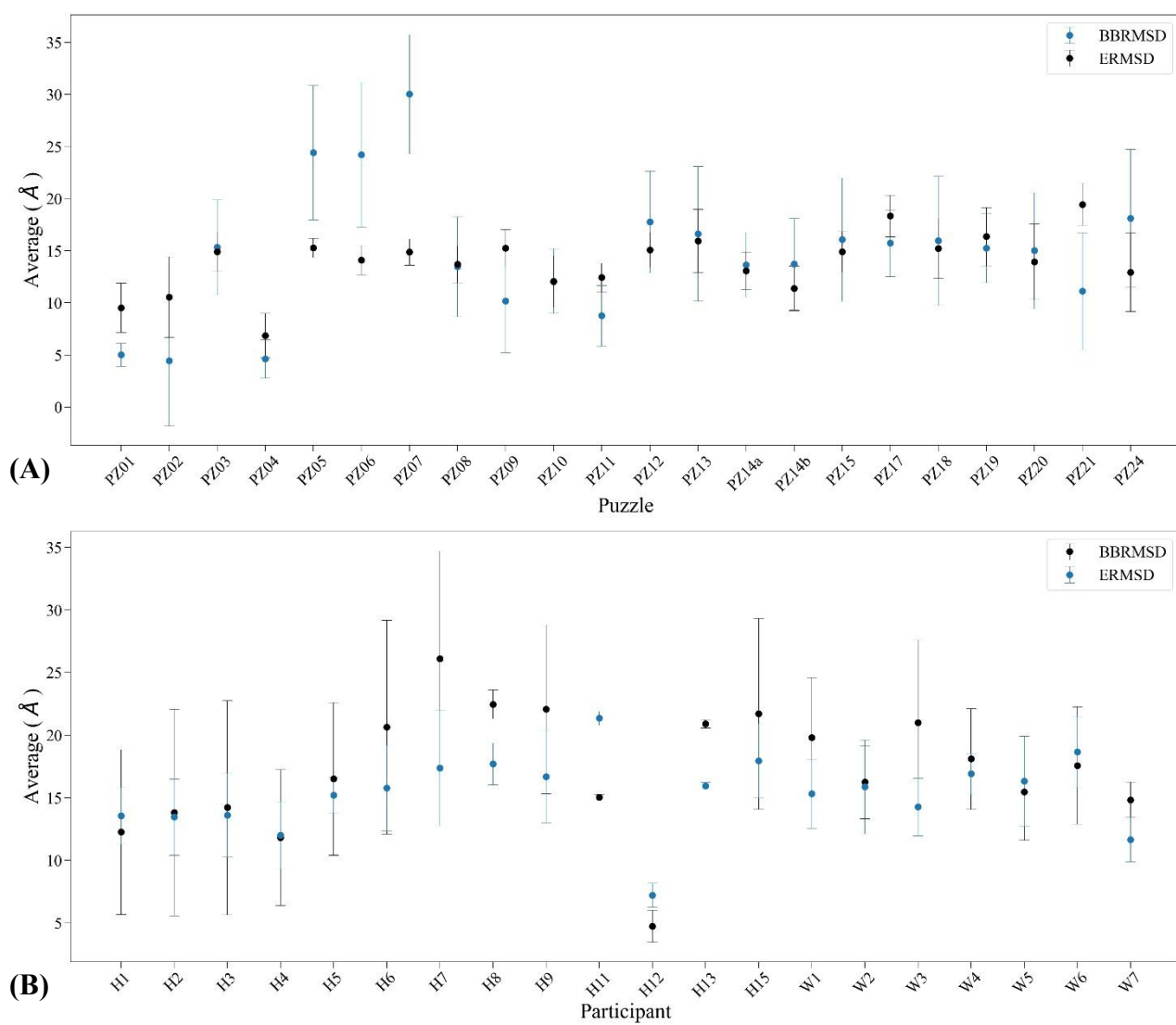


Figure S7. The average RMSD computed for the backbone (BBRMSD) and base pairs (eRMSD) over all models per puzzle (A), and per participant (B). Bars represent the standard deviation for every mean value.

RCSB MAXIT reports on the stereochemistry of experimentally determined 3D structures includes:

- the number of identified too-close contacts between symmetry-related molecules,
- bond lengths and bond angles,
- the number of planarity deviations,
- the number of chirality errors,
- the number of identified polymer linkage artefacts.

Table S1. MAXIT report on the reference structures.

No.	Puzzle id	PDB id	Resolution	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ01	3MEI	1.97	1	5	35	0	0	1	42
2	PZ02	3P59	2.18	2	0	8	0	0	0	10
3	PZ03	3OWZ	2.95	0	0	1	0	0	0	1
4	PZ04	3V7E	2.80	21	0	4	0	0	0	25
5	PZ05	4P9R	2.70	15	0	0	0	0	0	15
6	PZ06	4GXY	3.05	0	0	0	0	0	2	2
7	PZ07	4R4V	3.07	0	3	53	0	0	0	56
8	PZ08	4L81	2.95	6	0	0	0	0	1	7
9	PZ09	5KPY	2.00	0	0	2	0	0	0	2
10	PZ10	4LCK	3.20	0	0	1	0	0	1	2
11	PZ11	5IEM	-	0	0	1	0	0	0	1
12	PZ12	4QLM	2.72	0	0	10	0	0	1	11
13	PZ13	4XW7	2.50	0	0	1	3	0	0	4
14	PZ14a	5DDO	3.10	0	0	7	0	0	2	9
15	PZ14b	5DDO	3.10	2	15	9	0	0	1	27
16	PZ15	5DI4	2.95	0	0	0	0	0	0	0
17	PZ17	5K7C	2.73	0	7	16	0	0	0	23
18	PZ18	5TPY	2.81	0	0	1	0	0	0	1
19	PZ19	5T5A	2.00	0	0	6	6	0	0	12
20	PZ20	5Y85	2.00	0	0	0	0	0	0	0
21	PZ21	5NZ6	2.94	0	2	27	0	0	0	29
22	PZ24	6OL3	2.74	7	0	1	0	0	0	8
Average				2.45	1.45	8.32	0.41	0.00	0.41	13.05
Standard deviation				5.47	3.56	13.54	1.40	0.00	0.67	14.95
Median				0	0	1.5	0	0	0	8.5

Table S2. MAXIT report on structures in Puzzle 01.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ1_Das_1	0	0	0	0	0	0	0
2	PZ1_Das_3	0	0	0	0	0	0	0
3	PZ01_Das_4	0	0	0	0	0	0	0
4	PZ01_Das_2	0	0	1	0	0	0	1
5	PZ01_Das_5	0	0	3	0	0	0	3
6	PZ01_Bujnicki_1	0	0	15	9	1	0	25
7	PZ01_refstructure	0	2	27	0	0	0	29
8	PZ01_Dokholyan_1	0	0	27	12	0	1	40
9	PZ01_Chén_1	0	1	30	9	0	0	40
10	PZ01_Santalucia_1	0	44	29	0	0	2	75
11	PZ01_Bujnicki_3	3	23	33	1	0	19	79
12	PZ01_Bujnicki_4	17	25	40	1	0	7	90
13	PZ01_Bujnicki_5	19	20	46	1	0	14	100
14	PZ01_Bujnicki_2	4	30	55	1	0	20	110
15	PZ01_Major_1	1	85	209	29	0	0	324
Average		2.93	15.33	34.33	4.20	0.07	4.20	61.07
Standard deviation		6.25	24.04	51.59	7.96	0.26	7.30	82.71
Median		0	1	27	1	0	0	40

Table S3. MAXIT report on structures in Puzzle 02.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ02_Das_3	0	0	9	0	0	0	9
2	PZ02_Das_1	1	0	9	0	0	0	10
3	PZ02_Das_2	1	0	9	0	0	0	10
4	PZ02_Das_4	1	1	9	0	0	0	11
5	PZ02_Das_5	2	1	9	0	0	0	12
6	PZ02_Major_1	0	12	18	0	0	0	30
7	PZ02_refstructure	1	5	35	0	0	1	42
8	PZ02_Bujnicki_3	0	0	35	29	0	0	64
9	PZ02_Bujnicki_2	0	3	36	30	0	0	69
10	PZ02_Dokholyan_1	0	0	52	22	0	0	74
11	PZ02_Santalucia_1	6	32	41	0	0	2	81
12	PZ02_Bujnicki_1	0	4	70	20	1	0	95
13	PZ02_Chén_1	5	21	196	30	2	0	254
14	PZ02_Wildauer_1	271	39	210	0	0	0	520
Average		20.57	8.43	52.71	9.36	0.21	0.21	91.50
Standard deviation		72.10	12.97	66.43	13.30	0.58	0.58	138.91
Median		1	2	35	0	0	0	53

Table S4. MAXIT report on structures in Puzzle 03.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ03_Das_4	0	0	0	0	0	1	1
2	PZ03_refstructure	0	0	1	0	0	0	1
3	PZ03_Das_1	0	0	0	0	0	1	1
4	PZ03_Das_2	0	0	0	0	0	1	1
5	PZ03_Das_3	0	0	2	0	0	0	2
6	PZ03_Das_5	0	1	0	0	0	1	2
7	PZ03_Bujnicki_2	0	0	35	29	0	0	64
8	PZ03_Bujnicki_1	0	0	44	37	0	0	81
9	PZ03_Dokholyan_2	0	0	59	30	0	0	89
10	PZ03_Dokholyan_1	0	0	68	29	0	0	97
11	PZ03_Chen_1	0	1	114	25	0	0	140
12	PZ03_Major_2	0	145	398	48	1	0	592
13	PZ03_Major_1	0	143	415	36	1	0	595
Average		0.00	22.31	87.38	18.00	0.15	0.31	128.15
Standard deviation		0.00	54.01	145.95	18.18	0.38	0.48	211.85
Median		0	0	35	25	0	0	64

Table S5. MAXIT report on structures in Puzzle 04.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ04_Adamiak_1	0	0	0	0	0	0	0
2	PZ04_Adamiak_2	0	0	0	0	0	0	0
3	PZ04_Adamiak_3	0	0	0	0	0	0	0
4	PZ04_Adamiak_4	0	0	0	0	0	0	0
5	PZ04_Adamiak_5	0	0	0	0	0	0	0
6	PZ04_Das_2	0	0	1	0	0	0	1
7	PZ04_Das_3	0	0	1	0	0	0	1
8	PZ04_Das_4	0	0	1	0	0	0	1
9	PZ04_Das_5	0	0	1	0	0	0	1
10	PZ04_Das_1	0	0	1	0	0	0	1
11	PZ04_refstructure	0	0	6	6	0	0	12
12	PZ04_Bujnicki_4	1	18	27	2	0	2	50
13	PZ04_Bujnicki_2	1	19	27	2	0	2	51
14	PZ04_Dokholyan_1	0	0	37	16	2	0	55
15	PZ04_Dokholyan_2	0	0	37	16	2	0	55
16	PZ04_Bujnicki_5	1	19	30	6	0	2	58
17	PZ04_Bujnicki_3	1	18	31	8	0	2	60
18	PZ04_Santalucia_1	0	26	29	0	2	5	62
19	PZ04_Bujnicki_1	1	20	34	7	0	2	64
20	PZ04_Mikolajczak_1	26	15	24	6	0	1	72
21	PZ04_Chen_1	0	1	122	16	0	0	139

22	PZ04_Chén_4	0	3	135	22	0	0	160
23	PZ04_Chén_2	0	2	149	19	0	0	170
24	PZ04_Major_1	0	0	150	32	1	0	183
25	PZ04_Chén_8	0	5	160	21	0	0	186
26	PZ04_Chén_6	0	2	163	24	0	0	189
27	PZ04_Chén_10	0	4	171	19	0	0	194
28	PZ04_Chén_7	0	3	169	23	0	0	195
29	PZ04_Chén_3	0	7	173	20	0	0	200
30	PZ04_Chén_5	0	14	177	18	0	0	209
31	PZ04_Chén_9	0	18	186	20	0	0	224
Average		1.00	6.26	65.87	9.77	0.23	0.52	83.65
Standard deviation		4.65	8.35	72.53	9.89	0.62	1.12	81.98
Median		0	2	30	6	0	0	58

Table S6. MAXIT report on structures in Puzzle 05.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ05_Adamiak_1	0	0	0	0	0	0	0
2	PZ05_refstructure	2	0	8	0	0	0	10
3	PZ05_Bujnicki_4	0	0	22	0	0	0	22
4	PZ05_Bujnicki_1	0	0	25	0	0	0	25
5	PZ05_Bujnicki_5	0	0	29	0	0	0	29
6	PZ05_Bujnicki_3	2	0	31	0	0	0	33
7	PZ05_Bujnicki_2	1	0	34	0	0	0	35
8	PZ05_Das_1	0	10	29	0	0	1	40
9	PZ05_Das_2	0	7	34	0	0	2	43
10	PZ05_Chén_7	0	0	65	3	5	0	73
11	PZ05_Chén_6	0	0	67	5	5	0	77
12	PZ05_Chén_1	1	10	94	9	5	0	119
13	PZ05_Chén_4	0	17	93	14	5	0	129
14	PZ05_Chén_2	0	20	97	16	5	0	138
15	PZ05_Chén_3	0	22	115	10	4	0	151
16	PZ05_Chén_5	1	26	108	7	6	3	151
17	PZ05_Dokholyan_6	0	0	145	59	0	0	204
18	PZ05_Dokholyan_7	0	0	149	59	0	0	208
19	PZ05_Dokholyan_8	0	1	162	60	0	0	223
20	PZ05_Dokholyan_3	0	4	178	125	0	0	307
21	PZ05_Dokholyan_5	0	3	191	134	0	0	328
22	PZ05_Dokholyan_4	0	5	217	135	0	0	357
23	PZ05_Dokholyan_2	0	5	217	135	0	0	357
24	PZ05_Dokholyan_1	0	3	222	135	0	0	360
25	PZ05_Xiao_1	0	14	331	71	3	0	419
26	PZ05_Xiao_2	0	45	368	71	5	4	493
Average		0.27	7.38	116.58	40.31	1.65	0.38	166.58

Standard deviation	0.60	10.93	97.85	51.91	2.37	1.02	145.96
Median	0	3	96.5	9.5	0	0	133.5

Table S7. MAXIT report on structures in Puzzle 06.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ06_refstructure	0	0	0	0	0	2	2
2	PZ06_Bujnicki_3	1	0	13	0	0	0	14
3	PZ06_Bujnicki_1	0	0	16	0	0	0	16
4	PZ06_Bujnicki_4	3	0	16	0	0	0	19
5	PZ06_Bujnicki_2	2	0	22	0	0	0	24
6	PZ06_Das_7	5	8	12	1	0	3	29
7	PZ06_Das_3	6	8	12	1	0	4	31
8	PZ06_Das_9	6	11	18	0	0	3	38
9	PZ06_Das_5	17	6	15	0	0	4	42
10	PZ06_Das_8	17	6	16	0	0	3	42
11	PZ06_Das_2	8	12	22	0	0	2	44
12	PZ06_Das_10	21	13	17	1	0	4	56
13	PZ06_Das_6	63	11	23	1	0	6	104
14	PZ06_Das_1	63	12	23	1	0	5	104
15	PZ06_Das_4	63	12	23	1	0	6	105
16	PZ06_Chén_1	0	0	97	23	0	0	120
17	PZ06_Chén_2	0	2	113	21	0	0	136
18	PZ06_Chén_4	0	0	115	29	0	0	144
19	PZ06_Chén_3	0	2	121	32	0	0	155
20	PZ06_Chén_6	0	5	115	37	0	0	157
21	PZ06_Dokholyan_1	0	0	113	50	0	0	163
22	PZ06_Dokholyan_5	0	0	112	53	0	0	165
23	PZ06_Dokholyan_4	0	0	122	46	0	0	168
24	PZ06_Chén_7	2	20	124	28	0	1	175
25	PZ06_Dokholyan_2	0	0	118	57	0	0	175
26	PZ06_Dokholyan_3	0	0	122	55	0	0	177
27	PZ06_Major_6	1	0	147	42	3	0	193
28	PZ06_Major_4	0	0	142	56	4	0	202
29	PZ06_Major_7	0	0	147	57	4	0	208
30	PZ06_Major_1	0	0	143	63	4	0	210
31	PZ06_Major_3	1	0	147	61	5	0	214
32	PZ06_Major_2	0	0	160	54	7	0	221
33	PZ06_Major_5	0	0	170	55	5	0	230
34	PZ06_Chén_5	3	29	185	59	1	1	278
35	PZ06_Dokholyan_6	0	2	199	124	0	0	325
Average		8.06	4.54	84.57	28.80	0.94	1.26	128.17
Standard deviation		17.86	6.86	63.18	29.85	1.92	1.93	84.66
Median		0	0	113	28	0	0	144

Table S8. MAXIT report on structures in Puzzle 07.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ07_Adamiak_1	0	0	0	0	0	0	0
2	PZ07_Adamiak_2	0	0	0	0	0	0	0
3	PZ07_Adamiak_3	0	0	0	0	0	0	0
4	PZ07_Adamiak_4	0	0	0	0	0	0	0
5	PZ07_Adamiak_5	0	0	0	0	0	0	0
6	PZ07_Das_5	0	1	2	0	0	0	3
7	PZ07_Das_8	0	3	5	0	0	0	8
8	PZ07_Das_3	0	3	5	0	0	1	9
9	PZ07_Das_7	0	0	0	0	0	1	9
10	PZ07_Das_6	1	3	6	0	0	0	10
11	PZ07_Das_2	0	3	6	0	0	3	12
12	PZ07_Das_4	0	4	6	0	0	2	12
13	PZ07_Das_1	0	3	6	0	0	2	11
14	PZ07_refstructure	0	3	53	0	0	0	56
15	PZ07_Ding_8	0	0	127	60	0	0	187
16	PZ07_Ding_10	0	1	138	58	0	0	197
17	PZ07_Ding_4	0	0	133	64	0	0	197
18	PZ07_Ding_7	0	0	149	58	0	0	207
19	PZ07_Ding_5	0	1	142	64	0	0	207
20	PZ07_Ding_9	0	1	142	66	0	0	209
21	PZ07_Ding_6	0	0	151	68	0	0	219
22	PZ07_Ding_1	0	0	154	68	0	0	222
23	PZ07_Ding_3	0	0	150	74	0	0	224
24	PZ07_Ding_2	0	0	170	59	0	0	229
25	PZ07_Chen_10	53	54	103	0	0	51	261
26	PZ07_Chen_8	86	53	98	0	0	51	288
27	PZ07_Chen_3	63	61	118	0	0	51	293
28	PZ07_Chen_7	78	55	114	0	0	47	294
29	PZ07_Chen_6	73	60	118	0	0	49	300
30	PZ07_Bujnicki_5	0	37	212	58	7	0	314
31	PZ07_Bujnicki_4	0	38	216	58	7	0	319
32	PZ07_Bujnicki_6	0	41	230	50	10	0	331
33	PZ07_Dokholyan_1	0	7	199	127	1	0	334
34	PZ07_Bujnicki_3	0	44	229	53	9	0	335
35	PZ07_Chen_2	131	54	106	0	0	50	341
36	PZ07_Dokholyan_2	0	7	199	137	0	0	343
37	PZ07_Bujnicki_7	0	33	242	64	5	0	344
38	PZ07_Chen_5	126	59	113	0	0	49	347
39	PZ07_Bujnicki_2	0	47	252	52	9	0	360
40	PZ07_Bujnicki_1	0	44	259	50	10	0	363
41	PZ07_Chen_4	172	62	125	0	0	50	409
42	PZ07_Chen_9	214	53	96	0	0	52	415

43	PZ07_Major_4	0	59	379	113	6	2	559
44	PZ07_Major_7	0	61	390	110	4	3	568
45	PZ07_Major_5	0	57	394	112	4	2	569
46	PZ07_Major_8	0	62	428	110	0	0	600
47	PZ07_Major_1	0	57	434	112	4	2	609
48	PZ07_Major_6	0	76	431	113	3	3	626
49	PZ07_Major_3	0	80	471	119	6	5	681
50	PZ07_Major_9	0	88	483	112	4	3	690
51	PZ07_Major_2	0	89	491	109	6	4	699
52	PZ07_Major_10	0	82	496	116	5	4	703
53	PZ07_Chén_1	0	371	555	98	3	0	1027
Average		18.81	36.17	179.74	47.40	1.94	9.19	293.40
Standard deviation		47.08	55.71	160.40	46.97	3.10	18.69	238.71
Median		0	33	142	53	0	0	293

Table S9. MAXIT report on structures in Puzzle 08.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ08_Adamiak_1	0	0	0	0	0	0	0
2	PZ08_Adamiak_2	0	0	0	0	0	0	0
3	PZ08_Das_4	0	0	0	0	0	0	0
4	PZ08_Das_6	0	0	0	0	0	0	0
5	PZ08_Das_5	0	0	1	0	0	0	1
6	PZ08_Das_2	2	0	0	0	0	0	2
7	PZ08_Das_1	2	0	1	0	0	0	3
8	PZ08_refstructure	0	0	1	3	0	0	4
9	PZ08_Das_3	2	1	2	0	0	1	6
10	PZ08_Chén_2	0	0	52	19	0	0	71
11	PZ08_Chén_5	0	2	59	16	0	0	77
12	PZ08_Chén_3	0	5	68	18	0	0	91
13	PZ08_Chén_4	0	0	75	22	0	0	97
14	PZ08_Chén_10	0	5	70	21	2	0	98
15	PZ08_Ding_7	0	0	65	38	0	0	103
16	PZ08_Ding_8	0	0	68	35	0	0	103
17	PZ08_Ding_4	0	1	72	34	0	0	107
18	PZ08_Ding_5	0	0	79	30	0	0	109
19	PZ08_Ding_6	0	0	76	37	0	0	113
20	PZ08_Ding_1	0	0	78	36	0	0	114
21	PZ08_Ding_10	0	0	83	35	0	0	118
22	PZ08_Ding_9	0	0	82	37	0	0	119
23	PZ08_Ding_2	0	0	84	38	0	0	122
24	PZ08_Ding_3	0	0	96	35	0	0	131
25	PZ08_Chén_1	0	19	91	22	1	0	133
26	PZ08_Bujnicki_7	0	20	105	15	8	0	148

27	PZ08_Dokholyan_1	0	3	117	72	0	0	192
28	PZ08_Dokholyan_3	0	1	126	73	0	0	200
29	PZ08_Dokholyan_4	0	1	126	73	0	0	200
30	PZ08_Chen_7	0	33	141	28	1	0	203
31	PZ08_Bujnicki_9	0	29	141	33	2	0	205
32	PZ08_Dokholyan_2	0	3	131	75	0	0	209
33	PZ08_Bujnicki_8	0	29	163	37	8	0	237
34	PZ08_Bujnicki_10	0	28	173	29	8	3	241
35	PZ08_Bujnicki_6	0	28	203	26	4	0	261
36	PZ08_Bujnicki_1	0	30	204	25	3	1	263
37	PZ08_Bujnicki_4	0	32	235	22	1	1	291
38	PZ08_Bujnicki_5	0	44	225	23	3	0	295
39	PZ08_Bujnicki_2	0	30	254	26	4	0	314
40	PZ08_Bujnicki_3	0	46	248	23	3	0	320
41	PZ08_Chen_8	0	197	284	49	1	0	531
42	PZ08_Chen_6	0	186	312	47	0	0	545
43	PZ08_Chen_9	0	211	365	61	1	0	638
Average		0.14	22.88	110.60	28.21	1.16	0.14	163.14
Standard deviation		0.52	50.58	92.76	20.94	2.21	0.52	147.84
Median		0	1	83	26	0	0	119

Table S10. MAXIT report on structures in Puzzle 09.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ09_Das_6	0	0	0	1	0	0	1
2	PZ09_Das_7	0	0	0	1	0	0	1
3	PZ09_refstructure	0	0	2	0	0	0	2
4	PZ09_Das_8	0	0	1	1	0	0	2
5	PZ09_Das_9	0	0	1	1	0	0	2
6	PZ09_Das_1	0	1	3	1	0	0	5
7	PZ09_Das_3	0	1	3	1	0	0	5
8	PZ09_Das_4	0	1	3	1	0	0	5
9	PZ09_Das_2	0	1	4	1	0	0	6
10	PZ09_Das_5	0	1	4	1	0	0	6
11	PZ09_Chen_4	17	0	2	0	0	2	21
12	PZ09_Chen_3	16	1	5	0	0	2	24
13	PZ09_Chen_2	20	1	4	0	0	1	26
14	PZ09_Chen_1	7	3	21	0	0	2	33
15	PZ09_Chen_5	22	2	8	0	0	1	33
16	PZ09_Chen_7	24	3	17	0	0	1	45
17	PZ09_Ding_5	0	0	42	24	0	0	66
18	PZ09_Ding_7	0	0	57	14	0	0	71
19	PZ09_Ding_6	0	0	52	21	0	0	73
20	PZ09_Chen_8	37	5	26	0	0	12	80

21	PZ09_Ding_8	0	1	62	20	0	0	83
22	PZ09_Ding_4	0	0	59	26	0	0	85
23	PZ09_Ding_9	0	1	64	20	0	0	85
24	PZ09_Ding_10	0	0	60	27	0	0	87
25	PZ09_Ding_3	0	0	59	29	0	0	88
26	PZ09_Chen_6	46	6	28	0	0	13	93
27	PZ09_Ding_1	0	1	69	25	0	0	95
28	PZ09_Ding_2	0	0	78	24	0	0	102
29	PZ09_Dokholyan_3	0	2	68	49	0	0	119
30	PZ09_Dokholyan_1	0	1	76	48	0	0	125
31	PZ09_Bujnicki_3	0	14	86	15	12	0	127
32	PZ09_Bujnicki_4	0	14	86	15	12	0	127
33	PZ09_Bujnicki_5	0	14	86	15	12	0	127
34	PZ09_Dokholyan_4	0	4	76	54	0	0	134
35	PZ09_Dokholyan_2	0	4	81	53	0	0	138
Average		5.40	2.34	36.94	13.94	1.03	0.97	60.63
Standard deviation		11.53	3.93	32.80	16.95	3.41	2.95	48.03
Median		0	1	28	1	0	0	71

Table S11. MAXIT report on structures in Puzzle 10.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ10_Das_5	1	3	7	0	0	2	13
2	PZ10_refstructure	15	0	0	0	0	0	15
3	PZ10_Das_4	1	4	11	0	0	2	18
4	PZ10_Das_1	1	4	11	0	0	3	19
5	PZ10_Das_2	1	5	11	0	0	2	19
6	PZ10_Das_3	1	5	13	0	0	3	22
7	PZ10_Dokholyan_7	0	1	126	51	0	0	178
8	PZ10_Dokholyan_5	0	0	125	61	0	0	186
9	PZ10_Dokholyan_4	0	1	129	59	0	0	189
10	PZ10_Dokholyan_3	0	1	129	62	0	0	192
11	PZ10_Dokholyan_6	0	0	134	58	1	0	193
12	PZ10_Dokholyan_9	0	0	133	60	0	0	193
13	PZ10_Dokholyan_1	0	0	137	58	0	0	195
14	PZ10_Dokholyan_2	0	1	138	66	0	0	205
15	PZ10_Dokholyan_8	0	1	144	66	0	0	211
16	PZ10_Dokholyan_10	0	0	142	72	1	0	215
17	PZ10_Chen_1	0	35	167	38	2	1	243
18	PZ10_Bujnicki_4	0	43	211	47	17	0	318
19	PZ10_Bujnicki_3	0	49	212	37	26	0	324
20	PZ10_Bujnicki_9	0	49	221	41	18	0	329
21	PZ10_Bujnicki_2	0	47	216	48	19	0	330
22	PZ10_Bujnicki_1	0	48	220	44	20	0	332

23	PZ10_Bujnicki_10	0	40	222	51	25	0	338
24	PZ10_Bujnicki_6	0	48	227	45	18	0	338
25	PZ10_Bujnicki_5	0	43	225	53	18	0	339
26	PZ10_Bujnicki_8	0	46	224	56	13	0	339
27	PZ10_Bujnicki_7	0	47	251	60	16	0	374
Average		0.74	19.30	140.22	41.96	7.19	0.48	209.89
Standard deviation		2.88	21.93	81.97	24.37	9.53	0.98	122.06
Median		0	4	138	51	0	0	205

Table S12. MAXIT report on structures in Puzzle 11.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ11_Adamiak_10	0	0	0	0	0	0	0
2	PZ11_Adamiak_1	0	0	0	0	0	0	0
3	PZ11_Adamiak_2	0	0	0	0	0	0	0
4	PZ11_Adamiak_3	0	0	0	0	0	0	0
5	PZ11_Adamiak_4	0	0	0	0	0	0	0
6	PZ11_Adamiak_5	0	0	0	0	0	0	0
7	PZ11_Adamiak_6	0	0	0	0	0	0	0
8	PZ11_Adamiak_7	0	0	0	0	0	0	0
9	PZ11_Adamiak_8	0	0	0	0	0	0	0
10	PZ11_Adamiak_9	0	0	0	0	0	0	0
11	PZ11_Chén_8	0	0	0	0	0	0	0
12	PZ11_Das_10	0	0	0	0	0	0	0
13	PZ11_Chén_10	0	0	1	0	0	0	1
14	PZ11_Das_9	1	0	0	0	0	0	1
15	PZ11_Chén_6	0	0	0	0	0	1	1
16	PZ11_Chén_9	0	0	0	0	0	1	1
17	PZ11_refstructure	0	0	1	0	0	0	1
18	PZ11_Chén_7	0	0	1	0	0	1	2
19	PZ11_Das_6	0	2	2	0	0	1	5
20	PZ11_Das_8	0	2	2	0	0	1	5
21	PZ11_Das_3	0	2	2	0	0	1	5
22	PZ11_Das_5	0	2	2	0	0	1	5
23	PZ11_Das_4	0	2	3	0	0	1	6
24	PZ11_Das_1	0	3	3	0	0	1	7
25	PZ11_Das_7	1	4	4	0	0	1	10
26	PZ11_Das_2	4	2	3	0	0	1	10
27	PZ11_Bujnicki_1	0	3	4	12	2	0	21
28	PZ11_Bujnicki_5	0	1	7	12	2	0	22
29	PZ11_Bujnicki_9	0	3	8	9	4	0	24
30	PZ11_Bujnicki_3	0	5	5	9	5	0	24
31	PZ11_Bujnicki_2	0	5	8	10	3	0	26
32	PZ11_Bujnicki_7	0	1	9	16	2	0	28

33	PZ11_Bujnicki_10	0	3	10	10	7	0	30
34	PZ11_Bujnicki_8	0	4	12	17	3	0	36
35	PZ11_Bujnicki_6	0	5	11	18	3	0	37
36	PZ11_Chen_4	0	0	34	5	0	0	39
37	PZ11_Chen_3	0	3	37	6	0	0	46
38	PZ11_Chen_1	0	2	42	6	0	0	50
39	PZ11_Chen_2	0	5	40	7	0	0	52
40	PZ11_Chen_5	0	1	42	9	0	0	52
41	PZ11_Ding_3	0	0	37	15	0	0	52
42	PZ11_Ding_6	0	0	38	19	0	0	57
43	PZ11_Ding_1	0	0	41	19	0	0	60
44	PZ11_Ding_8	0	0	44	16	0	0	60
45	PZ11_Ding_9	0	0	43	20	0	0	63
46	PZ11_Ding_5	0	0	48	20	0	0	68
47	PZ11_Ding_7	0	0	49	23	0	0	72
48	PZ11_Ding_10	0	0	55	18	0	0	73
49	PZ11_Ding_4	0	0	54	21	0	0	75
50	PZ11_Ding_2	0	0	52	24	0	0	76
51	PZ11_Xiao_3	0	0	68	28	0	0	96
52	PZ11_Xiao_2	0	0	75	29	0	0	104
53	PZ11_Xiao_1	0	0	80	28	0	0	108
54	PZ11_Bujnicki_4	0	78	254	37	5	0	374
Average		0.11	2.56	22.80	8.57	0.67	0.20	34.91
Standard deviation		0.57	10.59	39.60	10.12	1.57	0.41	56.38
Median		0	0	4.5	5.5	0	0	21.5

Table S13. MAXIT report on structures in Puzzle 12.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ12_Adamiak_1	0	0	0	0	0	0	0
2	PZ12_Adamiak_2	0	0	0	0	0	0	0
3	PZ12_Adamiak_3	0	0	0	0	0	0	0
4	PZ12_Bujnicki_6	1	0	0	0	0	0	1
5	PZ12_Das_5	1	0	1	0	0	0	2
6	PZ12_Das_9	0	1	1	0	0	0	2
7	PZ12_Das_8	0	1	1	0	0	0	2
8	PZ12_Bujnicki_7	2	0	0	0	0	0	2
9	PZ12_Bujnicki_8	3	0	0	0	0	0	3
10	PZ12_Bujnicki_10	4	0	0	0	0	0	4
11	PZ12_Das_3	0	1	3	0	0	0	4
12	PZ12_Das_10	0	1	2	0	0	1	4
13	PZ12_Bujnicki_1	4	0	2	0	0	0	6
14	PZ12_Das_1	0	1	4	0	0	1	6
15	PZ12_Bujnicki_5	1	0	5	0	0	0	6

16	PZ12_Bujnicki_4	3	0	3	0	0	0	6
17	PZ12_Das_4	2	3	1	0	0	1	7
18	PZ12_Bujnicki_3	5	0	2	0	0	0	7
19	PZ12_Bujnicki_9	3	0	5	0	0	0	8
20	PZ12_refstructure	0	0	7	0	0	2	9
21	PZ12_Das_2	0	2	6	0	0	1	9
22	PZ12_Das_7	0	3	4	0	0	2	9
23	PZ12_Das_6	1	3	5	0	0	2	11
24	PZ12_Bujnicki_2	0	0	24	0	0	0	24
25	PZ12_Chen_1	0	2	61	14	0	0	77
26	PZ12_Chen_3	0	5	66	19	0	0	90
27	PZ12_Chen_2	0	0	61	27	2	0	90
28	PZ12_Chen_4	0	11	81	10	1	0	103
29	PZ12_Chen_7	0	8	81	14	1	0	104
30	PZ12_Chen_6	0	17	81	20	0	0	118
31	PZ12_Chen_5	0	17	98	11	0	0	126
32	PZ12_Ding_6	0	2	88	46	0	0	136
33	PZ12_Ding_1	0	0	89	48	0	0	137
34	PZ12_Ding_10	0	1	87	54	0	0	142
35	PZ12_Ding_5	0	1	98	44	0	0	143
36	PZ12_Ding_3	7	0	88	50	0	0	145
37	PZ12_Ding_11	7	0	108	38	0	0	153
38	PZ12_Ding_4	0	0	102	51	0	0	153
39	PZ12_Ding_7	0	1	98	54	1	0	154
40	PZ12_Ding_12	0	0	110	51	0	0	161
41	PZ12_Ding_2	0	0	113	48	0	0	161
42	PZ12_Ding_9	0	1	112	50	0	0	163
43	PZ12_Chen_9	0	29	120	15	2	1	167
44	PZ12_Ding_8	0	0	117	57	0	0	174
45	PZ12_Weeks_2	0	0	94	89	0	0	183
46	PZ12_Chen_10	0	41	123	21	3	2	190
47	PZ12_Weeks_1	0	1	105	86	0	0	192
48	PZ12_Chen_8	0	36	143	13	0	1	193
49	PZ12_Weeks_3	0	4	127	87	0	0	218
50	PZ12_Xiao_3	0	29	252	51	6	0	338
51	PZ12_Xiao_2	3	68	376	59	6	0	512
52	PZ12_Xiao_1	4	67	384	59	1	1	516
Average		0.98	6.87	68.06	22.81	0.44	0.29	99.44
Standard deviation		1.82	15.45	84.33	27.20	1.27	0.61	117.18
Median		0	1	63.5	12	0	0	90

Table S14. MAXIT report on structures in Puzzle 13.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ13_Adamiak_1	0	0	0	0	0	0	0
2	PZ13_Das_10	0	0	0	0	0	0	0
3	PZ13_Das_4	0	0	0	0	0	0	0
4	PZ13_Das_1	0	0	0	0	0	0	0
5	PZ13_Das_6	0	0	0	0	0	0	0
6	PZ13_Das_9	0	0	0	0	0	0	0
7	PZ13_Das_2	0	0	0	0	0	0	0
8	PZ13_Das_5	0	0	0	0	0	0	0
9	PZ13_refstructure	0	0	1	0	0	1	2
10	PZ13_Das_8	0	1	1	0	0	0	2
11	PZ13_Das_7	0	0	3	0	1	0	4
12	PZ13_Das_3	0	2	2	0	6	1	11
13	PZ13_Bujnicki_8	0	9	12	10	0	0	31
14	PZ13_Bujnicki_10	0	11	17	8	4	0	40
15	PZ13_Chen_1	0	0	37	7	2	0	46
16	PZ13_Chen_4	0	0	43	5	2	0	50
17	PZ13_Ding_7	0	0	37	14	0	0	51
18	PZ13_Chen_6	0	3	37	11	1	0	52
19	PZ13_Chen_3	0	1	42	16	1	0	60
20	PZ13_Ding_5	0	0	38	23	0	0	61
21	PZ13_Ding_3	0	0	43	21	0	0	64
22	PZ13_Bujnicki_9	0	11	37	15	5	0	68
23	PZ13_Ding_8	0	0	49	20	0	0	69
24	PZ13_Ding_10	0	0	43	27	0	0	70
25	PZ13_Ding_4	0	0	50	21	0	0	71
26	PZ13_Chen_8	0	2	53	16	1	0	72
27	PZ13_Ding_1	0	0	46	26	0	0	72
28	PZ13_Ding_9	0	0	58	20	0	0	78
29	PZ13_Chen_7	0	2	65	11	1	0	79
30	PZ13_Ding_6	0	0	53	26	0	0	79
31	PZ13_Bujnicki_6	0	13	52	14	0	0	79
32	PZ13_Chen_9	0	13	48	15	4	0	80
33	PZ13_Chen_5	0	2	61	14	3	0	80
34	PZ13_Ding_2	0	0	63	27	0	0	90
35	PZ13_Chen_2	0	7	69	12	5	0	93
36	PZ13_Dokholyan_2	0	4	65	50	0	0	119
37	PZ13_Bujnicki_7	0	16	92	12	2	0	122
38	PZ13_Bujnicki_5	0	14	94	17	2	0	127
39	PZ13_Xiao_10	0	0	100	26	1	0	127
40	PZ13_Dokholyan_3	0	7	74	47	0	0	128
41	PZ13_Dokholyan_1	0	6	79	45	0	0	130
42	PZ13_Xiao_6	0	1	112	22	2	0	137

43	PZ13_Dokholyan_4	0	1	87	49	2	0	139
44	PZ13_Bujnicki_2	0	20	101	18	1	0	140
45	PZ13_Xiao_8	0	1	117	24	3	0	145
46	PZ13_Xiao_9	0	2	116	32	3	0	153
47	PZ13_Dokholyan_5	3	2	100	52	0	0	157
48	PZ13_Bujnicki_3	0	25	120	16	2	0	163
49	PZ13_Xiao_7	4	37	204	28	1	1	275
50	PZ13_Bujnicki_4	0	48	220	22	0	0	290
51	PZ13_Bujnicki_1	0	55	224	21	3	0	303
52	PZ13_Xiao_1	1	98	269	37	2	1	408
53	PZ13_Xiao_4	0	93	281	39	1	0	414
54	PZ13_Xiao_2	5	112	279	33	6	1	436
55	PZ13_Xiao_5	0	117	288	38	1	0	444
56	PZ13_Xiao_3	4	119	313	30	5	1	472
Average		0.30	15.27	78.48	18.52	1.30	0.11	113.98
Standard deviation		1.06	31.51	83.43	14.55	1.72	0.31	122.69
Median		0	1.5	52.5	16.5	1	0	78.5

Table S15. MAXIT report on structures in Puzzle 14 (bound).

No .	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ14_AdamiakPostExp_1	0	0	0	0	0	0	0
2	PZ14_AdamiakPostExp_2	0	0	0	0	0	0	0
3	PZ14_DasPostExp_9	0	0	0	0	0	0	0
4	PZ14_AdamiakPreExp_1	0	0	0	0	0	0	0
5	PZ14_DasPreExp_10	0	0	0	0	0	0	0
6	PZ14_AdamiakPreExp_2	0	0	0	0	0	0	0
7	PZ14_DasPreExp_1	0	0	0	0	0	0	0
8	PZ14_DasPreExp_6	0	0	0	0	0	0	0
9	PZ14_DasPostExp_6	0	0	0	0	0	0	0
10	PZ14_ChenPostExp_2	0	0	0	0	0	0	0
11	PZ14_ChenPostExp_10	0	0	0	0	0	0	0
12	PZ14_ChenPostExp_1	0	0	0	0	0	0	0
13	PZ14_ChenPostExp_4	0	0	0	0	0	0	0
14	PZ14_ChenPostExp_5	0	0	0	0	0	0	0
15	PZ14_ChenPostExp_8	0	0	0	0	0	0	0
16	PZ14_ChenPostExp_7	0	0	0	0	0	0	0
17	PZ14_ChenPostExp_9	0	0	0	0	0	0	0
18	PZ14_ChenPostExp_6	0	0	0	0	0	0	0
19	PZ14_ChenPostExp_3	0	0	0	0	0	0	0
20	PZ14_DasPostExp_4	0	0	1	0	0	0	1
21	PZ14_DasPostExp_1	0	0	2	0	0	0	2
22	PZ14_DasPreExp_5	4	0	0	0	0	0	4
23	PZ14_DasPreExp_7	1	1	2	0	0	0	4

24	PZ14_DasPostExp_10	4	0	0	0	0	0	4
25	PZ14_DasPostExp_2	4	0	0	0	0	0	4
26	PZ14_DasPostExp_5	4	0	0	0	0	0	4
27	PZ14_refstructure_bound	7	0	1	0	0	0	8
28	PZ14_DasPostExp_3	5	1	2	0	0	0	8
29	PZ14_DasPreExp_4	8	0	1	0	0	0	9
30	PZ14_DasPostExp_7	7	0	4	0	0	0	11
31	PZ14_DasPreExp_2	7	0	4	0	0	0	11
32	PZ14_DasPostExp_8	10	0	2	0	0	0	12
33	PZ14_DasPreExp_3	10	0	2	0	0	0	12
34	PZ14_DasPreExp_8	8	0	5	0	0	0	13
35	PZ14_DasPreExp_9	11	0	3	0	0	0	14
36	PZ14_BujnickiPreExp_4	9	4	7	1	2	0	23
37	PZ14_BujnickiPreExp_5	0	15	8	3	2	0	28
38	PZ14_DingPreExp_1	0	0	45	17	0	0	62
39	PZ14_DingPostExp_3	0	1	47	18	0	0	66
40	PZ14_DingPreExp_5	0	0	43	24	0	0	67
41	PZ14_DingPostExp_10	0	0	46	24	0	0	70
42	PZ14_DingPostExp_6	0	1	45	25	0	0	71
43	PZ14_DingPostExp_5	0	0	48	26	0	0	74
44	PZ14_DingPreExp_3	0	1	49	24	0	0	74
45	PZ14_DingPostExp_4	0	1	44	30	0	0	75
46	PZ14_DingPostExp_1	0	0	53	24	0	0	77
47	PZ14_DingPostExp_9	0	0	53	25	0	0	78
48	PZ14_BujnickiPreExp_6	0	16	53	5	5	0	79
49	PZ14_DingPreExp_8	0	0	57	23	0	0	80
50	PZ14_DingPreExp_4	0	1	56	24	0	0	81
51	PZ14_DingPreExp_6	0	0	57	25	0	0	82
52	PZ14_DingPreExp_2	0	0	55	27	0	0	82
53	PZ14_DingPostExp_2	0	2	56	25	0	0	83
54	PZ14_DingPreExp_7	0	0	60	24	0	0	84
55	PZ14_DingPostExp_7	0	2	57	29	0	0	88
56	PZ14_DingPostExp_8	0	0	63	24	0	1	88
57	PZ14_BujnickiPreExp_7	0	14	62	13	10	0	99
58	PZ14_BujnickiPostExp_3	0	23	73	11	9	0	116
59	PZ14_BujnickiPostExp_5	2	41	104	24	15	0	186
60	PZ14_BujnickiPostExp_1	0	48	125	13	5	0	191
61	PZ14_BujnickiPostExp_4	3	54	159	10	3	0	229
62	PZ14_BujnickiPostExp_2	3	50	160	24	5	0	242
Average		1.73	4.45	27.65	8.74	0.90	0.02	43.48
Standard deviation		3.15	12.42	38.67	11.33	2.71	0.13	57.82
Median		0	0	2.5	0	0	0	11.5

Table S16. MAXIT report on structures in Puzzle 14 (free).

No.	3D RNA model	Close con- tacts	Bond lengths	Bond angles	Plana- rity	Chira- lity	Poly- mer linkage	Total
1	PZ14_DasPreExp_5	0	0	0	0	0	0	0
2	PZ14_DasPostExp_10	0	0	0	0	0	0	0
3	PZ14_DasPostExp_3	0	0	0	0	0	0	0
4	PZ14_DasPostExp_2	0	0	0	0	0	0	0
5	PZ14_DasPreExp_1	0	0	0	0	0	0	0
6	PZ14_DasPostExp_6	0	0	0	0	0	0	0
7	PZ14_DasPostExp_9	0	0	1	0	0	0	1
8	PZ14_DasPreExp_10	0	0	1	0	0	0	1
9	PZ14_DasPostExp_4	1	0	0	0	0	0	1
10	PZ14_DasPostExp_5	0	0	2	0	0	0	2
11	PZ14_DasPreExp_2	0	0	3	0	0	0	3
12	PZ14_DasPostExp_7	0	0	3	0	0	0	3
13	PZ14_DasPostExp_8	0	0	3	0	0	0	3
14	PZ14_DasPreExp_4	0	0	3	0	0	0	3
15	PZ14_DasPreExp_6	0	1	2	0	0	1	4
16	PZ14_DasPostExp_1	0	1	2	0	0	1	4
17	PZ14_DasPreExp_9	0	0	4	0	0	0	4
18	PZ14_DasPreExp_3	5	0	0	0	0	0	5
19	PZ14_DasPreExp_8	0	0	5	0	0	0	5
20	PZ14_DasPreExp_7	6	0	0	0	0	0	6
21	PZ14_refstructure_free	21	0	4	0	0	0	26
22	PZ14_ChenPostExp_2	0	4	33	6	2	1	46
23	PZ14_ChenPostExp_4	0	7	40	7	2	1	57
24	PZ14_ChenPostExp_8	0	7	39	10	0	1	57
25	PZ14_ChenPostExp_1	0	6	45	7	1	0	59
26	PZ14_ChenPostExp_5	0	6	47	4	1	1	59
27	PZ14_DingPostExp_1	0	1	34	26	0	0	61
28	PZ14_DingPreExp_4	0	0	41	20	0	0	61
29	PZ14_DingPostExp_2	0	0	39	23	0	0	62
30	PZ14_ChenPostExp_10	0	15	41	4	2	1	63
31	PZ14_ChenPostExp_6	0	8	44	11	0	1	64
32	PZ14_ChenPostExp_7	0	11	44	10	0	1	66
33	PZ14_DingPostExp_5	0	1	43	23	0	0	67
34	PZ14_ChenPostExp_9	0	10	43	12	2	1	68
35	PZ14_DingPreExp_1	0	0	46	25	0	0	71
36	PZ14_DingPostExp_7	0	0	51	24	0	0	75
37	PZ14_DingPostExp_10	0	0	61	14	0	0	75
38	PZ14_DingPostExp_3	0	1	49	26	0	0	76
39	PZ14_DingPostExp_9	0	0	56	20	0	0	76
40	PZ14_DingPostExp_8	0	0	55	22	0	0	77
41	PZ14_DingPostExp_4	0	0	53	24	1	0	78
42	PZ14_DingPostExp_6	0	0	53	26	0	0	79

43	PZ14_DingPreExp_3	0	0	52	27	0	0	79
44	PZ14_BujnickiPreExp_4	0	13	52	11	6	0	82
45	PZ14_BujnickiPreExp_2	0	12	53	8	10	0	83
46	PZ14_BujnickiPreExp_3	0	14	53	12	8	0	87
47	PZ14_DingPreExp_2	0	1	67	24	0	0	92
48	PZ14_ChenPostExp_3	0	22	61	9	1	1	94
49	PZ14_BujnickiPostExp_1	0	19	65	6	4	0	94
50	PZ14_BujnickiPostExp_2	0	21	76	10	5	0	112
51	PZ14_BujnickiPreExp_1	0	16	96	6	7	0	125
52	PZ14_BujnickiPostExp_3	1	26	85	17	3	0	132
53	PZ14_BujnickiPostExp_4	0	35	99	23	14	1	172
Average		0.64	4.87	33.00	9.38	1.30	0.23	49.43
Standard deviation		3.05	8.08	28.60	9.82	2.86	0.42	42.64
Median		0	0	41	7	0	0	61

Table S17. MAXIT report on structures in Puzzle 15.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ15_FARFAR2_6	0	0	0	0	0	0	0
2	PZ15_FARFAR2_8	0	0	0	0	0	0	0
3	PZ15_RNAComposer1_1	0	0	0	0	0	0	0
4	PZ15_RNAComposer1_2	0	0	0	0	0	0	0
5	PZ15_RNAComposer2_1	0	0	0	0	0	0	0
6	PZ15_RNAComposer2_2	0	0	0	0	0	0	0
7	PZ15_Adamiak_10	0	0	0	0	0	0	0
8	PZ15_Adamiak_1	0	0	0	0	0	0	0
9	PZ15_Adamiak_2	0	0	0	0	0	0	0
10	PZ15_Adamiak_3	0	0	0	0	0	0	0
11	PZ15_Adamiak_4	0	0	0	0	0	0	0
12	PZ15_Adamiak_5	0	0	0	0	0	0	0
13	PZ15_Adamiak_6	0	0	0	0	0	0	0
14	PZ15_Adamiak_7	0	0	0	0	0	0	0
15	PZ15_Adamiak_8	0	0	0	0	0	0	0
16	PZ15_Adamiak_9	0	0	0	0	0	0	0
17	PZ15_FARFAR2_1	0	0	0	0	0	0	0
18	PZ15_FARFAR2_4	0	0	0	0	0	0	0
19	PZ15_refstructure	0	0	0	0	0	0	0
20	PZ15_FARFAR2_7	0	1	0	0	0	0	1
21	PZ15_FARFAR2_2	0	0	1	0	0	0	1
22	PZ15_FARFAR2_3	0	0	1	0	0	0	1
23	PZ15_FARFAR1_8	0	1	1	0	0	0	2
24	PZ15_FARFAR2_10	0	0	2	0	0	0	2
25	PZ15_FARFAR2_5	0	1	1	0	0	0	2
26	PZ15_FARFAR2_9	0	1	2	0	0	0	3

27	PZ15_FARFAR1_10	0	1	3	0	0	0	4
28	PZ15_FARFAR1_1	0	1	3	0	0	0	4
29	PZ15_FARFAR1_2	0	1	2	0	0	0	3
30	PZ15_FARFAR1_3	0	1	2	0	0	0	3
31	PZ15_FARFAR1_5	0	1	3	0	0	0	4
32	PZ15_FARFAR1_6	0	1	2	0	0	0	3
33	PZ15_FARFAR1_7	0	2	2	0	0	0	4
34	PZ15_FARFAR1_9	0	2	2	0	0	0	4
35	PZ15_FARFAR1_4	1	2	3	0	0	0	6
36	PZ15_Chén_3	0	1	38	8	0	0	47
37	PZ15_Chén_2	0	0	40	8	0	0	48
38	PZ15_Chén_1	0	2	43	11	0	0	56
39	PZ15_Chén_4	0	4	55	10	0	0	69
40	PZ15_Chén_6	0	5	54	11	0	0	70
41	PZ15_Chén_5	0	6	60	12	0	0	78
42	PZ15_Chén_9	0	5	55	16	3	0	79
43	PZ15_Chén_8	0	16	57	17	2	0	92
44	PZ15_Chén_7	0	12	70	18	0	0	100
45	PZ15_Chén_10	0	17	77	13	2	0	109
46	PZ15_SimRNA2_10	13	42	122	22	0	12	211
47	PZ15_SimRNA2_2	7	49	125	17	0	18	216
48	PZ15_SimRNA1_7	10	53	129	15	0	12	219
49	PZ15_SimRNA2_4	8	47	145	17	0	13	230
50	PZ15_SimRNA1_6	10	49	141	16	1	18	235
51	PZ15_SimRNA1_1	21	49	133	14	1	17	235
52	PZ15_SimRNA1_10	10	51	139	15	3	18	236
53	PZ15_SimRNA1_8	12	55	132	21	2	15	237
54	PZ15_SimRNA1_5	14	52	139	16	2	16	239
55	PZ15_SimRNA1_2	14	45	152	22	1	13	247
56	PZ15_SimRNA1_9	24	52	136	18	1	20	251
57	PZ15_SimRNA1_3	18	51	146	21	0	16	252
58	PZ15_SimRNA2_9	15	56	148	19	3	16	257
59	PZ15_SimRNA2_5	33	54	139	18	0	13	257
60	PZ15_SimRNA2_7	35	49	137	19	1	19	260
61	PZ15_3dRNA2_8	2	19	183	35	22	1	262
62	PZ15_SimRNA2_6	20	56	150	18	1	18	263
63	PZ15_SimRNA2_8	6	56	156	19	3	24	264
64	PZ15_SimRNA2_1	7	51	162	25	2	17	264
65	PZ15_3dRNA2_10	1	21	186	35	22	1	266
66	PZ15_3dRNA2_1	2	20	193	33	22	1	271
67	PZ15_3dRNA2_2	2	21	191	35	22	1	272
68	PZ15_3dRNA2_4	2	18	192	37	22	1	272
69	PZ15_3dRNA2_7	2	22	189	36	22	2	273
70	PZ15_3dRNA2_6	3	23	193	32	22	2	275
71	PZ15_3dRNA2_3	2	22	191	37	22	2	276

72	PZ15_3dRNA2_9	2	17	199	36	22	1	277
73	PZ15_SimRNA1_4	26	57	144	28	1	24	280
74	PZ15_SimRNA2_3	33	56	147	23	1	21	281
75	PZ15_3dRNA2_5	2	21	199	35	22	2	281
Average		4.76	17.57	70.89	11.44	3.33	4.72	112.72
Standard deviation		8.69	21.81	75.53	12.61	7.42	7.68	120.51
Median		0	2	43	10	0	0	56

Table S18. MAXIT report on structures in Puzzle 17.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ17_Adamiak_1	0	0	0	0	0	0	0
2	PZ17_Adamiak_2	0	0	0	0	0	0	0
3	PZ17_Adamiak_3	0	0	0	0	0	0	0
4	PZ17_RNAComposer1_10	0	0	0	0	0	0	0
5	PZ17_RNAComposer1_1	0	0	0	0	0	0	0
6	PZ17_RNAComposer1_2	0	0	0	0	0	0	0
7	PZ17_RNAComposer1_3	0	0	0	0	0	0	0
8	PZ17_RNAComposer1_4	0	0	0	0	0	0	0
9	PZ17_RNAComposer1_5	0	0	0	0	0	0	0
10	PZ17_RNAComposer1_6	0	0	0	0	0	0	0
11	PZ17_RNAComposer1_7	0	0	0	0	0	0	0
12	PZ17_RNAComposer1_8	0	0	0	0	0	0	0
13	PZ17_RNAComposer1_9	0	0	0	0	0	0	0
14	PZ17_RNAComposer2_10	0	0	0	0	0	0	0
15	PZ17_Das_10	0	0	0	0	0	0	0
16	PZ17_RNAComposer2_9	0	0	0	0	0	0	0
17	PZ17_Das_4	0	0	0	0	0	0	0
18	PZ17_Das_5	0	0	0	0	0	0	0
19	PZ17_Das_6	0	0	0	0	0	0	0
20	PZ17_Das_7	0	0	0	0	0	0	0
21	PZ17_Das_8	0	0	0	0	0	0	0
22	PZ17_Das_9	0	0	0	0	0	0	0
23	PZ17_DasExtraInfo_1	0	0	0	0	0	0	0
24	PZ17_RNAComposer2_5	1	0	0	0	0	0	1
25	PZ17_Das_2	1	0	0	0	0	0	1
26	PZ17_Das_3	1	0	0	0	0	0	1
27	PZ17_Das_1	0	1	2	0	0	0	3
28	PZ17_DasExtraInfo_3	0	1	1	0	0	1	3
29	PZ17_RNAComposer2_2	4	0	0	0	0	0	4
30	PZ17_RNAComposer2_8	5	0	0	0	0	0	5
31	PZ17_RNAComposer2_6	6	0	0	0	0	0	6
32	PZ17_RNAComposer2_7	6	0	0	0	0	0	6
33	PZ17_DasExtraInfo_2	0	1	3	0	1	1	6

34	PZ17_RNAComposer2_4	9	0	0	0	0	0	9
35	PZ17_refstructure	0	0	10	0	0	1	11
36	PZ17_RNAComposer2_1	12	0	0	0	0	0	12
37	PZ17_Chén_10	0	0	21	3	1	0	25
38	PZ17_Chén_3	0	0	34	11	2	0	47
39	PZ17_Ding_2	0	0	32	22	0	0	54
40	PZ17_Ding_4	0	0	39	20	0	0	59
41	PZ17_Bujnicki_4	0	0	50	8	1	0	59
42	PZ17_Ding_8	0	1	39	20	0	0	60
43	PZ17_Ding_1	0	0	43	19	0	0	62
44	PZ17_Ding_5	0	0	39	24	0	0	63
45	PZ17_Ding_3	0	0	45	19	0	0	64
46	PZ17_Bujnicki_6	0	0	54	12	0	0	66
47	PZ17_Ding_10	0	0	46	24	0	0	70
48	PZ17_Ding_6	0	0	50	20	0	0	70
49	PZ17_Bujnicki_10	0	0	56	16	1	0	73
50	PZ17_Bujnicki_2	0	0	56	16	1	0	73
51	PZ17_Bujnicki_3	0	0	53	20	1	0	74
52	PZ17_Major_2	0	1	57	16	0	0	74
53	PZ17_Bujnicki_8	0	13	63	1	0	0	77
54	PZ17_Ding_9	0	0	55	24	0	0	79
55	PZ17_Bujnicki_7	0	13	65	3	0	0	81
56	PZ17_Ding_7	0	0	64	18	0	0	82
57	PZ17_Major_3	0	0	61	18	3	0	82
58	PZ17_Major_1	0	0	62	25	0	0	87
59	PZ17_Major_4	0	0	70	17	0	0	87
60	PZ17_Major_6	0	0	65	21	5	0	91
61	PZ17_Major_8	0	0	65	26	4	0	95
62	PZ17_Major_5	0	0	72	23	0	0	95
63	PZ17_Chén_7	0	20	64	20	3	0	107
64	PZ17_Major_7	0	0	82	24	4	0	110
65	PZ17_Major_9	4	8	85	13	9	0	119
66	PZ17_Dohkolyan_1	0	4	68	48	0	0	120
67	PZ17_Chén_8	0	28	74	17	3	0	122
68	PZ17_Dohkolyan_2	2	2	73	47	0	0	124
69	PZ17_Dohkolyan_3	0	0	75	49	0	0	124
70	PZ17_Bujnicki_1	0	15	105	13	4	0	137
71	PZ17_Bujnicki_9	0	15	105	13	4	0	137
72	PZ17_Major_10	4	7	102	27	5	0	145
73	PZ17_Xiao_4	0	1	100	22	27	0	150
74	PZ17_Xiao_2	0	1	92	28	36	0	157
75	PZ17_SimRNA2_2	5	37	95	11	1	14	163
76	PZ17_Xiao_3	0	1	93	32	40	0	166
77	PZ17_Xiao_1	0	10	110	29	17	0	166
78	PZ17_Xiao_7	0	1	100	37	31	0	169

79	PZ17_Xiao_10	0	1	93	33	45	0	172
80	PZ17_SimRNA1_2	19	39	91	14	0	12	175
81	PZ17_SimRNA1_8	19	28	105	14	1	9	176
82	PZ17_SimRNA2_4	7	46	100	12	1	13	179
83	PZ17_Bujnicki_5	0	20	138	16	6	0	180
84	PZ17_SimRNA1_7	6	44	95	20	0	18	183
85	PZ17_SimRNA2_8	12	35	95	20	1	21	184
86	PZ17_SimRNA2_3	13	47	99	13	1	13	186
87	PZ17_SimRNA1_1	33	35	100	9	1	17	195
88	PZ17_SimRNA1_3	23	41	101	16	0	14	195
89	PZ17_SimRNA1_6	18	45	99	17	1	16	196
90	PZ17_Chén_9	28	29	116	4	0	20	197
91	PZ17_SimRNA1_9	7	41	117	18	0	16	199
92	PZ17_Xiao_5	4	20	129	27	20	0	200
93	PZ17_SimRNA2_5	10	44	111	19	2	19	205
94	PZ17_SimRNA2_1	25	44	112	15	1	10	207
95	PZ17_Chén_2	29	36	120	1	0	21	207
96	PZ17_SimRNA2_7	20	43	112	17	0	18	210
97	PZ17_Xiao_8	4	13	132	31	38	0	218
98	PZ17_Chén_1	46	28	133	0	0	12	219
99	PZ17_Xiao_6	5	23	143	35	16	0	222
100	PZ17_Xiao_9	0	12	135	40	36	0	223
101	PZ17_SimRNA2_9	31	47	113	13	2	17	223
102	PZ17_SimRNA2_6	15	46	133	22	2	12	230
103	PZ17_SimRNA1_5	44	42	114	15	0	20	235
104	PZ17_SimRNA1_4	38	46	134	17	0	19	254
105	PZ17_Chén_6	82	33	119	2	0	21	257
106	PZ17_Chén_4	58	39	139	3	0	20	259
107	PZ17_Chén_5	100	26	125	3	1	24	279
108	PZ17_RNAComposer2_3	5	142	144	33	0	0	324
Average		7.05	12.19	58.26	12.73	3.51	3.69	97.43
Standard deviation		16.11	20.71	48.69	12.56	9.30	7.12	87.64
Median		0	0	61.5	13	0	0	80

Table S19. MAXIT report on structures in Puzzle 18.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ18_RNAComposer_3	0	0	0	0	0	0	0
2	PZ18_RNAComposer_4	0	0	0	0	0	0	0
3	PZ18_RNAComposer_5	0	0	0	0	0	0	0
4	PZ18_FARFAR_10	0	0	0	0	0	0	0
5	PZ18_FARFAR_1	0	0	0	0	0	0	0
6	PZ18_FARFAR_3	0	0	0	0	0	0	0
7	PZ18_FARFAR_4	0	0	0	0	0	0	0
8	PZ18_FARFAR_7	0	0	0	0	0	0	0
9	PZ18_FARFAR_8	0	0	0	0	0	0	0
10	PZ18_RNAComposer_1	0	0	0	0	0	0	0
11	PZ18_RNAComposer_2	0	0	0	0	0	0	0
12	PZ18_refstructure	0	0	1	0	0	0	1
13	PZ18_FARFAR_5	0	0	1	0	0	0	1
14	PZ18_FARFAR_6	1	0	0	0	0	0	1
15	PZ18_FARFAR_9	0	1	0	0	0	0	1
16	PZ18_YagoubAli_1	1	1	1	0	0	0	3
17	PZ18_FARFAR_2	4	0	0	0	0	0	4
18	PZ18_Lee_2	0	1	2	5	0	0	8
19	PZ18_LeeServer_2	0	1	2	5	0	0	8
20	PZ18_Lee_1	0	1	2	7	0	0	10
21	PZ18_LeeServer_4	2	1	1	7	0	0	11
22	PZ18_LeeServer_5	2	1	2	7	0	0	12
23	PZ18_Lee_3	0	1	2	10	0	0	13
24	PZ18_Lee_4	2	1	2	8	0	0	13
25	PZ18_LeeServer_1	0	1	2	10	0	0	13
26	PZ18_Lee_5	1	1	2	10	0	0	14
27	PZ18_LeeServer_3	0	1	3	10	0	0	14
28	PZ18_Das_3	0	4	11	0	0	0	15
29	PZ18_Das_4	0	4	11	0	0	0	15
30	PZ18_Das_5	0	5	12	0	0	0	17
31	PZ18_Das_2	2	5	10	0	0	1	18
32	PZ18_Das_1	1	5	14	0	0	0	20
33	PZ18_Chen_5	0	13	34	5	0	0	52
34	PZ18_Chen_1	0	2	44	13	0	0	59
35	PZ18_Chen_2	0	3	45	13	0	0	61
36	PZ18_Ding_2	0	0	40	26	0	0	66
37	PZ18_Chen_4	0	6	52	11	0	0	69
38	PZ18_Chen_3	0	3	51	16	1	0	71
39	PZ18_Ding_4	0	0	50	24	0	0	74
40	PZ18_Ding_1	0	0	47	30	0	0	77
41	PZ18_Ding_5	0	0	60	25	0	0	85
42	PZ18_Ding_3	0	1	57	30	0	0	88

43	PZ18_3dRNA_2	0	1	105	22	3	0	131
44	PZ18_Dokholyan_2	0	7	85	52	0	0	144
45	PZ18_Dokholyan_3	0	7	89	51	0	0	147
46	PZ18_Dokholyan_1	0	6	97	51	0	0	154
47	PZ18_3dRNA_4	0	1	121	18	19	0	159
48	PZ18_3dRNA_5	0	1	129	24	16	0	170
49	PZ18_3dRNA_3	0	11	145	25	9	0	190
50	PZ18_SimRNA_1	12	47	95	19	1	16	190
51	PZ18_SimRNA_3	8	51	107	13	0	19	198
52	PZ18_3dRNA_1	1	10	154	26	13	0	204
53	PZ18_SimRNA_2	5	47	128	13	1	21	215
Average		0.79	4.75	34.26	11.06	1.19	1.08	53.13
Standard deviation		2.13	11.20	46.11	13.79	3.93	4.38	67.99
Median		0	1	3	7	0	0	14

Table S20. MAXIT report on structures in Puzzle 19.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ19_RNAComposer_1	0	0	0	0	0	0	0
2	PZ19_RNAComposer_2	0	0	0	0	0	0	0
3	PZ19_RNAComposer_3	0	0	0	0	0	0	0
4	PZ19_RNAComposer_4	0	0	0	0	0	0	0
5	PZ19_RNAComposer_5	0	0	0	0	0	0	0
6	PZ19_Adamiak_1	0	0	0	0	0	0	0
7	PZ19_Adamiak_2	0	0	0	0	0	0	0
8	PZ19_Adamiak_3	0	0	0	0	0	0	0
9	PZ19_Adamiak_4	0	0	0	0	0	0	0
10	PZ19_Adamiak_5	0	0	0	0	0	0	0
11	PZ19_FARFAR_1	1	0	0	0	0	0	1
12	PZ19_FARFAR_2	1	0	0	0	0	0	1
13	PZ19_FARFAR_7	1	0	0	0	0	0	1
14	PZ19_FARFAR_9	1	0	0	0	0	0	1
15	PZ19_FARFAR_10	1	1	0	0	0	0	2
16	PZ19_FARFAR_3	1	0	1	0	0	0	2
17	PZ19_FARFAR_4	1	0	1	0	0	0	2
18	PZ19_FARFAR_5	1	0	1	0	0	0	2
19	PZ19_FARFAR_6	1	1	0	0	0	0	2
20	PZ19_Das_1	0	1	3	0	0	0	4
21	PZ19_Das_5	0	2	2	0	0	0	4
22	PZ19_FARFAR_8	1	1	2	0	0	0	4
23	PZ19_Das_4	1	1	4	0	0	0	6
24	PZ19_Das_3	0	3	4	0	0	0	7
25	PZ19_Das_2	0	3	5	0	0	0	8
26	PZ19_LeeServer_5	0	2	4	12	0	0	18

27	PZ19_refstructure	0	7	16	0	0	0	23
28	PZ19_LeeServer_4	0	2	5	17	0	0	24
29	PZ19_Chen_2	0	2	37	11	0	0	50
30	PZ19_Chen_4	0	7	43	5	0	0	55
31	PZ19_Ding_4	0	1	41	19	0	0	61
32	PZ19_Chen_3	0	1	44	16	0	0	61
33	PZ19_Ding_2	0	0	38	26	0	0	64
34	PZ19_LeeServer_1	0	2	4	14	50	0	70
35	PZ19_Ding_5	0	1	45	25	0	0	71
36	PZ19_LeeServer_2	0	2	5	13	51	0	71
37	PZ19_LeeServer_3	0	2	5	15	49	0	71
38	PZ19_Ding_3	0	0	49	26	0	0	75
39	PZ19_Ding_1	0	1	52	26	0	0	79
40	PZ19_Bujnicki_1	0	8	60	9	2	0	79
41	PZ19_Bujnicki_2	0	6	84	9	5	0	104
42	PZ19_Dokholyan_1	0	0	61	46	0	0	107
43	PZ19_Bujnicki_5	0	10	80	9	11	0	110
44	PZ19_Chen_1	0	18	89	20	1	0	128
45	PZ19_Bujnicki_3	0	6	102	19	4	0	131
46	PZ19_SimRNA_1	14	38	91	12	1	11	167
47	PZ19_Chen_5	0	30	110	23	4	0	167
48	PZ19_3dRNA_5	1	13	117	27	11	0	169
49	PZ19_3dRNA_2	1	13	118	33	11	0	176
50	PZ19_Bujnicki_4	0	12	132	22	10	0	176
51	PZ19_3dRNA_4	1	12	121	29	15	0	178
52	PZ19_3dRNA_3	1	8	119	36	15	0	179
53	PZ19_3dRNA_1	1	13	128	33	12	0	187
54	PZ19_SimRNA_3	10	50	110	11	2	14	197
55	PZ19_SimRNA_2	8	43	117	17	0	17	202
Average		0.87	5.87	37.27	10.55	4.62	0.76	59.95
Standard deviation		2.49	10.86	46.13	12.21	11.75	3.26	68.27
Median		0	1	5	9	0	0	24

Table S21. MAXIT report on structures in Puzzle 20.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ20_RNAComposer_5	0	0	0	0	0	0	0
2	PZ20_FARFAR_8	0	0	0	0	0	0	0
3	PZ20_Adamiak_1	0	0	0	0	0	0	0
4	PZ20_FARFAR_9	0	0	0	0	0	0	0
5	PZ20_Adamiak_2	0	0	0	0	0	0	0
6	PZ20_Adamiak_3	0	0	0	0	0	0	0
7	PZ20_Adamiak_4	0	0	0	0	0	0	0
8	PZ20_Adamiak_5	0	0	0	0	0	0	0

9	PZ20_FARFAR_1	0	0	0	0	0	0	0
10	PZ20_refstructure	0	0	0	0	0	0	0
11	PZ20_FARFAR_5	0	0	0	0	0	0	0
12	PZ20_RNAComposer_3	0	0	0	0	0	0	0
13	PZ20_FARFAR_6	0	0	0	0	0	0	0
14	PZ20_RNAComposer_4	0	0	0	0	0	0	0
15	PZ20_FARFAR_2	1	0	0	0	0	0	1
16	PZ20_FARFAR_3	0	0	1	0	0	0	1
17	PZ20_FARFAR_4	0	0	1	0	0	0	1
18	PZ20_RNAComposer_2	1	0	0	0	0	0	1
19	PZ20_FARFAR_10	0	0	2	0	0	0	2
20	PZ20_FARFAR_7	0	0	1	0	1	0	2
21	PZ20_RNAComposer_1	4	0	0	0	0	0	4
22	PZ20_Das_2	0	1	4	0	0	0	5
23	PZ20_Das_4	3	1	2	0	0	0	6
24	PZ20_Das_5	2	1	2	0	0	1	6
25	PZ20_Das_1	2	1	4	0	0	0	7
26	PZ20_Das_3	1	3	3	0	0	1	8
27	PZ20_Bujnicki_5	0	9	80	17	3	0	109
28	PZ20_Bujnicki_1	3	13	115	14	1	2	148
29	PZ20_Xiao3_5	1	1	115	34	34	0	185
30	PZ20_SimRNA_5	12	45	122	19	0	10	208
31	PZ20_SimRNA_2	25	48	107	17	1	21	219
32	PZ20_Xiao3_2	1	9	133	39	37	0	219
33	PZ20_Xiao3_4	1	9	120	43	50	0	223
34	PZ20_SimRNA_4	5	58	124	16	0	22	225
35	PZ20_SimRNA_1	18	54	119	17	1	17	226
36	PZ20_SimRNA_3	15	52	133	22	2	14	238
37	PZ20_Xiao3_1	1	19	142	42	53	0	257
38	PZ20_Xiao3_3	1	28	165	38	25	0	257
39	PZ20_Bujnicki_2	3	33	207	15	3	2	263
40	PZ20_Bujnicki_4	4	39	206	14	1	3	267
41	PZ20_Bujnicki_3	5	56	205	12	2	3	283
Average		2.66	11.71	51.54	8.76	5.22	2.34	82.22
Standard deviation		5.37	19.37	71.48	13.53	13.58	5.73	110.79
Median		1	0	2	0	0	0	4

Table S22. MAXIT report on structures in Puzzle 21.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ21_FARFAR_10	0	0	0	0	0	0	0
2	PZ21_FARFAR_1	0	0	0	0	0	0	0
3	PZ21_FARFAR_3	0	0	0	0	0	0	0
4	PZ21_FARFAR_4	0	0	0	0	0	0	0
5	PZ21_Adamiak_1	0	0	0	0	0	0	0

6	PZ21_Das_1	0	0	0	0	0	0	0
7	PZ21_FARFAR_5	0	0	0	0	0	0	0
8	PZ21_Adamiak_2	0	0	0	0	0	0	0
9	PZ21_Das_2	0	0	0	0	0	0	0
10	PZ21_FARFAR_6	0	0	0	0	0	0	0
11	PZ21_Adamiak_3	0	0	0	0	0	0	0
12	PZ21_FARFAR_7	0	0	0	0	0	0	0
13	PZ21_Adamiak_4	0	0	0	0	0	0	0
14	PZ21_Das_4	0	0	0	0	0	0	0
15	PZ21_FARFAR_8	0	0	0	0	0	0	0
16	PZ21_Adamiak_5	0	0	0	0	0	0	0
17	PZ21_FARFAR_9	0	0	0	0	0	0	0
18	PZ21_DasLORES_1	0	0	0	0	0	0	0
19	PZ21_DasLORES_4	0	0	0	0	0	0	0
20	PZ21_RNAComposer_1	0	0	0	0	0	0	0
21	PZ21_RNAComposer_2	0	0	0	0	0	0	0
22	PZ21_RNAComposer_4	0	0	0	0	0	0	0
23	PZ21_RNAComposer_5	0	0	0	0	0	0	0
24	PZ21_DasLORES_2	1	0	0	0	0	0	1
25	PZ21_DasLORES_5	1	0	0	0	0	0	1
26	PZ21_RNAComposer_3	1	0	0	0	0	0	1
27	PZ21_FARFAR_2	0	1	1	0	0	0	2
28	PZ21_Das_3	0	0	3	0	0	0	3
29	PZ21_DasLORES_3	0	1	2	0	0	0	3
30	PZ21_Das_5	0	0	5	0	0	0	5
31	PZ21_refstructure	2	15	9	0	0	1	27
32	PZ21_Bujnicki_4	0	7	40	5	4	0	56
33	PZ21_Sanbonmatsu_1	6	14	25	0	12	0	57
34	PZ21_Sanbonmatsu_2	6	14	25	0	12	0	57
35	PZ21_Bujnicki_2	2	13	34	3	2	5	59
36	PZ21_Bujnicki_1	0	8	52	4	4	0	68
37	PZ21_Bujnicki_3	0	8	50	4	6	0	68
38	PZ21_Sanbonmatsu_3	23	14	29	0	8	0	74
39	PZ21_Sanbonmatsu_4	23	14	29	0	8	0	74
40	PZ21_Bujnicki_5	0	6	59	6	4	0	75
41	PZ21_3dRNA_5	0	0	75	12	22	0	109
42	PZ21_3dRNA_3	0	0	69	22	21	0	112
43	PZ21_SimRNA_2	2	25	66	11	2	10	116
44	PZ21_3dRNA_4	0	1	79	11	26	0	117
45	PZ21_SimRNA_4	8	27	76	12	0	10	133
46	PZ21_SimRNA_1	7	30	79	9	0	13	138
47	PZ21_3dRNA_1	0	19	95	23	13	0	150
48	PZ21_SimRNA_3	12	36	89	15	1	13	166
49	PZ21_SimRNA_5	12	36	89	15	1	13	166
50	PZ21_3dRNA_2	0	21	107	25	22	0	175

51	PZ21_ChenHighLig_2	9	23	153	2	0	5	192
52	PZ21_ChenLowLig_2	9	23	154	2	0	5	193
53	PZ21_ChenLowLig_5	33	25	123	1	0	12	194
54	PZ21_ChenHighLig_5	33	25	123	1	0	12	194
55	PZ21_ChenLowLig_3	30	32	135	2	0	9	208
56	PZ21_ChenHighLig_3	30	32	135	2	0	9	208
57	PZ21_ChenHighLig_1	36	31	130	1	0	15	213
58	PZ21_ChenLowLig_1	36	31	131	1	0	15	214
59	PZ21_ChenHighLig_4	49	37	134	4	0	13	237
60	PZ21_ChenLowLig_4	49	37	135	4	0	13	238
Average		7.00	10.10	42.33	3.28	2.80	2.88	68.40
Standard deviation		13.11	12.98	52.13	6.11	6.23	5.08	81.87
Median		0	0.5	7	0	0	0	16

Table S23. MAXIT report on structures in Puzzle 24.

No.	3D RNA model	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total
1	PZ24_RNAComposer_1	0	0	0	0	0	0	0
2	PZ24_RNAComposer_2	0	0	0	0	0	0	0
3	PZ24_RNAComposer_3	0	0	0	0	0	0	0
4	PZ24_RNAComposer_4	0	0	0	0	0	0	0
5	PZ24_RNAComposer_5	0	0	0	0	0	0	0
6	PZ24_Adamiak_1	0	0	0	0	0	0	0
7	PZ24_Adamiak_2	0	0	0	0	0	0	0
8	PZ24_Adamiak_3	0	0	0	0	0	0	0
9	PZ24_Das_1	0	0	0	0	0	0	0
10	PZ24_Adamiak_4	0	0	0	0	0	0	0
11	PZ24_Das_2	0	0	0	0	0	0	0
12	PZ24_Adamiak_5	0	0	0	0	0	0	0
13	PZ24_Das_3	0	0	0	0	0	0	0
14	PZ24_Das_4	0	0	0	0	0	0	0
15	PZ24_FARFAR2_5	0	0	0	0	0	0	0
16	PZ24_Das_5	0	0	0	0	0	0	0
17	PZ24_FARFAR2_7	0	0	0	0	0	0	0
18	PZ24_Das_8	0	0	0	0	0	0	0
19	PZ24_FARFAR2_9	0	0	0	0	0	0	0
20	PZ24_DasTFN_10	0	0	0	0	0	0	0
21	PZ24_DasTFN_4	0	0	0	0	0	0	0
22	PZ24_FARFAR2_10	1	0	0	0	0	0	1
23	PZ24_Das_10	0	0	0	1	0	0	1
24	PZ24_FARFAR2_1	0	0	1	0	0	0	1
25	PZ24_FARFAR2_2	0	0	0	1	0	0	1
26	PZ24_FARFAR2_6	0	1	0	0	0	0	1
27	PZ24_FARFAR2_8	0	0	1	0	0	0	1
28	PZ24_Das_9	0	0	0	1	0	0	1

29	PZ24_DasTFN_3	0	0	1	0	0	0	1
30	PZ24_DasTFN_7	0	0	1	0	0	0	1
31	PZ24_DasTFN_9	0	1	0	0	0	0	1
32	PZ24_FARFAR2_3	0	0	0	2	0	0	2
33	PZ24_Das_6	0	0	0	2	0	0	2
34	PZ24_Das_7	0	0	0	2	0	0	2
35	PZ24_FARFAR2_4	0	0	1	2	0	0	3
36	PZ24_DasTFN_2	1	0	1	1	0	0	3
37	PZ24_DasTFN_6	0	1	1	1	0	0	3
38	PZ24_DasTFN_8	0	0	3	0	0	0	3
39	PZ24_DasTFN_5	0	0	2	2	0	0	4
40	PZ24_DasTFN_1	2	0	2	2	0	0	6
41	PZ24_refstructure	6	0	0	0	0	1	7
42	PZ24_Vfold3D_4	0	2	50	17	2	0	71
43	PZ24_Vfold3D_2	0	0	67	21	0	0	88
44	PZ24_Vfold3D_5	0	4	66	20	0	0	90
45	PZ24_Vfold3D_1	0	4	69	19	0	0	92
46	PZ24_Vfold3D_3	0	10	67	24	0	0	101
47	PZ24_3dRNA_4	0	0	106	17	0	0	123
48	PZ24_3dRNA_2	0	0	109	19	0	0	128
49	PZ24_3dRNA_3	0	0	115	18	1	0	134
50	PZ24_3dRNA_1	0	0	119	18	0	0	137
51	PZ24_3dRNA_5	0	0	113	27	0	0	140
52	PZ24_Bujnicki_4	0	11	124	15	6	0	156
53	PZ24_Bujnicki_2	0	12	124	17	6	0	159
54	PZ24_Bujnicki_1	0	14	120	15	16	0	165
55	PZ24_Ding_9	0	3	92	74	0	0	169
56	PZ24_Bujnicki_3	0	12	130	25	9	0	176
57	PZ24_Ding_7	0	0	111	78	0	0	189
58	PZ24_Ding_4	0	1	112	78	0	0	191
59	PZ24_Ding_6	0	1	120	71	0	0	192
60	PZ24_Ding_10	0	0	119	76	0	0	195
61	PZ24_Ding_5	0	1	121	74	0	0	196
62	PZ24_Ding_1	0	2	118	77	0	0	197
63	PZ24_iFoldRNA_4	0	1	151	48	0	0	200
64	PZ24_Ding_8	0	3	115	86	0	0	204
65	PZ24_Ding_2	0	2	124	79	0	0	205
66	PZ24_Ding_3	0	0	121	84	0	0	205
67	PZ24_iFoldRNA_2	0	1	159	49	0	0	209
68	PZ24_iFoldRNA_1	0	1	168	48	0	0	217
69	PZ24_iFoldRNA_5	0	1	158	59	0	0	218
70	PZ24_iFoldRNA_3	0	1	172	45	0	0	218
71	PZ24_Bujnicki_5	0	15	183	25	7	0	230
72	PZ24_Kollmann_7	22	41	151	24	4	9	251
73	PZ24_Kollmann_6	33	46	158	27	1	16	281

74	PZ24_Kollmann_2	69	44	141	16	2	10	282
75	PZ24_Kollmann_9	26	55	183	26	3	12	305
76	PZ24_Kollmann_4	67	51	152	24	2	15	311
77	PZ24_Kollmann_10	50	47	174	29	1	12	313
78	PZ24_Kollmann_8	62	46	176	26	0	9	319
79	PZ24_Kollmann_5	46	62	173	27	1	15	324
80	PZ24_SimRNA_2	23	72	185	25	0	24	329
81	PZ24_Kollmann_3	47	58	183	29	1	13	331
82	PZ24_Kollmann_1	67	61	188	31	4	19	370
83	PZ24_SimRNA_5	27	84	200	30	3	33	377
84	PZ24_SimRNA_3	25	95	222	32	0	24	398
85	PZ24_SimRNA_4	12	98	247	27	1	32	417
86	PZ24_SimRNA_1	45	83	229	39	2	26	424
87	PZ24_VfoldLA_4	61	70	284	0	0	71	486
88	PZ24_VfoldLA_1	124	51	252	7	0	61	495
89	PZ24_VfoldLA_3	119	58	262	8	0	65	512
90	PZ24_VfoldLA_5	98	77	277	7	1	61	521
91	PZ24_VfoldLA_2	135	69	271	7	0	57	539
Average		12.84	15.09	84.01	19.57	0.80	6.43	138.74
Standard deviation		29.22	27.12	87.30	24.99	2.29	15.61	155.32
Median		0	0	69	8	0	0	101

Table S24. Total number of errors of different types by cluster and the average number over all types of errors (ATN) per model in every cluster.

No.	Cluster	Total number of models	Close contacts	Bond lengths	Bond angles	Planarity	Chirality	Polymer linkage	Total	ATN
1	H1	64	0	0	0	0	0	0	0	0.00
2	H2	131	118	2,426	12,444	2,231	584	91	17,894	136.60
3	H3	145	1,854	2,817	12,188	1,712	110	732	19,413	133.88
4	H4	188	414	254	642	27	8	93	1,446	7.69
5	H5	124	14	44	8,710	4,241	2	1	13,012	104.94
6	H6	52	5	107	6,036	3,313	9	1	9,471	182.13
7	H7	10	489	511	1,679	259	19	130	3,087	308.70
8	H8	5	3	5	10	40	0	0	58	11.60
9	H9	32	11	1,112	7,364	1,869	107	28	10,491	327.84
10	H10	1	26	15	24	6	0	1	72	72.00
11	H11	4	58	56	108	0	40	0	262	65.50
12	H12	3	6	102	99	0	2	9	218	72.67
13	H13	3	0	5	326	262	0	0	593	197.67
14	H14	1	271	39	210	0	0	0	520	520.00
15	H15	33	39	952	5,815	1,215	551	9	8,581	260.03
16	H16	1	1	1	1	0	0	0	3	3.00
17	W1	30	26	328	4,160	816	443	14	5,787	192.90
18	W2	70	18	22	45	5	1	0	91	1.30
19	W3	5	0	5	808	249	0	0	1,062	212.40

20	W4	10	4	15	33	110	150	0	312	31.20
21	W5	49	54	142	144	33	0	0	373	7.61
22	W6	59	986	2,899	7,483	1,056	56	998	13,478	228.44
23	W7	10	537	345	1,665	130	3	315	2,995	299.50

BARNABA reports

BBRMSD - RMSD is calculated using backbone atoms only.

ERMSD - eRMSD measures the distance between structures by considering only the relative positions and orientations of nucleobases.

Table S25. BARNABA report on structures in Puzzle 01.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ01_Das_3	0.35	0.55	3.50	5.53
2	PZ01_Santalucia_1	0.62	0.71	6.19	7.08
3	PZ01_Das_1	0.39	0.73	3.93	7.30
4	PZ01_Das_4	0.37	0.82	3.73	8.18
5	PZ01_Das_2	0.45	0.91	4.55	9.05
6	PZ01_Bujnicki_1	0.59	0.93	5.87	9.27
7	PZ01_Major_1	0.43	0.94	4.31	9.44
8	PZ01_Chen_1	0.43	0.95	4.35	9.47
9	PZ01_Bujnicki_3	0.54	0.97	5.42	9.66
10	PZ01_Das_5	0.43	0.98	4.35	9.80
11	PZ01_Dokholyan_1	0.73	1.02	7.34	10.19
12	PZ01_Bujnicki_2	0.64	1.02	6.42	10.23
13	PZ01_Bujnicki_5	0.53	1.38	5.25	13.82
14	PZ01_Bujnicki_4	0.51	1.44	5.09	14.40
	Average	0.50	0.95	5.02	9.53
	Standard deviation	0.35	0.55	3.50	5.53
	Median	0.73	1.44	7.34	14.40

Table S26. BARNABA report on structures in Puzzle 02.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ02_Santalucia_1	0.38	0.83	3.79	8.25
2	PZ02_Das_1	0.23	0.86	2.28	8.57
3	PZ02_Bujnicki_1	0.23	0.87	2.34	8.65
4	PZ02_Bujnicki_3	0.21	0.88	2.09	8.76
5	PZ02_Bujnicki_2	0.20	0.88	2.04	8.84
6	PZ02_Dokholyan_1	0.23	0.89	2.35	8.94
7	PZ02_Das_2	0.29	0.97	2.86	9.74
8	PZ02_Chen_1	0.27	1.00	2.69	10.00
9	PZ02_Das_4	0.26	1.01	2.56	10.11
10	PZ02_Das_3	0.30	1.04	2.96	10.36
11	PZ02_Das_5	0.35	1.05	3.48	10.52
12	PZ02_Wildauer_1	0.32	1.13	3.17	11.34
13	PZ02_Major_1	2.51	2.31	25.14	23.10
	Average	0.44	1.06	4.44	10.55
	Standard deviation	0.20	0.83	2.04	8.25
	Median	2.51	2.31	25.14	23.10

Table S27. BARNABA report on structures in Puzzle 03.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ03_Das_5	1.26	1.33	12.57	13.34
2	PZ03_Das_2	1.27	1.36	12.73	13.58
3	PZ03_Chen_1	0.77	1.37	7.75	13.72
4	PZ03_Das_1	1.75	1.37	17.47	13.73
5	PZ03_Das_3	1.86	1.42	18.56	14.21
6	PZ03_Das_4	1.85	1.44	18.49	14.39
7	PZ03_Dokholyan_2	1.18	1.47	11.81	14.71
8	PZ03_Bujnicki_1	1.22	1.49	12.21	14.90
9	PZ03_Bujnicki_2	1.50	1.50	14.97	14.99
10	PZ03_Dokholyan_1	1.81	1.50	18.10	15.02
11	PZ03_Major_2	1.41	1.60	14.15	16.05
12	PZ03_Major_1	2.53	2.03	25.30	20.27
	Average	1.53	1.49	15.34	14.91
	Standard deviation	0.77	1.33	7.75	13.34
	Median	0.73	1.44	7.34	14.40

Table S28. BARNABA report on structures in Puzzle 04.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ04_Das_1	0.47	0.50	4.73	5.00
2	PZ04_Das_4	0.47	0.50	4.73	5.02
3	PZ04_Das_3	0.47	0.50	4.73	5.02
4	PZ04_Das_2	0.47	0.50	4.73	5.03
5	PZ04_Das_5	0.47	0.50	4.73	5.03
6	PZ04_Chen_9	0.35	0.55	3.45	5.51
7	PZ04_Chen_2	0.35	0.55	3.45	5.52
8	PZ04_Chen_4	0.35	0.55	3.47	5.53
9	PZ04_Chen_8	0.35	0.56	3.47	5.56
10	PZ04_Chen_10	0.35	0.56	3.46	5.59
11	PZ04_Chen_7	0.35	0.56	3.46	5.60
12	PZ04_Chen_3	0.35	0.56	3.47	5.63
13	PZ04_Chen_6	0.35	0.57	3.47	5.70
14	PZ04_Chen_5	0.35	0.58	3.47	5.77
15	PZ04_Major_1	0.46	0.59	4.65	5.89
16	PZ04_Chen_1	0.35	0.59	3.45	5.90
17	PZ04_Dokholyan_1	0.56	0.63	5.59	6.31
18	PZ04_Dokholyan_2	0.56	0.63	5.59	6.31
19	PZ04_Santalucia_1	0.42	0.64	4.24	6.35
20	PZ04_Bujnicki_1	0.43	0.73	4.27	7.34
21	PZ04_Bujnicki_3	0.43	0.74	4.27	7.36
22	PZ04_Bujnicki_5	0.43	0.74	4.27	7.37
23	PZ04_Bujnicki_2	0.43	0.74	4.27	7.40
24	PZ04_Bujnicki_4	0.43	0.74	4.27	7.40
25	PZ04_Adamiak_3	0.44	0.85	4.39	8.53
26	PZ04_Adamiak_2	0.46	0.87	4.58	8.70
27	PZ04_Adamiak_1	0.47	0.87	4.67	8.74
28	PZ04_Adamiak_4	0.67	1.12	6.72	11.24

29	PZ04_Adamiak_5	0.47	1.19	4.72	11.94
30	PZ04_Mikolajczak_1	1.34	1.34	13.40	13.40
	Average	0.46	0.69	4.61	6.86
	Standard deviation	0.35	0.50	3.45	5.00
	Median	1.34	1.34	13.40	13.40

Table S29. BARNABA report on structures in Puzzle 05.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ05_Das_2	0.94	1.30	9.41	13.00
2	PZ05_Das_1	1.02	1.33	10.20	13.26
3	PZ05_Bujnicki_2	2.11	1.44	21.11	14.38
4	PZ05_Adamiak_1	1.71	1.48	17.12	14.75
5	PZ05_Chen_5	3.13	1.48	31.30	14.85
6	PZ05_Chen_2	2.63	1.50	26.30	15.02
7	PZ05_Ding_3	2.34	1.50	23.39	15.03
8	PZ05_Chen_1	2.69	1.52	26.92	15.15
9	PZ05_Ding_5	2.29	1.52	22.93	15.22
10	PZ05_Bujnicki_5	2.41	1.53	24.12	15.27
11	PZ05_Chen_4	3.22	1.53	32.25	15.30
12	PZ05_Chen_6	3.22	1.53	32.24	15.34
13	PZ05_Dokholyan_1	2.21	1.54	22.07	15.36
14	PZ05_Ding_1	2.74	1.54	27.40	15.40
15	PZ05_Chen_7	2.67	1.54	26.74	15.42
16	PZ05_Dokholyan_3	2.53	1.54	25.30	15.44
17	PZ05_Ding_2	1.96	1.55	19.59	15.52
18	PZ05_Ding_4	1.96	1.55	19.59	15.52
19	PZ05_Dokholyan_2	2.27	1.56	22.72	15.58
20	PZ05_Xiao_1	3.65	1.57	36.48	15.66
21	PZ05_Bujnicki_1	2.53	1.58	25.32	15.75
22	PZ05_Xiao_2	3.29	1.58	32.89	15.81
23	PZ05_Bujnicki_4	2.29	1.60	22.92	15.99
24	PZ05_Chen_3	2.99	1.64	29.90	16.40
25	PZ05_Bujnicki_3	2.25	1.79	22.48	17.90
	Average	2.44	1.53	24.43	15.29
	Standard deviation	0.94	1.30	9.41	13.00
	Median	3.65	1.79	36.48	17.90

Table S30. BARNABA report on structures in Puzzle 06.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ06_Das_1	1.45	1.17	14.51	11.74
2	PZ06_Das_6	1.27	1.18	12.71	11.78
3	PZ06_Das_4	1.21	1.19	12.13	11.88
4	PZ06_Das_2	1.41	1.20	14.05	12.02
5	PZ06_Das_9	1.54	1.21	15.43	12.07
6	PZ06_Das_5	1.60	1.22	16.01	12.21
7	PZ06_Das_8	1.84	1.24	18.40	12.37
8	PZ06_Das_7	1.84	1.25	18.43	12.55

9	PZ06_Das_3	1.60	1.27	16.00	12.66
10	PZ06_Das_10	2.98	1.31	29.77	13.12
11	PZ06_Major_6	2.45	1.34	24.48	13.38
12	PZ06_Major_2	2.29	1.36	22.93	13.60
13	PZ06_Major_7	2.36	1.37	23.59	13.69
14	PZ06_Major_1	2.36	1.38	23.62	13.76
15	PZ06_Major_4	2.34	1.39	23.38	13.88
16	PZ06_Major_3	2.25	1.40	22.49	13.96
17	PZ06_Major_5	2.51	1.45	25.12	14.45
18	PZ06_Bujnicki_1	3.76	1.46	37.59	14.60
19	PZ06_Dokholyan_3	2.70	1.48	26.98	14.80
20	PZ06_Bujnicki_2	3.15	1.49	31.51	14.88
21	PZ06_Chen_4	2.28	1.50	22.84	15.02
22	PZ06_Dokholyan_5	2.33	1.51	23.30	15.13
23	PZ06_Dokholyan_4	2.59	1.52	25.88	15.21
24	PZ06_Chen_1	2.51	1.52	25.05	15.21
25	PZ06_Chen_3	2.42	1.52	24.22	15.22
26	PZ06_Dokholyan_1	2.71	1.52	27.09	15.24
27	PZ06_Dokholyan_2	2.74	1.52	27.39	15.24
28	PZ06_Chen_6	3.65	1.54	36.54	15.40
29	PZ06_Chen_2	2.29	1.54	22.91	15.40
30	PZ06_Chen_5	2.40	1.55	24.04	15.47
31	PZ06_Bujnicki_4	3.26	1.56	32.57	15.63
32	PZ06_Chen_7	3.14	1.58	31.44	15.77
33	PZ06_Dokholyan_6	3.81	1.58	38.14	15.83
34	PZ06_Bujnicki_3	3.25	1.63	32.50	16.27
	Average	2.42	1.41	24.21	14.10
	Standard deviation	1.21	1.17	12.13	11.74
	Median	3.81	1.63	38.14	16.27

Table S31. BARNABA report on structures in Puzzle 07.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ07_Das_1	2.10	1.27	20.99	12.69
2	PZ07_Chen_8	3.08	1.28	30.77	12.84
3	PZ07_Chen_10	3.24	1.32	32.41	13.22
4	PZ07_Chen_2	3.50	1.33	34.99	13.25
5	PZ07_Das_6	2.58	1.33	25.81	13.30
6	PZ07_Chen_9	3.40	1.34	34.01	13.42
7	PZ07_Chen_5	2.42	1.35	24.15	13.49
8	PZ07_Das_2	2.42	1.36	24.16	13.56
9	PZ07_Chen_4	2.85	1.36	28.48	13.59
10	PZ07_Bujnicki_3	2.70	1.36	27.04	13.64
11	PZ07_Chen_3	3.05	1.37	30.50	13.67
12	PZ07_Das_3	2.51	1.37	25.08	13.68
13	PZ07_Das_5	2.52	1.37	25.23	13.71
14	PZ07_Chen_6	2.98	1.37	29.78	13.71
15	PZ07_Bujnicki_6	2.71	1.37	27.07	13.75
16	PZ07_Chen_7	2.98	1.38	29.78	13.75
17	PZ07_Das_8	2.74	1.40	27.37	13.99

18	PZ07_Das_4	2.58	1.40	25.83	14.02
19	PZ07_Das_7	2.57	1.41	25.68	14.08
20	PZ07_Bujnicki_4	2.58	1.41	25.82	14.08
21	PZ07_Bujnicki_5	2.58	1.41	25.82	14.09
22	PZ07_Bujnicki_7	2.78	1.43	27.83	14.32
23	PZ07_Adamiak_5	2.93	1.48	29.33	14.77
24	PZ07_Dokholyan_1	3.09	1.48	30.90	14.82
25	PZ07_Ding_4	3.27	1.50	32.66	14.98
26	PZ07_Ding_6	2.99	1.51	29.92	15.09
27	PZ07_Ding_1	2.98	1.51	29.76	15.10
28	PZ07_Ding_10	3.73	1.52	37.26	15.17
29	PZ07_Ding_8	2.80	1.52	28.05	15.20
30	PZ07_Ding_9	2.75	1.53	27.47	15.26
31	PZ07_Ding_7	3.05	1.53	30.54	15.28
32	PZ07_Adamiak_3	3.15	1.55	31.53	15.47
33	PZ07_Adamiak_1	2.97	1.55	29.75	15.50
34	PZ07_Ding_2	3.34	1.56	33.42	15.61
35	PZ07_Ding_3	3.25	1.56	32.46	15.63
36	PZ07_Ding_5	3.02	1.58	30.25	15.79
37	PZ07_Bujnicki_2	6.11	1.58	61.11	15.82
38	PZ07_Adamiak_2	2.97	1.58	29.66	15.84
39	PZ07_Major_7	2.90	1.58	29.04	15.84
40	PZ07_Major_5	2.90	1.58	29.03	15.84
41	PZ07_Major_2	2.88	1.59	28.78	15.87
42	PZ07_Adamiak_4	3.07	1.59	30.74	15.87
43	PZ07_Major_9	2.80	1.59	28.01	15.93
44	PZ07_Major_6	2.84	1.60	28.36	15.98
45	PZ07_Major_1	2.96	1.60	29.60	16.05
46	PZ07_Major_8	2.82	1.61	28.19	16.08
47	PZ07_Major_3	2.76	1.61	27.61	16.12
48	PZ07_Major_4	2.82	1.62	28.17	16.23
49	PZ07_Major_10	3.22	1.62	32.16	16.25
50	PZ07_Bujnicki_1	4.30	1.67	43.04	16.68
51	PZ07_Chen_1	2.90	1.80	29.01	18.04
52	PZ07_Dokholyan_2	3.74	1.82	37.37	18.17
	Average	3.00	1.49	30.03	14.89
	Standard deviation	2.10	1.27	20.99	12.69
	Median	6.11	1.82	61.11	18.17

Table S32. BARNABA report on structures in Puzzle 08

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ08_Das_2	1.13	1.10	11.30	11.04
2	PZ08_Das_1	0.64	1.14	6.40	11.40
3	PZ08_Das_3	0.47	1.15	4.73	11.51
4	PZ08_Bujnicki_4	1.29	1.17	12.95	11.66
5	PZ08_Das_6	1.12	1.17	11.21	11.68
6	PZ08_Das_5	1.16	1.18	11.62	11.78
7	PZ08_Bujnicki_2	1.27	1.19	12.66	11.85
8	PZ08_Das_4	1.12	1.19	11.20	11.87

9	PZ08_Bujnicki_5	1.16	1.23	11.57	12.32
10	PZ08_Bujnicki_1	1.31	1.24	13.11	12.44
11	PZ08_Bujnicki_8	1.20	1.25	12.02	12.46
12	PZ08_Bujnicki_9	0.68	1.25	6.82	12.55
13	PZ08_Chen_1	1.33	1.29	13.30	12.85
14	PZ08_Bujnicki_7	0.67	1.29	6.67	12.92
15	PZ08_Bujnicki_6	1.27	1.30	12.65	12.97
16	PZ08_Bujnicki_3	1.20	1.31	12.03	13.09
17	PZ08_Chen_2	1.30	1.31	13.01	13.14
18	PZ08_Chen_3	1.14	1.32	11.39	13.23
19	PZ08_Chen_5	1.18	1.33	11.83	13.26
20	PZ08_Chen_10	1.24	1.33	12.38	13.30
21	PZ08_Ding_4	1.59	1.35	15.88	13.52
22	PZ08_Chen_4	1.30	1.37	13.05	13.70
23	PZ08_Ding_7	1.33	1.37	13.32	13.73
24	PZ08_Ding_5	1.32	1.39	13.18	13.88
25	PZ08_Ding_8	1.58	1.40	15.75	13.98
26	PZ08_Ding_10	1.21	1.40	12.07	14.04
27	PZ08_Bujnicki_10	1.13	1.41	11.30	14.09
28	PZ08_Chen_7	1.29	1.42	12.88	14.21
29	PZ08_Adamiak_2	1.51	1.42	15.13	14.23
30	PZ08_Ding_6	1.46	1.43	14.64	14.28
31	PZ08_Adamiak_1	1.46	1.44	14.62	14.37
32	PZ08_Ding_1	1.26	1.44	12.65	14.40
33	PZ08_Ding_3	1.16	1.45	11.62	14.47
34	PZ08_Ding_2	1.42	1.46	14.23	14.62
35	PZ08_Ding_9	1.71	1.47	17.06	14.67
36	PZ08_Chen_6	1.18	1.49	11.82	14.92
37	PZ08_Chen_8	1.60	1.49	15.96	14.93
38	PZ08_Chen_9	1.13	1.55	11.34	15.46
39	PZ08_Dokholyan_1	2.46	1.60	24.56	15.97
40	PZ08_Dokholyan_3	2.57	1.67	25.73	16.67
41	PZ08_Dokholyan_2	1.87	1.71	18.70	17.10
42	PZ08_Dokholyan_4	3.17	2.06	31.68	20.57
	Average	1.35	1.37	13.48	13.69
	Standard deviation	0.47	1.10	4.73	11.04
	Median	3.17	2.06	31.68	20.57

Table S33. BARNABA report on structures in Puzzle 9.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ09_Das_1	0.90	1.20	9.03	11.95
2	PZ09_Das_4	1.00	1.24	9.95	12.42
3	PZ09_Das_5	0.80	1.25	7.99	12.49
4	PZ09_Das_2	0.81	1.29	8.13	12.90
5	PZ09_Das_8	1.12	1.34	11.22	13.36
6	PZ09_Das_3	0.88	1.35	8.84	13.54
7	PZ09_Das_7	0.94	1.35	9.43	13.55
8	PZ09_Das_6	0.91	1.36	9.07	13.56
9	PZ09_Chen_1	0.64	1.36	6.40	13.59

10	PZ09_Chen_8	0.65	1.39	6.46	13.90
11	PZ09_Das_9	1.00	1.43	10.01	14.33
12	PZ09_Chen_5	0.63	1.44	6.33	14.42
13	PZ09_Chen_6	0.65	1.44	6.52	14.44
14	PZ09_Chen_4	0.64	1.45	6.40	14.52
15	PZ09_Chen_2	0.63	1.46	6.32	14.56
16	PZ09_Chen_3	0.63	1.46	6.32	14.60
17	PZ09_Chen_7	0.59	1.51	5.90	15.10
18	PZ09_Ding_7	0.98	1.54	9.77	15.44
19	PZ09_Bujnicki_3	0.60	1.57	5.98	15.69
20	PZ09_Bujnicki_4	0.60	1.57	5.98	15.69
21	PZ09_Bujnicki_5	0.60	1.57	5.98	15.69
22	PZ09_Ding_5	0.93	1.68	9.25	16.76
23	PZ09_Ding_10	1.16	1.68	11.61	16.81
24	PZ09_Ding_4	0.99	1.68	9.94	16.83
25	PZ09_Ding_3	0.93	1.69	9.31	16.90
26	PZ09_Ding_9	1.01	1.69	10.13	16.95
27	PZ09_Ding_6	1.25	1.70	12.49	17.03
28	PZ09_Dokholyan_1	2.06	1.71	20.56	17.07
29	PZ09_Dokholyan_2	2.61	1.71	26.11	17.11
30	PZ09_Ding_8	1.15	1.71	11.53	17.13
31	PZ09_Ding_1	1.01	1.75	10.06	17.47
32	PZ09_Ding_2	1.02	1.75	10.24	17.48
33	PZ09_Dokholyan_4	2.00	1.78	19.99	17.75
34	PZ09_Dokholyan_3	2.28	1.78	22.81	17.80
	Average	1.02	1.53	10.18	15.26
	Standard deviation	0.59	1.20	5.90	11.95
	Average	1.02	1.53	10.18	15.26

Table S34. BARNABA report on structures in Puzzle 10.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ10_Das_5	1.08	0.82	10.77	8.16
2	PZ10_Das_4	0.73	0.89	7.31	8.92
3	PZ10_Das_2	1.08	0.91	10.81	9.07
4	PZ10_Das_1	0.79	0.91	7.86	9.14
5	PZ10_Das_3	0.70	0.92	7.03	9.16
6	PZ10_Bujnicki_8	1.05	1.00	10.50	10.01
7	PZ10_Bujnicki_1	1.05	1.01	10.54	10.05
8	PZ10_Bujnicki_9	1.06	1.04	10.60	10.40
9	PZ10_Bujnicki_7	1.05	1.05	10.54	10.49
10	PZ10_Bujnicki_3	1.06	1.08	10.60	10.76
11	PZ10_Bujnicki_5	1.06	1.08	10.56	10.83
12	PZ10_Bujnicki_10	1.07	1.09	10.66	10.89
13	PZ10_Bujnicki_2	1.07	1.10	10.67	10.96
14	PZ10_Bujnicki_6	1.06	1.12	10.63	11.20
15	PZ10_Bujnicki_4	0.96	1.22	9.55	12.21
16	PZ10_Chen_1	1.17	1.25	11.73	12.47
17	PZ10_Ding_4	1.36	1.43	13.64	14.35
18	PZ10_Ding_3	1.32	1.45	13.23	14.51

19	PZ10_Ding_8	1.61	1.46	16.13	14.59
20	PZ10_Ding_6	1.82	1.46	18.21	14.65
21	PZ10_Ding_1	1.34	1.48	13.39	14.83
22	PZ10_Ding_10	1.35	1.49	13.52	14.88
23	PZ10_Ding_7	1.68	1.50	16.80	15.00
24	PZ10_Ding_2	1.45	1.51	14.54	15.13
25	PZ10_Ding_5	1.72	1.51	17.25	15.14
26	PZ10_Ding_9	1.72	1.55	17.22	15.46
	Average	1.21	1.20	12.09	12.05
	Standard deviation	0.70	0.82	7.03	8.16
	Median	1.82	1.55	18.21	15.46

Table S35. BARNABA report on structures in Puzzle 11.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ11_Das_2	0.87	0.99	8.72	9.94
2	PZ11_Das_4	0.69	1.03	6.91	10.28
3	PZ11_Chén_1	0.56	1.07	5.60	10.65
4	PZ11_Chén_3	0.49	1.07	4.91	10.69
5	PZ11_Das_1	0.57	1.08	5.71	10.78
6	PZ11_Das_8	0.98	1.09	9.76	10.89
7	PZ11_Chén_9	0.78	1.09	7.76	10.90
8	PZ11_Chén_5	0.88	1.09	8.79	10.93
9	PZ11_Bujnicki_9	0.52	1.09	5.18	10.95
10	PZ11_Chén_2	0.74	1.09	7.37	10.95
11	PZ11_Das_7	0.82	1.10	8.18	11.01
12	PZ11_Chén_10	0.84	1.10	8.37	11.02
13	PZ11_Adamiak_5	0.95	1.11	9.50	11.15
14	PZ11_Chén_7	0.76	1.12	7.56	11.24
15	PZ11_Chén_8	0.81	1.14	8.06	11.40
16	PZ11_Das_6	0.66	1.15	6.64	11.45
17	PZ11_Bujnicki_1	0.66	1.15	6.56	11.54
18	PZ11_Ding_1	0.57	1.16	5.67	11.56
19	PZ11_Chén_4	0.65	1.16	6.54	11.58
20	PZ11_Das_10	0.97	1.17	9.72	11.69
21	PZ11_Das_3	0.81	1.17	8.10	11.72
22	PZ11_Adamiak_7	0.74	1.18	7.42	11.76
23	PZ11_Bujnicki_3	0.69	1.19	6.86	11.94
24	PZ11_Chén_6	0.70	1.21	7.02	12.08
25	PZ11_Ding_6	0.71	1.21	7.06	12.15
26	PZ11_Ding_7	0.57	1.22	5.69	12.18
27	PZ11_Das_5	0.77	1.23	7.68	12.35
28	PZ11_Ding_10	1.13	1.24	11.32	12.41
29	PZ11_Bujnicki_4	0.66	1.24	6.64	12.43
30	PZ11_Das_9	1.93	1.25	19.34	12.46
31	PZ11_Xiao_3	1.13	1.25	11.32	12.49
32	PZ11_Ding_2	1.13	1.27	11.26	12.73
33	PZ11_Ding_3	1.06	1.28	10.64	12.78
34	PZ11_Ding_9	0.83	1.30	8.28	13.01
35	PZ11_Xiao_2	1.32	1.33	13.16	13.31

36	PZ11_Ding_8	0.66	1.33	6.61	13.33
37	PZ11_Ding_5	0.66	1.34	6.62	13.39
38	PZ11_Adamiak_6	0.67	1.34	6.67	13.43
39	PZ11_Ding_4	0.64	1.35	6.44	13.46
40	PZ11_Adamiak_4	0.93	1.35	9.25	13.50
41	PZ11_Adamiak_9	0.87	1.36	8.74	13.65
42	PZ11_Bujnicki_6	1.29	1.38	12.89	13.81
43	PZ11_Adamiak_2	1.11	1.39	11.14	13.91
44	PZ11_Adamiak_10	1.03	1.39	10.34	13.95
45	PZ11_Adamiak_1	0.89	1.40	8.94	13.96
46	PZ11_Bujnicki_10	0.81	1.42	8.12	14.24
47	PZ11_Adamiak_8	1.10	1.44	10.97	14.37
48	PZ11_Bujnicki_7	0.78	1.44	7.75	14.41
49	PZ11_Bujnicki_5	0.99	1.45	9.87	14.47
50	PZ11_Adamiak_3	1.01	1.45	10.07	14.51
51	PZ11_Bujnicki_8	1.22	1.46	12.22	14.57
52	PZ11_Bujnicki_2	1.92	1.48	19.23	14.81
53	PZ11_Xiao_1	0.97	1.53	9.72	15.28
	Average	0.88	1.24	8.77	12.44
	Standard deviation	0.49	0.99	4.91	9.94
	Median	1.93	1.53	19.34	15.28

Table S36. BARNABA report on structures in Puzzle 12.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ12_Das_2	1.40	1.16	13.97	11.62
2	PZ12_Das_5	1.47	1.28	14.65	12.80
3	PZ12_Das_1	1.47	1.30	14.69	13.03
4	PZ12_Das_8	1.35	1.31	13.52	13.10
5	PZ12_Das_10	1.80	1.32	17.98	13.17
6	PZ12_Das_7	1.33	1.34	13.27	13.38
7	PZ12_Das_4	1.83	1.34	18.35	13.43
8	PZ12_Das_3	1.44	1.35	14.40	13.45
9	PZ12_Adamiak_1	1.75	1.37	17.54	13.74
10	PZ12_Bujnicki_10	1.41	1.39	14.10	13.89
11	PZ12_Bujnicki_4	1.61	1.40	16.10	13.98
12	PZ12_Bujnicki_3	1.24	1.42	12.41	14.24
13	PZ12_Adamiak_3	1.64	1.43	16.44	14.31
14	PZ12_Das_9	1.42	1.44	14.17	14.35
15	PZ12_Das_6	1.41	1.44	14.11	14.41
16	PZ12_Adamiak_2	1.63	1.44	16.31	14.41
17	PZ12_Chén_1	2.34	1.44	23.41	14.45
18	PZ12_Chén_8	1.86	1.45	18.65	14.47
19	PZ12_Bujnicki_5	1.30	1.46	13.04	14.56
20	PZ12_Chén_7	2.09	1.47	20.92	14.73
21	PZ12_Bujnicki_6	1.61	1.47	16.14	14.75
22	PZ12_Bujnicki_1	2.24	1.48	22.35	14.80
23	PZ12_Bujnicki_8	1.14	1.48	11.38	14.85
24	PZ12_Chén_6	2.05	1.50	20.54	14.97
25	PZ12_Chén_9	1.90	1.51	18.98	15.08

26	PZ12_Ding_12	1.06	1.51	10.60	15.09
27	PZ12_Bujnicki_2	1.92	1.51	19.25	15.14
28	PZ12_Ding_2	2.11	1.52	21.12	15.18
29	PZ12_Ding_11	1.07	1.53	10.74	15.25
30	PZ12_Chen_2	1.95	1.53	19.52	15.27
31	PZ12_Chen_3	1.98	1.53	19.76	15.29
32	PZ12_Ding_3	1.82	1.53	18.20	15.32
33	PZ12_Ding_10	1.94	1.54	19.35	15.37
34	PZ12_Chen_10	2.01	1.54	20.11	15.41
35	PZ12_Ding_5	2.18	1.55	21.76	15.48
36	PZ12_Ding_8	1.34	1.55	13.41	15.53
37	PZ12_Bujnicki_7	1.68	1.56	16.83	15.56
38	PZ12_Chen_4	1.68	1.56	16.80	15.58
39	PZ12_Weeks_3	2.06	1.56	20.57	15.64
40	PZ12_Ding_4	1.42	1.57	14.24	15.73
41	PZ12_Ding_7	1.85	1.57	18.55	15.74
42	PZ12_Chen_5	2.09	1.58	20.93	15.76
43	PZ12_Ding_6	1.61	1.58	16.07	15.79
44	PZ12_Bujnicki_9	1.41	1.58	14.08	15.84
45	PZ12_Ding_9	1.52	1.60	15.25	16.05
46	PZ12_Weeks_2	2.09	1.61	20.92	16.11
47	PZ12_Weeks_1	2.12	1.61	21.23	16.12
48	PZ12_Ding_1	1.35	1.63	13.52	16.25
49	PZ12_Xiao_3	3.63	1.87	36.26	18.67
50	PZ12_Xiao_1	3.01	2.11	30.14	21.09
51	PZ12_Xiao_2	2.97	2.12	29.72	21.20
	Average	1.78	1.51	17.77	15.09
	Standard deviation	1.06	1.16	10.60	11.62
	Median	3.63	2.12	36.26	21.20

Table S37. BARNABA report on structures in Puzzle 13.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ13_Chen_6	1.68	1.23	16.79	12.30
2	PZ13_Chen_8	1.53	1.27	15.35	12.69
3	PZ13_Das_1	0.78	1.27	7.79	12.75
4	PZ13_Das_2	0.55	1.28	5.53	12.78
5	PZ13_Das_4	1.17	1.31	11.67	13.13
6	PZ13_Adamiak_1	1.00	1.32	10.04	13.23
7	PZ13_Das_7	0.56	1.34	5.63	13.40
8	PZ13_Chen_3	1.00	1.34	10.00	13.44
9	PZ13_Chen_9	1.60	1.37	16.03	13.66
10	PZ13_Chen_7	1.58	1.37	15.77	13.67
11	PZ13_Chen_5	0.62	1.37	6.17	13.74
12	PZ13_Ding_3	1.40	1.37	14.02	13.75
13	PZ13_Das_10	1.33	1.38	13.30	13.81
14	PZ13_Das_8	1.42	1.38	14.24	13.82
15	PZ13_Das_3	0.90	1.38	9.03	13.84
16	PZ13_Chen_2	0.97	1.39	9.74	13.86
17	PZ13_Bujnicki_8	1.30	1.39	13.01	13.90

18	PZ13_Bujnicki_5	1.27	1.40	12.74	13.96
19	PZ13_Ding_5	1.54	1.41	15.44	14.11
20	PZ13_Das_5	1.32	1.42	13.24	14.19
21	PZ13_Ding_7	1.69	1.43	16.88	14.27
22	PZ13_Das_6	1.52	1.44	15.22	14.42
23	PZ13_Ding_6	1.51	1.44	15.10	14.43
24	PZ13_Bujnicki_6	1.59	1.44	15.92	14.43
25	PZ13_Bujnicki_7	1.33	1.46	13.30	14.59
26	PZ13_Ding_10	1.74	1.46	17.42	14.59
27	PZ13_Ding_1	1.69	1.46	16.89	14.62
28	PZ13_Chen_1	1.56	1.46	15.64	14.64
29	PZ13_Ding_4	1.46	1.46	14.63	14.65
30	PZ13_Bujnicki_2	1.43	1.47	14.28	14.66
31	PZ13_Ding_2	1.71	1.47	17.11	14.71
32	PZ13_Ding_8	1.53	1.48	15.31	14.75
33	PZ13_Bujnicki_3	0.88	1.49	8.75	14.92
34	PZ13_Ding_9	1.82	1.49	18.16	14.94
35	PZ13_Das_9	1.26	1.50	12.56	15.04
36	PZ13_Bujnicki_1	0.96	1.59	9.57	15.89
37	PZ13_Bujnicki_4	1.59	1.59	15.88	15.92
38	PZ13_Chen_4	1.60	1.60	15.98	15.97
39	PZ13_Xiao_5	2.93	1.61	29.33	16.12
40	PZ13_Dokholyan_2	2.64	1.61	26.40	16.14
41	PZ13_Dokholyan_1	2.28	1.78	22.81	17.79
42	PZ13_Dokholyan_5	1.88	1.80	18.80	18.01
43	PZ13_Bujnicki_10	1.56	1.95	15.64	19.53
44	PZ13_Bujnicki_9	1.75	1.97	17.51	19.65
45	PZ13_Dokholyan_3	2.35	1.98	23.52	19.75
46	PZ13_Xiao_1	1.76	2.03	17.63	20.34
47	PZ13_Xiao_6	2.82	2.05	28.24	20.46
48	PZ13_Xiao_4	2.85	2.07	28.51	20.67
49	PZ13_Xiao_10	2.81	2.07	28.07	20.72
50	PZ13_Xiao_9	3.15	2.08	31.54	20.76
51	PZ13_Xiao_8	2.93	2.08	29.25	20.80
52	PZ13_Dokholyan_4	2.32	2.11	23.20	21.07
53	PZ13_Xiao_7	2.78	2.18	27.85	21.77
54	PZ13_Xiao_3	1.76	2.31	17.56	23.09
55	PZ13_Xiao_2	2.51	2.34	25.08	23.37
	Average	1.66	1.60	16.64	15.95
	Standard deviation	0.55	1.23	5.53	12.30
	Median	3.15	2.34	31.54	23.37

Table S38. BARNABA report on structures in Puzzle 14a.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ14_ChenPostExp_8	1.58	1.01	15.79	10.05
2	PZ14_DasPreExp_9	0.80	1.05	8.02	10.49
3	PZ14_DasPostExp_2	1.23	1.05	12.34	10.53
4	PZ14_DasPreExp_6	0.80	1.08	7.97	10.78
5	PZ14_DasPostExp_5	1.25	1.10	12.54	11.02

6	PZ14_ChenPostExp_3	1.71	1.10	17.15	11.04
7	PZ14_AdamiakPreExp_1	1.69	1.13	16.85	11.30
8	PZ14_BujnickiPreExp_5	0.78	1.14	7.77	11.36
9	PZ14_DasPreExp_7	1.28	1.14	12.80	11.38
10	PZ14_AdamiakPostExp_2	1.53	1.14	15.28	11.44
11	PZ14_BujnickiPreExp_6	1.15	1.15	11.50	11.48
12	PZ14_AdamiakPostExp_1	1.60	1.15	15.97	11.49
13	PZ14_DasPostExp_4	1.34	1.15	13.38	11.53
14	PZ14_DasPreExp_8	0.86	1.15	8.57	11.53
15	PZ14_BujnickiPreExp_4	0.61	1.15	6.09	11.54
16	PZ14_DasPostExp_10	1.02	1.16	10.18	11.58
17	PZ14_DasPreExp_5	1.02	1.16	10.18	11.58
18	PZ14_DasPostExp_6	1.28	1.16	12.83	11.61
19	PZ14_DasPreExp_1	1.28	1.16	12.83	11.61
20	PZ14_DasPostExp_8	1.26	1.16	12.61	11.63
21	PZ14_DasPreExp_3	1.26	1.16	12.61	11.63
22	PZ14_ChenPostExp_4	1.63	1.16	16.32	11.65
23	PZ14_AdamiakPreExp_2	1.71	1.18	17.10	11.82
24	PZ14_ChenPostExp_10	1.71	1.18	17.12	11.85
25	PZ14_ChenPostExp_5	0.86	1.21	8.56	12.08
26	PZ14_DasPostExp_7	1.23	1.22	12.27	12.22
27	PZ14_DasPreExp_2	1.23	1.22	12.27	12.22
28	PZ14_ChenPostExp_9	1.11	1.22	11.11	12.23
29	PZ14_DasPreExp_4	1.78	1.23	17.81	12.29
30	PZ14_ChenPostExp_6	0.76	1.23	7.61	12.29
31	PZ14_BujnickiPostExp_1	1.46	1.24	14.61	12.36
32	PZ14_DasPostExp_1	1.50	1.26	14.95	12.58
33	PZ14_ChenPostExp_2	0.80	1.27	7.99	12.69
34	PZ14_DasPostExp_3	1.47	1.28	14.74	12.81
35	PZ14_BujnickiPostExp_5	1.21	1.33	12.12	13.30
36	PZ14_ChenPostExp_7	1.18	1.37	11.81	13.65
37	PZ14_ChenPostExp_1	1.83	1.37	18.34	13.71
38	PZ14_DingPostExp_8	1.22	1.37	12.24	13.73
39	PZ14_DasPostExp_9	1.73	1.39	17.25	13.85
40	PZ14_DasPreExp_10	1.73	1.39	17.25	13.85
41	PZ14_DingPostExp_2	1.25	1.39	12.49	13.88
42	PZ14_DingPreExp_5	1.79	1.45	17.93	14.49
43	PZ14_DingPostExp_3	1.55	1.45	15.54	14.51
44	PZ14_DingPostExp_6	1.84	1.47	18.40	14.73
45	PZ14_DingPostExp_9	1.35	1.48	13.46	14.76
46	PZ14_DingPreExp_3	1.38	1.48	13.85	14.80
47	PZ14_DingPostExp_1	1.15	1.48	11.52	14.84
48	PZ14_BujnickiPostExp_4	1.33	1.52	13.35	15.20
49	PZ14_DingPreExp_1	1.45	1.52	14.54	15.20
50	PZ14_DingPreExp_6	1.65	1.53	16.55	15.29
51	PZ14_DingPreExp_8	1.68	1.54	16.75	15.35
52	PZ14_BujnickiPostExp_2	1.42	1.54	14.20	15.41
53	PZ14_DingPostExp_4	1.68	1.56	16.79	15.59
54	PZ14_DingPreExp_4	1.57	1.56	15.70	15.60
55	PZ14_DingPreExp_7	1.54	1.56	15.38	15.61
56	PZ14_BujnickiPostExp_3	1.64	1.57	16.37	15.65

57	PZ14_DingPreExp_2	1.37	1.57	13.75	15.73
58	PZ14_DingPostExp_10	1.64	1.59	16.40	15.86
59	PZ14_DingPostExp_7	1.63	1.59	16.33	15.89
60	PZ14_DingPostExp_5	1.37	1.59	13.70	15.92
61	PZ14_BujnickiPreExp_7	1.58	1.61	15.76	16.08
	Average	1.37	1.31	13.66	13.08
	Standard deviation	0.61	1.01	6.09	10.05
	Median	1.84	1.61	18.40	16.08

Table S39. BARNABA report on structures in Puzzle 14b.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ14_BujnickiPreExp_1	1.34	0.72	13.41	7.17
2	PZ14_DasPostExp_6	0.74	0.82	7.38	8.24
3	PZ14_DasPreExp_1	0.74	0.82	7.38	8.24
4	PZ14_BujnickiPreExp_3	1.26	0.87	12.62	8.70
5	PZ14_BujnickiPreExp_2	1.80	0.87	17.95	8.72
6	PZ14_DasPostExp_3	0.73	0.89	7.34	8.89
7	PZ14_ChenPostExp_3	2.37	0.90	23.69	8.97
8	PZ14_DasPreExp_9	0.89	0.91	8.87	9.11
9	PZ14_ChenPostExp_8	1.93	0.95	19.27	9.49
10	PZ14_DasPostExp_2	0.74	0.95	7.40	9.51
11	PZ14_DasPostExp_10	1.03	0.96	10.29	9.65
12	PZ14_DasPreExp_5	1.03	0.96	10.29	9.65
13	PZ14_DasPostExp_4	1.24	0.97	12.35	9.67
14	PZ14_DasPostExp_7	1.20	0.99	12.01	9.87
15	PZ14_DasPreExp_2	1.20	0.99	12.01	9.87
16	PZ14_DasPreExp_8	1.65	0.99	16.48	9.93
17	PZ14_ChenPostExp_4	1.94	1.01	19.35	10.06
18	PZ14_DasPostExp_5	0.91	1.02	9.13	10.22
19	PZ14_DasPostExp_8	2.05	1.03	20.47	10.35
20	PZ14_DasPreExp_4	2.05	1.03	20.47	10.35
21	PZ14_ChenPostExp_10	1.61	1.04	16.12	10.40
22	PZ14_DasPreExp_3	1.11	1.05	11.11	10.46
23	PZ14_ChenPostExp_5	1.08	1.06	10.84	10.55
24	PZ14_DasPostExp_1	1.41	1.06	14.05	10.56
25	PZ14_DasPreExp_6	1.41	1.06	14.05	10.56
26	PZ14_ChenPostExp_6	1.18	1.09	11.76	10.92
27	PZ14_DasPreExp_7	1.77	1.10	17.69	10.97
28	PZ14_ChenPostExp_9	1.96	1.10	19.63	11.03
29	PZ14_BujnickiPostExp_2	1.58	1.14	15.81	11.35
30	PZ14_ChenPostExp_2	0.98	1.14	9.78	11.38
31	PZ14_ChenPostExp_7	1.39	1.15	13.87	11.45
32	PZ14_BujnickiPostExp_4	1.87	1.19	18.75	11.88
33	PZ14_BujnickiPostExp_1	1.38	1.19	13.76	11.93
34	PZ14_DasPostExp_9	1.25	1.19	12.52	11.93
35	PZ14_DasPreExp_10	1.25	1.19	12.52	11.93
36	PZ14_ChenPostExp_1	1.79	1.23	17.91	12.31
37	PZ14_DingPostExp_8	0.70	1.31	6.99	13.11
38	PZ14_DingPostExp_2	1.88	1.32	18.76	13.17

39	PZ14_DingPostExp_1	1.69	1.32	16.94	13.25
40	PZ14_DingPreExp_4	0.92	1.33	9.17	13.33
41	PZ14_DingPostExp_5	1.76	1.37	17.60	13.72
42	PZ14_DingPostExp_3	1.29	1.37	12.90	13.73
43	PZ14_DingPostExp_10	1.12	1.38	11.19	13.82
44	PZ14_BujnickiPreExp_4	1.41	1.40	14.11	13.96
45	PZ14_DingPreExp_1	0.96	1.41	9.59	14.11
46	PZ14_DingPostExp_7	1.75	1.43	17.48	14.26
47	PZ14_DingPostExp_9	0.83	1.46	8.33	14.62
48	PZ14_BujnickiPostExp_3	1.63	1.47	16.31	14.74
49	PZ14_DingPostExp_4	0.88	1.48	8.79	14.77
50	PZ14_DingPreExp_2	1.89	1.48	18.94	14.80
51	PZ14_DingPreExp_3	2.09	1.52	20.90	15.15
52	PZ14_DingPostExp_6	0.83	1.54	8.29	15.39
	Average	1.37	1.14	13.74	11.39
	Standard deviation	0.70	0.72	6.99	7.17
	Median	1.84	1.61	18.40	16.08

Table S40. BARNABA report on structures in Puzzle 15.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ15_Adamiak_2	0.85	1.04	8.52	10.44
2	PZ15_RNAComposer1_1	0.85	1.04	8.52	10.44
3	PZ15_Adamiak_3	0.88	1.05	8.82	10.51
4	PZ15_RNAComposer1_2	0.88	1.05	8.82	10.51
5	PZ15_Chén_3	0.92	1.08	9.22	10.76
6	PZ15_Adamiak_6	0.92	1.28	9.25	12.85
7	PZ15_Adamiak_10	0.71	1.29	7.06	12.86
8	PZ15_Adamiak_7	0.87	1.29	8.72	12.87
9	PZ15_Adamiak_8	0.69	1.30	6.88	13.01
10	PZ15_Adamiak_4	0.91	1.35	9.07	13.46
11	PZ15_RNAComposer2_1	0.91	1.35	9.07	13.46
12	PZ15_Adamiak_9	0.82	1.36	8.25	13.56
13	PZ15_Chén_1	1.00	1.36	9.99	13.62
14	PZ15_Chén_4	1.09	1.38	10.86	13.78
15	PZ15_Adamiak_5	0.90	1.38	8.97	13.82
16	PZ15_RNAComposer2_2	0.90	1.38	8.97	13.82
17	PZ15_Adamiak_1	0.94	1.38	9.42	13.83
18	PZ15_FARFAR2_1	1.28	1.40	12.77	13.98
19	PZ15_FARFAR2_10	1.50	1.40	15.04	13.99
20	PZ15_Chén_2	1.66	1.43	16.57	14.28
21	PZ15_FARFAR2_9	1.56	1.43	15.64	14.34
22	PZ15_SimRNA2_2	1.94	1.45	19.38	14.46
23	PZ15_Chén_5	1.70	1.46	16.95	14.58
24	PZ15_Chén_6	0.89	1.46	8.94	14.59
25	PZ15_FARFAR2_6	1.84	1.46	18.41	14.61
26	PZ15_FARFAR1_5	1.44	1.46	14.40	14.61
27	PZ15_FARFAR1_1	1.92	1.47	19.16	14.67
28	PZ15_SimRNA2_1	1.58	1.47	15.79	14.71
29	PZ15_SimRNA2_4	1.22	1.47	12.25	14.74

30	PZ15_Chen_9	1.45	1.48	14.48	14.75
31	PZ15_3dRNA2_10	2.55	1.48	25.49	14.85
32	PZ15_3dRNA2_1	2.55	1.49	25.49	14.86
33	PZ15_3dRNA2_3	2.54	1.49	25.45	14.86
34	PZ15_3dRNA2_8	2.56	1.49	25.56	14.86
35	PZ15_3dRNA2_9	2.54	1.49	25.44	14.88
36	PZ15_3dRNA2_7	2.54	1.49	25.42	14.89
37	PZ15_3dRNA2_5	2.54	1.49	25.43	14.89
38	PZ15_3dRNA2_4	2.54	1.49	25.42	14.90
39	PZ15_3dRNA2_2	2.54	1.49	25.41	14.91
40	PZ15_FARFAR1_3	1.65	1.49	16.53	14.94
41	PZ15_FARFAR1_10	1.94	1.50	19.39	14.98
42	PZ15_3dRNA2_6	2.55	1.50	25.49	14.98
43	PZ15_FARFAR1_9	1.61	1.50	16.11	15.04
44	PZ15_FARFAR1_7	1.64	1.52	16.41	15.15
45	PZ15_FARFAR1_4	1.60	1.52	16.02	15.21
46	PZ15_SimRNA2_10	2.02	1.53	20.20	15.29
47	PZ15_FARFAR2_5	1.12	1.53	11.24	15.30
48	PZ15_FARFAR1_6	1.65	1.54	16.47	15.37
49	PZ15_FARFAR1_8	2.13	1.54	21.33	15.39
50	PZ15_SimRNA2_8	2.32	1.54	23.21	15.44
51	PZ15_FARFAR1_2	1.70	1.55	17.03	15.45
52	PZ15_SimRNA2_9	1.51	1.55	15.10	15.49
53	PZ15_FARFAR2_3	1.69	1.55	16.93	15.53
54	PZ15_FARFAR2_2	1.71	1.56	17.09	15.56
55	PZ15_SimRNA2_3	2.03	1.56	20.33	15.59
56	PZ15_SimRNA2_6	2.12	1.56	21.18	15.63
57	PZ15_FARFAR2_8	1.45	1.57	14.55	15.70
58	PZ15_SimRNA2_5	2.05	1.57	20.47	15.71
59	PZ15_Chen_7	1.22	1.57	12.19	15.73
60	PZ15_Chen_8	1.27	1.58	12.73	15.78
61	PZ15_SimRNA1_10	2.04	1.58	20.43	15.80
62	PZ15_SimRNA1_1	0.73	1.58	7.33	15.82
63	PZ15_FARFAR2_4	1.05	1.59	10.52	15.91
64	PZ15_Chen_10	1.00	1.60	9.99	15.97
65	PZ15_SimRNA1_7	1.87	1.60	18.74	15.99
66	PZ15_FARFAR2_7	1.40	1.63	14.02	16.27
67	PZ15_SimRNA1_9	1.98	1.64	19.84	16.39
68	PZ15_SimRNA1_8	2.09	1.64	20.89	16.40
69	PZ15_SimRNA2_7	0.98	1.67	9.77	16.65
70	PZ15_SimRNA1_5	2.17	1.79	21.74	17.93
71	PZ15_SimRNA1_2	2.18	1.83	21.75	18.35
72	PZ15_SimRNA1_4	2.47	2.04	24.75	20.39
73	PZ15_SimRNA1_6	2.27	2.09	22.66	20.88
74	PZ15_SimRNA1_3	1.76	2.14	17.63	21.42
	Average	1.61	1.49	16.07	14.91
	Standard deviation	0.69	1.04	6.88	10.44
	Median	1.84	1.61	18.40	16.08

Table S41. BARNABA report on structures in Puzzle 17.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ17_Das_1	0.90	1.36	8.95	13.61
2	PZ17_Das_8	0.92	1.51	9.19	15.09
3	PZ17_Bujnicki_8	1.31	1.52	13.10	15.20
4	PZ17_Bujnicki_7	1.15	1.53	11.53	15.34
5	PZ17_DasExtraInfo_2	1.31	1.58	13.07	15.84
6	PZ17_DasExtraInfo_3	1.40	1.58	13.98	15.85
7	PZ17_DasExtraInfo_1	1.17	1.59	11.72	15.86
8	PZ17_Das_7	1.14	1.59	11.38	15.89
9	PZ17_Bujnicki_6	1.55	1.60	15.50	15.96
10	PZ17_Chén_2	1.24	1.60	12.37	16.04
11	PZ17_Das_4	0.68	1.61	6.83	16.07
12	PZ17_Das_3	1.52	1.61	15.16	16.08
13	PZ17_Chén_8	1.75	1.61	17.49	16.11
14	PZ17_Das_9	0.93	1.62	9.26	16.17
15	PZ17_Das_5	1.62	1.62	16.20	16.18
16	PZ17_Das_6	1.22	1.62	12.24	16.21
17	PZ17_SimRNA2_1	0.52	1.62	5.23	16.23
18	PZ17_Bujnicki_1	1.48	1.63	14.83	16.29
19	PZ17_Bujnicki_9	1.48	1.63	14.83	16.29
20	PZ17_Das_2	1.15	1.65	11.54	16.45
21	PZ17_Das_10	1.84	1.65	18.45	16.47
22	PZ17_Bujnicki_5	1.49	1.65	14.92	16.50
23	PZ17_SimRNA2_8	1.36	1.67	13.60	16.69
24	PZ17_Chén_7	1.80	1.67	17.99	16.74
25	PZ17_SimRNA2_3	1.66	1.68	16.64	16.78
26	PZ17_Xiao_2	1.76	1.68	17.63	16.81
27	PZ17_Ding_7	1.45	1.69	14.47	16.88
28	PZ17_Dohkolyan_3	1.55	1.70	15.49	16.95
29	PZ17_Adamiak_3	1.25	1.70	12.49	16.98
30	PZ17_Bujnicki_4	1.71	1.70	17.08	17.02
31	PZ17_Adamiak_1	1.28	1.71	12.77	17.07
32	PZ17_Bujnicki_10	1.54	1.71	15.41	17.07
33	PZ17_Bujnicki_2	1.54	1.71	15.41	17.07
34	PZ17_Ding_8	1.61	1.71	16.06	17.11
35	PZ17_Adamiak_2	1.22	1.71	12.19	17.13
36	PZ17_RNAComposer2_8	1.40	1.72	13.98	17.22
37	PZ17_Chén_3	1.83	1.74	18.33	17.39
38	PZ17_Bujnicki_3	1.56	1.74	15.55	17.40
39	PZ17_Xiao_3	1.64	1.74	16.40	17.43
40	PZ17_Ding_10	1.49	1.75	14.92	17.48
41	PZ17_SimRNA2_7	0.81	1.75	8.07	17.48
42	PZ17_RNAComposer2_7	1.31	1.75	13.14	17.50
43	PZ17_Xiao_9	1.44	1.76	14.42	17.56
44	PZ17_Ding_9	1.75	1.76	17.52	17.58
45	PZ17_SimRNA2_2	1.67	1.77	16.71	17.68
46	PZ17_Xiao_5	1.54	1.77	15.40	17.69
47	PZ17_Xiao_8	1.66	1.77	16.58	17.72
48	PZ17_SimRNA2_4	1.59	1.77	15.93	17.73

49	PZ17_RNAComposer2_2	1.27	1.78	12.67	17.75
50	PZ17_RNAComposer2_4	1.41	1.78	14.13	17.78
51	PZ17_Chén_1	1.75	1.78	17.45	17.84
52	PZ17_Xiao_1	1.54	1.79	15.35	17.85
53	PZ17_RNAComposer2_1	1.29	1.79	12.95	17.86
54	PZ17_RNAComposer2_6	1.34	1.79	13.39	17.94
55	PZ17_Ding_6	1.80	1.80	17.99	17.96
56	PZ17_SimRNA2_6	1.24	1.80	12.39	17.97
57	PZ17_SimRNA2_5	1.93	1.81	19.30	18.09
58	PZ17_Chén_6	1.56	1.81	15.57	18.13
59	PZ17_RNAComposer2_5	1.32	1.81	13.19	18.14
60	PZ17_Chén_9	1.65	1.82	16.50	18.18
61	PZ17_Xiao_10	1.62	1.82	16.17	18.19
62	PZ17_Ding_5	1.69	1.82	16.94	18.24
63	PZ17_Ding_3	1.53	1.84	15.27	18.37
64	PZ17_Xiao_6	1.78	1.84	17.78	18.43
65	PZ17_SimRNA2_9	1.50	1.85	14.97	18.54
66	PZ17_Ding_1	1.59	1.87	15.90	18.67
67	PZ17_RNAComposer2_10	1.63	1.87	16.33	18.70
68	PZ17_Xiao_4	1.83	1.87	18.26	18.70
69	PZ17_RNAComposer2_3	1.25	1.90	12.46	18.97
70	PZ17_RNAComposer2_9	1.68	1.90	16.82	18.97
71	PZ17_Ding_2	1.70	1.92	17.02	19.18
72	PZ17_Ding_4	1.67	1.92	16.72	19.23
73	PZ17_Major_5	1.98	1.93	19.80	19.28
74	PZ17_Major_3	1.86	1.93	18.55	19.30
75	PZ17_Major_1	1.79	1.93	17.91	19.34
76	PZ17_Dohkolyan_2	1.73	1.94	17.32	19.45
77	PZ17_Xiao_7	1.41	1.96	14.15	19.57
78	PZ17_RNAComposer1_3	1.79	1.96	17.92	19.62
79	PZ17_Major_2	1.93	1.96	19.32	19.63
80	PZ17_Major_4	1.95	1.96	19.52	19.64
81	PZ17_RNAComposer1_1	1.96	1.98	19.61	19.77
82	PZ17_RNAComposer1_4	2.05	2.01	20.48	20.07
83	PZ17_RNAComposer1_6	1.93	2.01	19.29	20.09
84	PZ17_RNAComposer1_5	2.03	2.01	20.28	20.10
85	PZ17_RNAComposer1_8	1.79	2.01	17.92	20.14
86	PZ17_SimRNA1_6	1.58	2.02	15.81	20.18
87	PZ17_SimRNA1_8	1.73	2.02	17.27	20.19
88	PZ17_SimRNA1_2	1.72	2.02	17.21	20.20
89	PZ17_RNAComposer1_9	2.00	2.03	19.97	20.28
90	PZ17_SimRNA1_5	1.77	2.04	17.66	20.39
91	PZ17_Major_7	1.72	2.04	17.23	20.45
92	PZ17_Major_6	1.64	2.05	16.43	20.53
93	PZ17_RNAComposer1_10	1.89	2.06	18.91	20.63
94	PZ17_Major_8	1.76	2.06	17.63	20.65
95	PZ17_Chén_5	1.01	2.07	10.11	20.74
96	PZ17_SimRNA1_4	1.73	2.09	17.33	20.92
97	PZ17_SimRNA1_3	1.77	2.11	17.74	21.09
98	PZ17_Major_9	1.75	2.12	17.45	21.18
99	PZ17_SimRNA1_1	1.61	2.12	16.10	21.21

100	PZ17_Chen_4	1.56	2.15	15.62	21.53
101	PZ17_Major_10	1.42	2.21	14.22	22.08
102	PZ17_RNAComposer1_2	2.24	2.22	22.38	22.24
103	PZ17_RNAComposer1_7	2.13	2.23	21.25	22.31
104	PZ17_Dohkolyan_1	2.23	2.24	22.30	22.41
105	PZ17_Chen_10	2.00	2.26	20.03	22.64
106	PZ17_SimRNA1_7	1.96	2.33	19.57	23.28
107	PZ17_SimRNA1_9	2.10	2.37	21.04	23.65
	Average	1.57	1.83	15.73	18.34
	Standard deviation	0.52	1.36	5.23	13.61
	Median	2.37	1.54	23.69	15.39

Table S42. BARNABA report on structures in Puzzle 18.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ18_Das_1	0.55	0.78	5.52	7.85
2	PZ18_Das_3	0.57	0.81	5.69	8.14
3	PZ18_Das_2	0.40	0.88	3.95	8.79
4	PZ18_Das_4	0.56	0.94	5.63	9.35
5	PZ18_Chen_1	0.35	0.98	3.53	9.80
6	PZ18_Chen_2	0.69	0.99	6.91	9.89
7	PZ18_Das_5	1.10	1.10	11.05	10.98
8	PZ18_FARFAR_7	1.53	1.43	15.33	14.32
9	PZ18_Chen_3	0.89	1.44	8.87	14.42
10	PZ18_Chen_4	0.89	1.45	8.90	14.45
11	PZ18_FARFAR_1	1.65	1.45	16.55	14.50
12	PZ18_3dRNA_2	1.94	1.46	19.35	14.56
13	PZ18_Dokholyan_2	1.19	1.46	11.93	14.58
14	PZ18_FARFAR_4	1.18	1.46	11.76	14.62
15	PZ18_FARFAR_2	0.97	1.46	9.74	14.64
16	PZ18_Dokholyan_1	0.87	1.48	8.66	14.76
17	PZ18_FARFAR_10	1.34	1.48	13.35	14.80
18	PZ18_FARFAR_3	1.27	1.48	12.68	14.84
19	PZ18_FARFAR_8	1.58	1.48	15.76	14.85
20	PZ18_FARFAR_9	1.78	1.50	17.78	14.96
21	PZ18_Chen_5	1.58	1.50	15.80	15.03
22	PZ18_FARFAR_6	1.01	1.50	10.10	15.04
23	PZ18_FARFAR_5	1.33	1.52	13.34	15.22
24	PZ18_RNAComposer_2	2.16	1.52	21.56	15.24
25	PZ18_Ding_2	2.08	1.53	20.80	15.34
26	PZ18_Dokholyan_3	0.77	1.54	7.72	15.40
27	PZ18_3dRNA_1	1.91	1.54	19.13	15.42
28	PZ18_RNAComposer_5	1.55	1.55	15.46	15.51
29	PZ18_3dRNA_4	1.24	1.57	12.40	15.73
30	PZ18_RNAComposer_4	2.13	1.57	21.32	15.74
31	PZ18_Ding_5	1.62	1.58	16.19	15.81
32	PZ18_RNAComposer_1	2.11	1.58	21.14	15.82
33	PZ18_YagoubAli_1	1.90	1.58	19.04	15.83
34	PZ18_Lee_2	2.16	1.60	21.64	16.04
35	PZ18_3dRNA_3	2.03	1.61	20.28	16.06

36	PZ18_Ding_1	1.99	1.61	19.89	16.10
37	PZ18_SimRNA_2	1.10	1.63	11.01	16.32
38	PZ18_LeeServer_2	2.30	1.64	23.02	16.38
39	PZ18_3dRNA_5	2.41	1.67	24.05	16.68
40	PZ18_Ding_3	1.64	1.69	16.40	16.90
41	PZ18_LeeServer_5	1.88	1.69	18.83	16.93
42	PZ18_RNAComposer_3	2.10	1.70	21.02	16.97
43	PZ18_Lee_5	2.44	1.71	24.38	17.12
44	PZ18_Lee_1	2.23	1.73	22.34	17.30
45	PZ18_LeeServer_1	2.26	1.75	22.63	17.45
46	PZ18_Lee_4	2.25	1.76	22.52	17.57
47	PZ18_LeeServer_4	1.96	1.76	19.56	17.58
48	PZ18_SimRNA_3	2.48	1.81	24.77	18.12
49	PZ18_Ding_4	2.49	1.98	24.94	19.83
50	PZ18_SimRNA_1	2.30	2.04	23.03	20.44
51	PZ18_Lee_3	2.15	2.05	21.46	20.52
52	PZ18_LeeServer_3	2.12	2.10	21.20	21.00
	Average	1.60	1.52	15.96	15.22
	Standard deviation	0.35	0.78	3.53	7.85
	Median	2.49	2.10	24.94	21.00

Table S43. BARNABA report on structures in Puzzle 19.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ19_Chen_4	1.05	1.30	10.54	12.98
2	PZ19_Bujnicki_3	1.60	1.32	16.05	13.15
3	PZ19_SimRNA_2	1.53	1.32	15.30	13.21
4	PZ19_Chen_1	0.58	1.35	5.81	13.52
5	PZ19_Das_2	1.20	1.39	11.98	13.87
6	PZ19_Das_4	1.53	1.39	15.26	13.87
7	PZ19_RNAComposer_5	1.21	1.39	12.05	13.90
8	PZ19_Das_3	1.52	1.40	15.17	14.02
9	PZ19_Chen_3	1.59	1.41	15.85	14.11
10	PZ19_RNAComposer_2	1.13	1.41	11.34	14.14
11	PZ19_Bujnicki_1	1.51	1.42	15.08	14.21
12	PZ19_3dRNA_5	1.62	1.44	16.22	14.39
13	PZ19_3dRNA_2	1.47	1.45	14.66	14.48
14	PZ19_Das_1	1.91	1.45	19.07	14.48
15	PZ19_Das_5	1.17	1.45	11.72	14.53
16	PZ19_Chen_2	0.76	1.45	7.63	14.54
17	PZ19_Ding_3	1.84	1.47	18.45	14.67
18	PZ19_Ding_1	1.61	1.47	16.06	14.69
19	PZ19_RNAComposer_1	1.62	1.47	16.22	14.70
20	PZ19_3dRNA_1	1.63	1.47	16.29	14.72
21	PZ19_Dokholyan_1	1.77	1.48	17.71	14.77
22	PZ19_Ding_2	1.72	1.49	17.20	14.89
23	PZ19_3dRNA_3	1.66	1.50	16.64	15.02
24	PZ19_LeeServer_1	1.53	1.51	15.35	15.14
25	PZ19_Adamiak_1	1.17	1.52	11.67	15.16
26	PZ19_RNAComposer_3	1.00	1.53	9.98	15.31

27	PZ19_Bujnicki_2	1.08	1.54	10.80	15.37
28	PZ19_Bujnicki_5	1.76	1.54	17.62	15.44
29	PZ19_Ding_4	1.87	1.54	18.73	15.44
30	PZ19_SimRNA_1	1.48	1.55	14.82	15.54
31	PZ19_3dRNA_4	1.41	1.56	14.12	15.56
32	PZ19_RNAComposer_4	1.30	1.58	13.00	15.79
33	PZ19_Adamiak_4	1.31	1.59	13.05	15.92
34	PZ19_LeeServer_3	2.02	1.59	20.15	15.93
35	PZ19_Ding_5	2.13	1.60	21.26	16.01
36	PZ19_Adamiak_5	1.02	1.60	10.22	16.04
37	PZ19_LeeServer_2	1.16	1.60	11.62	16.04
38	PZ19_LeeServer_5	1.61	1.62	16.08	16.16
39	PZ19_Bujnicki_4	1.54	1.62	15.39	16.18
40	PZ19_Adamiak_2	1.75	1.63	17.49	16.26
41	PZ19_LeeServer_4	1.26	1.65	12.62	16.52
42	PZ19_Adamiak_3	1.51	1.78	15.11	17.79
43	PZ19_SimRNA_3	1.34	1.96	13.40	19.56
44	PZ19_FARFAR_8	1.78	2.11	17.79	21.13
45	PZ19_FARFAR_9	1.87	2.12	18.72	21.19
46	PZ19_FARFAR_5	1.62	2.12	16.20	21.22
47	PZ19_FARFAR_1	1.75	2.13	17.54	21.26
48	PZ19_FARFAR_7	1.84	2.13	18.42	21.26
49	PZ19_Chen_5	2.23	2.13	22.27	21.30
50	PZ19_FARFAR_2	1.71	2.13	17.08	21.30
51	PZ19_FARFAR_10	1.88	2.13	18.82	21.32
52	PZ19_FARFAR_3	1.83	2.16	18.33	21.59
53	PZ19_FARFAR_6	1.75	2.16	17.47	21.64
54	PZ19_FARFAR_4	1.64	2.20	16.41	22.00
	Average	1.53	1.64	15.26	16.36
	Standard deviation	0.58	1.30	5.81	12.98
	Median	2.23	2.20	22.27	22.00

Table S44. BARNABA report on structures in Puzzle 20.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ20_Bujnicki_3	0.68	0.98	6.81	9.80
2	PZ20_Bujnicki_2	0.71	0.98	7.14	9.81
3	PZ20_Bujnicki_1	0.55	1.00	5.49	9.99
4	PZ20_Adamiak_5	0.71	1.02	7.14	10.22
5	PZ20_Bujnicki_4	0.47	1.03	4.74	10.35
6	PZ20_RNAComposer_5	1.37	1.07	13.66	10.69
7	PZ20_RNAComposer_4	1.19	1.12	11.91	11.18
8	PZ20_Bujnicki_5	0.53	1.13	5.34	11.28
9	PZ20_Das_3	0.72	1.16	7.15	11.60
10	PZ20_RNAComposer_1	1.78	1.16	17.85	11.62
11	PZ20_RNAComposer_2	1.73	1.18	17.34	11.79
12	PZ20_RNAComposer_3	1.36	1.22	13.59	12.18
13	PZ20_Adamiak_2	1.65	1.24	16.55	12.44
14	PZ20_Adamiak_4	1.46	1.30	14.62	13.04
15	PZ20_Das_5	1.70	1.31	17.01	13.05

16	PZ20_FARFAR_6	2.01	1.31	20.06	13.08
17	PZ20_Adamiak_1	1.23	1.31	12.25	13.09
18	PZ20_FARFAR_3	1.74	1.32	17.42	13.21
19	PZ20_FARFAR_5	1.99	1.32	19.92	13.22
20	PZ20_Adamiak_3	1.79	1.32	17.88	13.25
21	PZ20_FARFAR_1	1.86	1.35	18.56	13.55
22	PZ20_FARFAR_9	1.73	1.36	17.35	13.58
23	PZ20_FARFAR_8	1.72	1.36	17.18	13.64
24	PZ20_FARFAR_7	1.77	1.37	17.69	13.68
25	PZ20_FARFAR_10	1.79	1.38	17.93	13.84
26	PZ20_Xiao3_3	1.96	1.39	19.56	13.87
27	PZ20_FARFAR_4	1.78	1.39	17.84	13.88
28	PZ20_Das_2	0.61	1.39	6.08	13.93
29	PZ20_FARFAR_2	1.86	1.39	18.58	13.95
30	PZ20_Xiao3_4	2.03	1.40	20.34	14.02
31	PZ20_Das_4	1.00	1.42	9.97	14.24
32	PZ20_Xiao3_5	1.28	1.43	12.76	14.28
33	PZ20_Das_1	0.68	1.43	6.81	14.30
34	PZ20_Xiao3_1	1.86	1.44	18.61	14.39
35	PZ20_Xiao3_2	2.03	1.44	20.26	14.41
36	PZ20_SimRNA_4	2.08	2.07	20.79	20.65
37	PZ20_SimRNA_2	2.44	2.18	24.36	21.76
38	PZ20_SimRNA_5	2.13	2.23	21.30	22.31
39	PZ20_SimRNA_3	2.25	2.41	22.50	24.08
40	PZ20_SimRNA_1	1.89	2.43	18.95	24.30
	Average	1.50	1.39	15.03	13.94
	Standard deviation	0.47	0.98	4.74	9.80
	Median	2.44	2.43	24.36	24.30

Table S45. BARNABA report on structures in Puzzle 21.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ21_DasLORES_1	0.33	1.34	3.28	13.41
2	PZ21_Das_5	0.64	1.61	6.35	16.12
3	PZ21_Adamiak_4	0.45	1.65	4.50	16.52
4	PZ21_Adamiak_5	0.54	1.69	5.36	16.90
5	PZ21_Adamiak_3	0.44	1.70	4.38	16.98
6	PZ21_ChenHighLig_2	0.38	1.70	3.78	17.03
7	PZ21_ChenLowLig_2	0.38	1.70	3.78	17.03
8	PZ21_DasLORES_5	0.92	1.71	9.15	17.12
9	PZ21_Bujnicki_4	0.65	1.73	6.46	17.29
10	PZ21_RNAComposer_4	1.46	1.73	14.55	17.34
11	PZ21_RNAComposer_3	1.36	1.74	13.61	17.35
12	PZ21_DasLORES_4	0.62	1.74	6.23	17.36
13	PZ21_Adamiak_2	0.44	1.74	4.42	17.42
14	PZ21_DasLORES_2	0.38	1.75	3.85	17.46
15	PZ21_Adamiak_1	0.44	1.76	4.41	17.63
16	PZ21_ChenHighLig_5	0.73	1.81	7.32	18.08
17	PZ21_ChenLowLig_5	0.73	1.81	7.32	18.08
18	PZ21_Bujnicki_2	0.98	1.82	9.81	18.17

19	PZ21_ChenHighLig_1	0.42	1.84	4.16	18.41
20	PZ21_ChenLowLig_1	0.42	1.84	4.16	18.41
21	PZ21_Das_3	0.49	1.84	4.92	18.43
22	PZ21_Das_4	0.55	1.84	5.54	18.44
23	PZ21_DasLORES_3	1.53	1.88	15.34	18.78
24	PZ21_Bujnicki_1	0.73	1.88	7.26	18.81
25	PZ21_ChenHighLig_4	0.51	1.88	5.08	18.82
26	PZ21_ChenLowLig_4	0.51	1.88	5.08	18.82
27	PZ21_ChenHighLig_3	0.53	1.89	5.30	18.86
28	PZ21_ChenLowLig_3	0.53	1.89	5.30	18.86
29	PZ21_Das_1	0.57	1.89	5.71	18.91
30	PZ21_Das_2	0.56	1.93	5.64	19.34
31	PZ21_3dRNA_5	1.77	1.98	17.66	19.76
32	PZ21_3dRNA_1	1.28	2.01	12.83	20.06
33	PZ21_3dRNA_4	1.82	2.02	18.20	20.16
34	PZ21_3dRNA_3	1.28	2.03	12.82	20.29
35	PZ21_FARFAR_9	1.85	2.03	18.52	20.32
36	PZ21_FARFAR_3	1.81	2.05	18.12	20.50
37	PZ21_FARFAR_10	1.60	2.06	16.01	20.58
38	PZ21_RNAComposer_2	1.85	2.07	18.48	20.67
39	PZ21_FARFAR_6	1.67	2.07	16.66	20.72
40	PZ21_FARFAR_4	1.87	2.09	18.73	20.85
41	PZ21_Sanbonmatsu_1	1.52	2.09	15.24	20.89
42	PZ21_Sanbonmatsu_2	1.52	2.09	15.24	20.89
43	PZ21_RNAComposer_1	1.50	2.09	15.02	20.92
44	PZ21_FARFAR_8	1.82	2.09	18.17	20.94
45	PZ21_RNAComposer_5	1.76	2.11	17.56	21.06
46	PZ21_FARFAR_7	1.86	2.12	18.63	21.17
47	PZ21_FARFAR_2	1.66	2.12	16.64	21.20
48	PZ21_FARFAR_1	1.84	2.13	18.35	21.32
49	PZ21_3dRNA_2	1.32	2.16	13.23	21.63
50	PZ21_FARFAR_5	1.86	2.17	18.64	21.67
51	PZ21_SimRNA_4	1.16	2.18	11.58	21.76
52	PZ21_Sanbonmatsu_3	1.48	2.18	14.81	21.84
53	PZ21_Sanbonmatsu_4	1.48	2.18	14.81	21.84
54	PZ21_SimRNA_2	1.26	2.19	12.59	21.94
55	PZ21_Bujnicki_3	1.26	2.21	12.58	22.09
56	PZ21_SimRNA_3	1.41	2.23	14.08	22.26
57	PZ21_SimRNA_5	1.41	2.23	14.08	22.26
58	PZ21_SimRNA_1	1.24	2.24	12.41	22.36
59	PZ21_Bujnicki_5	2.19	2.38	21.93	23.76
	Average	1.11	1.95	11.11	19.45
	Standard deviation	0.33	1.34	3.28	13.41
	Median	2.19	2.38	21.93	23.76

Table 45. BARNABA report on structures in Puzzle 24.

No.	3D RNA model	BBRMSD [nm]	ERMSD [nm]	BBRMSD [Å]	ERMSD [Å]
1	PZ24_Bujnicki_4	1.90	0.89	18.95	8.87
2	PZ24_Bujnicki_5	1.51	0.91	15.07	9.12

3	PZ24_Vfold3D_1	1.54	0.92	15.43	9.18
4	PZ24_FARFAR2_8	1.34	0.94	13.45	9.44
5	PZ24_Bujnicki_2	1.03	0.94	10.27	9.44
6	PZ24_FARFAR2_10	1.05	0.97	10.51	9.70
7	PZ24_DasTFN_1	1.12	0.97	11.24	9.71
8	PZ24_DasTFN_9	0.92	0.97	9.24	9.73
9	PZ24_FARFAR2_6	0.92	0.97	9.24	9.73
10	PZ24_Das_3	1.74	0.99	17.42	9.89
11	PZ24_Das_2	1.77	0.99	17.72	9.90
12	PZ24_Das_10	1.69	0.99	16.88	9.90
13	PZ24_Das_6	1.49	0.99	14.94	9.90
14	PZ24_Das_8	1.56	0.99	15.59	9.91
15	PZ24_Das_5	1.48	0.99	14.82	9.92
16	PZ24_Das_1	1.64	0.99	16.37	9.92
17	PZ24_DasTFN_8	1.15	0.99	11.49	9.94
18	PZ24_Das_4	1.55	0.99	15.55	9.94
19	PZ24_Das_9	1.45	0.99	14.52	9.94
20	PZ24_Das_7	1.41	1.00	14.07	9.97
21	PZ24_FARFAR2_3	2.05	1.00	20.47	9.98
22	PZ24_Vfold3D_3	1.65	1.00	16.54	9.99
23	PZ24_FARFAR2_9	0.80	1.00	8.00	10.00
24	PZ24_Bujnicki_3	1.14	1.00	11.35	10.01
25	PZ24_FARFAR2_7	1.27	1.02	12.70	10.17
26	PZ24_Vfold3D_5	1.17	1.02	11.70	10.24
27	PZ24_DasTFN_7	1.72	1.02	17.21	10.24
28	PZ24_DasTFN_6	0.70	1.03	6.99	10.28
29	PZ24_Adamiak_4	1.54	1.04	15.39	10.43
30	PZ24_DasTFN_10	0.49	1.04	4.88	10.44
31	PZ24_RNAComposer_2	1.09	1.04	10.90	10.45
32	PZ24_Vfold3D_2	1.33	1.05	13.32	10.45
33	PZ24_FARFAR2_4	1.43	1.05	14.27	10.49
34	PZ24_Bujnicki_1	1.55	1.05	15.49	10.51
35	PZ24_DasTFN_3	1.75	1.06	17.46	10.58
36	PZ24_FARFAR2_1	1.75	1.06	17.46	10.58
37	PZ24_Vfold3D_4	1.49	1.06	14.93	10.63
38	PZ24_Adamiak_5	1.02	1.07	10.16	10.67
39	PZ24_RNAComposer_1	1.38	1.07	13.77	10.73
40	PZ24_Adamiak_3	1.47	1.08	14.69	10.76
41	PZ24_DasTFN_5	2.08	1.09	20.77	10.95
42	PZ24_3dRNA_5	1.95	1.11	19.46	11.14
43	PZ24_3dRNA_4	1.63	1.12	16.25	11.16
44	PZ24_DasTFN_4	2.24	1.12	22.38	11.17
45	PZ24_Adamiak_2	1.12	1.12	11.22	11.19
46	PZ24_DasTFN_2	1.41	1.12	14.08	11.21
47	PZ24_3dRNA_3	1.90	1.12	19.00	11.21
48	PZ24_FARFAR2_5	2.01	1.12	20.06	11.24
49	PZ24_Adamiak_1	1.07	1.13	10.71	11.27
50	PZ24_3dRNA_2	2.09	1.13	20.86	11.32
51	PZ24_3dRNA_1	1.66	1.15	16.55	11.45
52	PZ24_RNAComposer_4	1.32	1.15	13.17	11.51
53	PZ24_FARFAR2_2	1.79	1.16	17.88	11.55

54	PZ24_iFoldRNA_1	1.98	1.16	19.82	11.64
55	PZ24_VfoldLA_4	1.53	1.18	15.26	11.77
56	PZ24_iFoldRNA_2	1.06	1.20	10.61	11.98
57	PZ24_RNAComposer_3	1.34	1.22	13.38	12.19
58	PZ24_RNAComposer_5	1.76	1.25	17.58	12.55
59	PZ24_VfoldLA_1	1.56	1.32	15.57	13.16
60	PZ24_VfoldLA_2	1.61	1.36	16.06	13.63
61	PZ24_VfoldLA_3	1.52	1.37	15.21	13.72
62	PZ24_VfoldLA_5	1.43	1.38	14.30	13.79
63	PZ24_Ding_4	2.89	1.51	28.86	15.11
64	PZ24_Ding_3	2.15	1.52	21.50	15.17
65	PZ24_Ding_1	2.08	1.54	20.85	15.38
66	PZ24_iFoldRNA_3	2.20	1.54	22.03	15.42
67	PZ24_Ding_7	2.68	1.54	26.80	15.43
68	PZ24_Ding_5	2.03	1.55	20.30	15.50
69	PZ24_iFoldRNA_4	2.84	1.55	28.38	15.52
70	PZ24_Ding_10	2.10	1.56	20.97	15.62
71	PZ24_Ding_9	2.18	1.56	21.78	15.65
72	PZ24_Ding_8	2.49	1.59	24.91	15.93
73	PZ24_Ding_6	2.02	1.60	20.23	16.00
74	PZ24_Ding_2	2.17	1.62	21.71	16.17
75	PZ24_SimRNA_5	1.67	1.66	16.72	16.57
76	PZ24_SimRNA_3	1.50	1.67	15.03	16.70
77	PZ24_iFoldRNA_5	2.42	1.68	24.18	16.78
78	PZ24_Kollmann_5	3.35	1.84	33.48	18.38
79	PZ24_Kollmann_1	3.08	1.84	30.79	18.38
80	PZ24_SimRNA_1	2.22	1.87	22.23	18.69
81	PZ24_Kollmann_6	3.15	1.93	31.51	19.33
82	PZ24_SimRNA_4	2.67	1.94	26.68	19.37
83	PZ24_Kollmann_3	3.34	2.00	33.36	19.96
84	PZ24_Kollmann_8	3.35	2.06	33.49	20.60
85	PZ24_Kollmann_2	2.60	2.10	26.00	21.01
86	PZ24_Kollmann_4	3.30	2.12	33.01	21.17
87	PZ24_SimRNA_2	2.55	2.13	25.50	21.31
88	PZ24_Kollmann_7	2.96	2.18	29.64	21.80
89	PZ24_Kollmann_10	3.02	2.26	30.15	22.63
90	PZ24_Kollmann_9	3.05	2.28	30.52	22.82
	Average	1.81	1.29	18.12	12.94
	Standard deviation	0.49	0.89	4.88	8.87
	Median	3.35	2.28	33.49	22.82

X3DNA reports

Table S46. X3DNA report on reference structures.

			Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
No.	3D RNA model	#Helices	#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ01_refstructure	1	21	19	10	0	0	7	3	20
2	PZ02_refstructure	4	38	36	14	0	0	12	8	34
3	PZ03_refstructure	2	32	25	13	0	0	11	6	30
4	PZ04_refstructure	4	51	46	20	0	0	22	5	47
5	PZ05_refstructure	7	71	59	37	0	0	18	9	64
6	PZ06_refstructure	7	61	49	16	0	0	25	13	54
7	PZ07_refstructure	4	73	61	30	0	0	25	14	69
8	PZ08_refstructure	3	36	31	19	0	0	9	5	33
9	PZ09_refstructure	3	31	20	12	0	0	6	10	28
10	PZ10_refstructure	4	57	44	19	0	0	25	16	60
11	PZ11_refstructure	1	59	45	3	0	0	16	4	23
12	PZ12_refstructure	4	61	46	19	0	0	17	6	42
13	PZ13_refstructure	2	63	47	14	0	0	7	3	24
14	PZ14_refstructure_bound	2	65	48	10	0	0	7	3	20
15	PZ14_refstructure_free	2	67	49	9	0	0	8	2	19
16	PZ15_refstructure	2	69	50	13	0	0	2	4	19
17	PZ17_refstructure	2	71	51	8	0	0	9	4	21
18	PZ18_refstructure	2	73	52	12	0	0	9	6	27
19	PZ19_refstructure	2	75	53	12	0	0	6	7	25
20	PZ20_refstructure	2	78	54	17	0	0	4	7	28
21	PZ21_refstructure	2	80	56	6	0	0	2	3	11
22	PZ24_refstructure	3	82	57	32	0	0	11	3	46
	Average	2.95	84	58	15.68	0.00	0.00	11.73	6.41	33.82
	Standard deviation	1.62	86	59	8.35	0.00	0.00	7.36	3.87	16.27
	Median	2.00	88	60	13.50	0.00	0.00	9.00	5.50	28.00

Table S47. X3DNA report on structures in Puzzle 01.

			Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
No.	3D RNA model	#Helices	#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ01_Bujnicki_1	1	22	20	13	0	0	6	2	21
2	PZ01_Bujnicki_2	1	21	18	7	0	0	10	3	20
3	PZ01_Bujnicki_3	1	20	17	9	0	0	7	3	19
4	PZ01_Bujnicki_4	1	19	13	9	0	0	4	5	18
5	PZ01_Bujnicki_5	1	19	13	11	0	0	3	4	18
6	PZ01_Chen_1	1	21	16	7	0	0	9	4	20
7	PZ01_Das_1	1	22	20	11	0	0	8	2	21
8	PZ01_Das_2	1	22	20	11	0	0	8	2	21
9	PZ01_Das_3	1	22	20	11	0	0	8	2	21
10	PZ01_Das_4	1	22	20	11	0	0	8	2	21
11	PZ01_Das_5	1	21	20	11	0	0	6	3	20
12	PZ01_Dokholyan_1	1	22	20	9	0	0	9	3	21
13	PZ01_Major_1	1	21	18	5	0	0	12	3	20
14	PZ01_Santalucia_1	1	21	20	14	0	0	3	3	20
15	PZ01_refstructure	1	21	19	10	0	0	7	3	20
	Average	1.00	21.07	18.27	9.93	0.00	0.00	7.20	2.93	20.07
	Standard deviation	0.00	1.03	2.49	2.34	0.00	0.00	2.51	0.88	1.03
	Median	1.00	21.00	20.00	11.00	0.00	0.00	8.00	3.00	20.00

Table S49. X3DNA report on structures in Puzzle 02.

			Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
No.	3D RNA model	#Helices	#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ02_refstructure	4	38	36	14	0	0	12	8	34
2	PZ02_Bujnicki_1	4	38	37	5	0	0	21	8	34
3	PZ02_Bujnicki_2	3	40	38	0	1	0	26	10	37
4	PZ02_Bujnicki_3	3	40	38	0	1	0	26	10	37
5	PZ02_Chen_1	4	36	35	9	0	0	14	9	32
6	PZ02_Das_1	4	40	38	14	0	0	12	10	36
7	PZ02_Das_2	3	39	37	15	0	0	11	10	36
8	PZ02_Das_3	4	40	37	14	0	0	12	10	36
9	PZ02_Das_4	4	40	37	16	0	0	10	10	36
10	PZ02_Das_5	4	42	37	17	0	0	10	11	38
11	PZ02_Dokholyan_1	4	39	37	17	0	0	9	9	35
12	PZ02_Major_1	4	37	37	22	0	0	11	0	33
13	PZ02_Santalucia_1	4	40	40	28	0	0	0	8	36
14	PZ02_Wildauer_1	4	37	35	0	0	0	25	8	33
	Average	3.79	39.00	37.07	12.21	0.14	0.00	14.21	8.64	35.21
	Standard deviation	0.43	1.62	1.27	8.47	0.36	0.00	7.55	2.68	1.76
	Median	4.00	39.50	37.00	14.00	0.00	0.00	12.00	9.50	36.00

Table S50. X3DNA report on structures in Puzzle 03.

			Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
No.	3D RNA model	#Helices	#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ03_Bujnicki_1	2	33	23	6	0	0	21	4	31
2	PZ03_Bujnicki_2	2	34	22	12	0	0	15	5	32

3	PZ03_Chen_1	3	31	21	3	0	0	22	3	28
4	PZ03_Das_1	2	37	23	16	0	0	13	6	35
5	PZ03_Das_2	2	37	23	15	0	0	16	4	35
6	PZ03_Das_3	2	37	24	15	0	0	14	6	35
7	PZ03_Das_4	2	38	23	16	0	0	13	7	36
8	PZ03_Das_5	2	37	24	17	0	0	14	4	35
9	PZ03_Dokholyan_1	3	27	23	15	0	0	6	3	24
10	PZ03_Dokholyan_2	4	28	22	13	0	0	9	2	24
11	PZ03_Major_1	4	28	21	4	0	0	16	4	24
12	PZ03_Major_2	3	32	19	1	0	0	26	2	29
13	PZ03_refstructure	2	32	25	13	0	0	11	6	30
	Average	2.54	33.15	22.54	11.23	0.00	0.00	15.08	4.31	30.62
	Standard deviation	0.78	3.89	1.56	5.63	0.00	0.00	5.41	1.60	4.56
	Median	2.00	33.00	23.00	13.00	0.00	0.00	14.00	4.00	31.00

Table S51. X3DNA report on structures in Puzzle 04.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ04_refstructure	4	51	46	20	0	0	22	5	47
2	PZ04_Adamiak_1	4	49	44	9	0	0	32	4	45
3	PZ04_Adamiak_2	5	51	44	19	0	0	24	3	46
4	PZ04_Adamiak_3	5	52	44	20	0	0	23	4	47
5	PZ04_Adamiak_4	4	48	26	0	0	0	35	9	44
6	PZ04_Adamiak_5	4	42	18	0	0	0	30	8	38
7	PZ04_Bujnicki_1	4	51	46	32	0	0	10	5	47
8	PZ04_Bujnicki_2	4	51	46	32	0	0	10	5	47
9	PZ04_Bujnicki_3	4	51	46	32	0	0	10	5	47
10	PZ04_Bujnicki_4	4	51	46	32	0	0	10	5	47
11	PZ04_Bujnicki_5	4	51	46	32	0	0	10	5	47

12	PZ04_Chen_1	3	51	45	32	0	0	10	6	48
13	PZ04_Chen_10	3	51	45	31	0	0	11	6	48
14	PZ04_Chen_2	2	52	45	31	0	0	11	8	50
15	PZ04_Chen_3	4	51	45	31	0	0	11	5	47
16	PZ04_Chen_4	2	52	45	29	0	0	13	8	50
17	PZ04_Chen_5	4	51	45	31	0	0	11	5	47
18	PZ04_Chen_6	3	51	45	31	0	0	11	6	48
19	PZ04_Chen_7	3	51	45	31	0	0	11	6	48
20	PZ04_Chen_8	3	51	45	31	0	0	11	6	48
21	PZ04_Chen_9	3	52	45	31	0	0	11	7	49
22	PZ04_Das_1	3	52	46	28	0	0	15	6	49
23	PZ04_Das_2	3	52	46	28	0	0	15	6	49
24	PZ04_Das_3	3	52	46	28	0	0	15	6	49
25	PZ04_Das_4	3	52	46	28	0	0	15	6	49
26	PZ04_Das_5	3	52	46	28	0	0	15	6	49
27	PZ04_Dokholyan_1	3	53	46	24	0	0	19	7	50
28	PZ04_Dokholyan_2	3	53	46	24	0	0	19	7	50
29	PZ04_Major_1	4	52	47	16	0	0	27	5	48
30	PZ04_Mikolajczak_1	5	39	28	15	0	0	11	8	34
31	PZ04_Santalucia_1	4	52	46	29	0	0	14	5	48
	Average	3.55	50.65	43.39	25.32	0.00	0.00	15.87	5.90	47.10
	Standard deviation	0.77	2.90	6.63	9.00	0.00	0.00	7.21	1.35	3.32
	Median	4.00	51.00	45.00	29.00	0.00	0.00	13.00	6.00	48.00

Table S52. X3DNA report on structures in Puzzle 05.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ05_refstructure	7	71	59	37	0	0	18	9	64
2	PZ05_Adamiak_1	9	67	63	23	0	0	29	6	58

3	PZ05_Bujnicki_1	9	65	57	11	0	0	39	6	56
4	PZ05_Bujnicki_2	7	68	62	16	0	0	36	9	61
5	PZ05_Bujnicki_3	10	58	47	15	0	0	23	10	48
6	PZ05_Bujnicki_4	8	65	56	17	0	0	33	7	57
7	PZ05_Bujnicki_5	7	63	59	25	0	0	21	10	56
8	PZ05_Chen_1	9	60	47	30	0	0	16	5	51
9	PZ05_Chen_2	9	60	47	20	1	0	24	6	51
10	PZ05_Chen_3	9	59	51	28	0	0	18	4	50
11	PZ05_Chen_4	9	60	51	25	0	0	22	4	51
12	PZ05_Chen_5	8	63	47	31	0	0	16	8	55
13	PZ05_Chen_6	11	60	49	25	0	0	22	2	49
14	PZ05_Chen_7	8	55	42	18	1	0	22	6	47
15	PZ05_Das_1	6	77	67	35	0	0	25	11	71
16	PZ05_Das_2	6	76	64	31	0	0	27	12	70
17	PZ05_Dokholyan_1	6	67	63	23	0	0	28	10	61
18	PZ05_Dokholyan_2	6	67	62	20	0	0	31	10	61
19	PZ05_Dokholyan_3	8	68	63	21	0	0	32	7	60
20	PZ05_Dokholyan_4	6	67	62	20	0	0	31	10	61
21	PZ05_Dokholyan_5	6	69	62	26	0	0	28	9	63
22	PZ05_Dokholyan_6	7	71	62	28	0	0	28	8	64
23	PZ05_Dokholyan_7	7	68	62	22	0	0	32	7	61
24	PZ05_Dokholyan_8	7	66	61	17	0	0	33	9	59
25	PZ05_Xiao_1	9	61	52	6	0	0	43	3	52
26	PZ05_Xiao_2	9	60	52	7	0	0	40	4	51
	Average	7.81	65.04	56.50	22.19	0.08	0.00	27.58	7.38	57.23
	Standard deviation	1.41	5.41	7.03	7.75	0.27	0.00	7.34	2.65	6.51
	Median	8.00	65.50	59.00	22.50	0.00	0.00	28.00	7.50	57.50

Table S53. X3DNA report on structures in Puzzle 06.

			Base pairs	Dinucleotide steps			
				Right-handed	Left-handed	Other	Total

No.	3D RNA model	#Helices	#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ06_refstructure	7	61	49	16	0	0	25	13	54
2	PZ06_Bujnicki_1	5	60	54	13	0	0	33	9	55
3	PZ06_Bujnicki_2	6	59	54	24	0	0	24	5	53
4	PZ06_Bujnicki_3	5	62	51	18	0	0	32	7	57
5	PZ06_Bujnicki_4	4	57	50	15	0	0	27	11	53
6	PZ06_Chen_1	7	59	45	16	0	0	28	8	52
7	PZ06_Chen_2	9	57	46	7	0	0	38	3	48
8	PZ06_Chen_3	6	56	47	8	1	0	35	6	50
9	PZ06_Chen_4	5	61	47	32	0	0	15	9	56
10	PZ06_Chen_5	7	57	47	27	0	0	17	6	50
11	PZ06_Chen_6	5	61	46	37	0	0	10	9	56
12	PZ06_Chen_7	6	57	46	14	1	0	30	6	51
13	PZ06_Das_1	7	66	56	31	0	0	20	8	59
14	PZ06_Das_10	5	66	54	31	0	0	19	11	61
15	PZ06_Das_2	7	63	55	32	0	0	18	6	56
16	PZ06_Das_3	7	62	56	28	0	0	22	5	55
17	PZ06_Das_4	7	67	56	31	0	0	20	9	60
18	PZ06_Das_5	7	67	55	26	0	0	24	6	56
19	PZ06_Das_6	7	67	56	31	0	0	20	8	59
20	PZ06_Das_7	7	67	55	27	0	0	23	5	55
21	PZ06_Das_8	7	67	55	26	0	0	24	6	56
22	PZ06_Das_9	7	67	55	32	0	0	18	6	56
23	PZ06_Dokholyan_1	6	67	53	16	0	0	34	5	55
24	PZ06_Dokholyan_2	6	67	54	14	0	0	34	6	54
25	PZ06_Dokholyan_3	7	67	53	22	0	0	23	8	53
26	PZ06_Dokholyan_4	6	67	53	14	0	0	35	5	54
27	PZ06_Dokholyan_5	5	67	53	20	0	0	28	6	54
28	PZ06_Dokholyan_6	4	67	54	15	0	0	35	6	56
29	PZ06_Major_1	6	67	56	10	1	0	38	8	57

30	PZ06_Major_2	6	67	54	4	0	0	45	7	56
31	PZ06_Major_3	6	67	56	6	1	0	42	7	56
32	PZ06_Major_4	5	67	57	7	0	0	44	8	59
33	PZ06_Major_5	6	67	56	7	1	0	41	7	56
34	PZ06_Major_6	5	67	57	9	1	0	41	8	59
35	PZ06_Major_7	6	67	56	15	0	0	36	7	58
	Average	6.11	67	52.77	19.46	0.17	0.00	28.51	7.14	55.29
	Standard deviation	1.05	67	3.74	9.48	0.38	0.00	9.12	2.00	2.92
	Median	6.00	67	54.00	16.00	0.00	0.00	28.00	7.00	56.00

Table S54. X3DNA report on structures in Puzzle 07.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ07_refstructure	4	73	61	30	0	0	25	14	69
2	PZ07_Adamiak_1	4	76	62	29	0	0	30	13	72
3	PZ07_Adamiak_2	6	73	61	23	0	0	34	10	67
4	PZ07_Adamiak_3	6	72	60	26	0	0	29	11	66
5	PZ07_Adamiak_4	3	76	65	26	0	0	34	13	73
6	PZ07_Adamiak_5	5	74	65	29	0	0	30	10	69
7	PZ07_Bujnicki_1	3	41	32	16	0	0	14	8	38
8	PZ07_Bujnicki_2	3	37	33	13	0	0	17	4	34
9	PZ07_Bujnicki_3	3	77	68	40	0	0	21	13	74
10	PZ07_Bujnicki_4	3	76	68	31	0	0	30	12	73
11	PZ07_Bujnicki_5	3	76	68	31	0	0	30	12	73
12	PZ07_Bujnicki_6	3	77	68	40	0	0	21	13	74
13	PZ07_Bujnicki_7	3	77	68	36	0	0	25	13	74
14	PZ07_Chen_1	8	44	30	0	0	0	30	6	36
15	PZ07_Chen_10	5	70	59	43	0	0	11	11	65
16	PZ07_Chen_2	7	71	58	41	0	0	10	13	64

17	PZ07_Chen_3	5	68	58	41	0	0	10	12	63
18	PZ07_Chen_4	4	69	57	41	0	0	12	12	65
19	PZ07_Chen_5	5	69	58	41	0	0	10	13	64
20	PZ07_Chen_6	5	69	58	41	0	0	9	14	64
21	PZ07_Chen_7	6	69	57	40	0	0	11	12	63
22	PZ07_Chen_8	5	71	59	43	0	0	11	12	66
23	PZ07_Chen_9	6	70	58	40	0	0	12	12	64
24	PZ07_Das_1	4	75	62	39	0	0	21	11	71
25	PZ07_Das_2	4	75	63	41	0	0	19	11	71
26	PZ07_Das_3	4	74	61	40	0	0	20	10	70
27	PZ07_Das_4	4	73	61	34	0	0	24	11	69
28	PZ07_Das_5	5	80	65	38	0	0	25	12	75
29	PZ07_Das_6	3	75	62	37	0	0	24	11	72
30	PZ07_Das_7	5	71	62	36	0	0	20	10	66
31	PZ07_Das_8	4	73	62	39	0	0	15	15	69
32	PZ07_Ding_1	5	66	63	18	0	0	35	8	61
33	PZ07_Ding_10	4	68	63	24	0	0	29	11	64
34	PZ07_Ding_2	6	67	63	24	0	0	29	8	61
35	PZ07_Ding_3	5	70	63	13	0	0	41	11	65
36	PZ07_Ding_4	5	68	63	19	0	0	32	12	63
37	PZ07_Ding_5	5	66	63	18	0	0	31	12	61
38	PZ07_Ding_6	5	69	63	21	0	0	34	9	64
39	PZ07_Ding_7	5	66	63	28	0	0	24	9	61
40	PZ07_Ding_8	5	65	61	27	0	0	23	10	60
41	PZ07_Ding_9	6	65	63	22	0	0	29	8	59
42	PZ07_Dokholyan_1	7	68	61	14	0	0	40	7	61
43	PZ07_Dokholyan_2	6	60	56	17	0	0	30	7	54
44	PZ07_Major_1	6	72	61	0	2	0	53	11	66
45	PZ07_Major_10	6	72	60	1	1	0	51	13	66
46	PZ07_Major_2	6	72	61	0	1	0	53	12	66
47	PZ07_Major_3	6	73	62	1	0	0	53	13	67
48	PZ07_Major_4	6	72	60	9	0	0	45	12	66
49	PZ07_Major_5	6	70	60	8	0	0	43	13	64

50	PZ07_Major_6	6	72	62	3	0	0	51	12	66
51	PZ07_Major_7	6	70	60	8	0	0	43	13	64
52	PZ07_Major_8	6	73	60	0	1	0	53	13	67
53	PZ07_Major_9	6	72	61	0	0	0	55	11	66
	Average	4.94	69.57	60.02	24.91	0.09	0.00	28.51	11.11	64.62
	Standard deviation	1.23	8.09	7.58	14.41	0.35	0.00	13.29	2.19	8.34
	Median	5.00	71.00	61.00	27.00	0.00	0.00	29.00	12.00	66.00

Table S55. X3DNA report on structures in Puzzle 08.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					Total
					Right-handed		Left-handed	Other		
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ08_refstructure	3	36	31	19	0	0	9	5	33
2	PZ08_Adamiak_1	5	35	32	16	0	0	11	3	30
3	PZ08_Adamiak_2	4	35	32	17	0	0	10	4	31
4	PZ08_Bujnicki_1	4	37	32	17	0	0	11	5	33
5	PZ08_Bujnicki_10	5	33	30	19	0	0	6	3	28
6	PZ08_Bujnicki_2	2	35	31	15	0	0	11	7	33
7	PZ08_Bujnicki_3	3	35	30	11	0	0	15	6	32
8	PZ08_Bujnicki_4	2	34	30	17	0	0	8	7	32
9	PZ08_Bujnicki_5	3	36	32	16	0	0	11	6	33
10	PZ08_Bujnicki_6	3	37	32	16	0	0	12	6	34
11	PZ08_Bujnicki_7	5	35	31	11	0	0	15	4	30
12	PZ08_Bujnicki_8	4	37	30	21	0	0	8	4	33
13	PZ08_Bujnicki_9	6	33	29	15	0	0	9	3	27
14	PZ08_Chen_1	4	35	31	12	0	0	15	4	31
15	PZ08_Chen_10	4	33	29	14	0	0	11	4	29
16	PZ08_Chen_2	5	33	29	13	0	0	12	3	28
17	PZ08_Chen_3	3	34	30	12	0	0	13	6	31
18	PZ08_Chen_4	5	33	29	14	0	0	11	3	28

19	PZ08_Chen_5	3	35	31	14	0	0	13	5	32
20	PZ08_Chen_6	4	35	30	4	0	0	22	5	31
21	PZ08_Chen_7	4	32	28	12	0	0	12	4	28
22	PZ08_Chen_8	5	31	26	5	0	0	18	3	26
23	PZ08_Chen_9	5	33	28	3	0	0	20	5	28
24	PZ08_Das_1	3	37	32	16	0	0	13	5	34
25	PZ08_Das_2	3	36	32	19	0	0	9	5	33
26	PZ08_Das_3	3	36	31	20	0	0	8	5	33
27	PZ08_Das_4	2	35	32	15	0	0	12	6	33
28	PZ08_Das_5	3	37	32	15	0	0	12	7	34
29	PZ08_Das_6	2	35	32	16	0	0	11	6	33
30	PZ08_Ding_1	3	33	32	8	0	0	15	7	30
31	PZ08_Ding_10	4	33	31	8	0	0	17	4	29
32	PZ08_Ding_2	4	30	30	5	0	0	17	4	26
33	PZ08_Ding_3	5	31	30	6	0	0	17	3	26
34	PZ08_Ding_4	4	32	30	8	0	0	16	4	28
35	PZ08_Ding_5	4	32	29	9	0	0	15	4	28
36	PZ08_Ding_6	5	31	29	12	0	0	10	4	26
37	PZ08_Ding_7	2	35	29	10	0	0	16	7	33
38	PZ08_Ding_8	3	34	30	12	0	0	12	7	31
39	PZ08_Ding_9	3	35	32	5	0	0	22	5	32
40	PZ08_Dokholyan_1	4	32	29	10	0	0	14	4	28
41	PZ08_Dokholyan_2	4	32	29	1	0	0	23	4	28
42	PZ08_Dokholyan_3	5	32	29	9	0	0	15	3	27
43	PZ08_Dokholyan_4	3	35	32	8	0	0	19	5	32
	Average	3.72	34.07	30.35	12.21	0.00	0.00	13.40	4.74	30.35
	Standard deviation	1.03	1.88	1.45	4.96	0.00	0.00	4.02	1.31	2.57
	Median	4.00	35.00	30.00	12.00	0.00	0.00	12.00	5.00	31.00

Table S56. X3DNA report on structures in Puzzle 09.

			Base pairs	Dinucleotide steps			
				Right-handed	Left-handed	Other	Total

No.	3D RNA model	#Helices	#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ09_refstructure	3	31	20	12	0	0	6	10	28
2	PZ09_Bujnicki_3	4	30	15	10	0	0	10	6	26
3	PZ09_Bujnicki_4	4	30	15	10	0	0	10	6	26
4	PZ09_Bujnicki_5	4	30	15	10	0	0	10	6	26
5	PZ09_Chen_1	3	27	18	11	0	0	7	6	24
6	PZ09_Chen_2	4	27	18	9	0	0	8	6	23
7	PZ09_Chen_3	5	26	18	10	0	0	6	5	21
8	PZ09_Chen_4	4	27	18	9	0	0	7	7	23
9	PZ09_Chen_5	5	26	18	9	0	0	7	5	21
10	PZ09_Chen_6	4	24	17	8	0	0	8	4	20
11	PZ09_Chen_7	5	25	17	9	0	0	8	3	20
12	PZ09_Chen_8	3	27	17	8	0	0	7	9	24
13	PZ09_Das_1	3	29	19	12	0	0	8	6	26
14	PZ09_Das_2	3	29	19	12	0	0	6	8	26
15	PZ09_Das_3	3	28	18	3	0	0	15	7	25
16	PZ09_Das_4	3	30	20	12	0	0	10	5	27
17	PZ09_Das_5	4	26	18	12	0	0	7	3	22
18	PZ09_Das_6	3	29	20	13	0	0	10	3	26
19	PZ09_Das_7	4	27	18	12	0	0	8	3	23
20	PZ09_Das_8	4	25	18	12	0	0	7	2	21
21	PZ09_Das_9	4	28	18	13	0	0	7	4	24
22	PZ09_Ding_1	3	24	23	8	0	0	8	5	21
23	PZ09_Ding_10	3	22	21	5	0	0	11	3	19
24	PZ09_Ding_2	2	24	23	8	0	0	8	6	22
25	PZ09_Ding_3	2	24	23	7	0	0	9	6	22
26	PZ09_Ding_4	2	26	23	7	0	0	11	6	24
27	PZ09_Ding_5	2	27	24	10	0	0	7	8	25
28	PZ09_Ding_6	2	25	22	9	0	0	8	6	23
29	PZ09_Ding_7	3	20	18	8	0	0	7	2	17

30	PZ09_Ding_8	2	24	23	12	0	0	5	5	22
31	PZ09_Ding_9	2	23	22	9	0	0	8	4	21
32	PZ09_Dokholyan_1	3	22	20	7	0	0	11	1	19
33	PZ09_Dokholyan_2	3	21	20	5	0	0	12	1	18
34	PZ09_Dokholyan_3	3	23	22	4	0	0	13	3	20
35	PZ09_Dokholyan_4	3	26	23	7	0	0	14	2	23
	Average	3.26	26.06	19.46	9.20	0.00	0.00	8.69	4.91	22.80
	Standard deviation	0.89	2.79	2.55	2.58	0.00	0.00	2.35	2.19	2.71
	Median	3.00	26.00	19.00	9.00	0.00	0.00	8.00	5.00	23.00

Table S57. X3DNA report on structures in Puzzle 10.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ10_refstructure	4	64	47	19	0	0	25	16	60
2	PZ10_Bujnicki_1	5	63	47	23	0	0	17	18	58
3	PZ10_Bujnicki_10	7	61	44	18	0	0	23	13	54
4	PZ10_Bujnicki_2	8	64	47	22	0	0	19	15	56
5	PZ10_Bujnicki_3	4	61	46	26	0	0	15	16	57
6	PZ10_Bujnicki_4	5	62	49	26	0	0	14	17	57
7	PZ10_Bujnicki_5	6	61	46	22	0	0	17	16	55
8	PZ10_Bujnicki_6	5	60	47	26	0	0	13	16	55
9	PZ10_Bujnicki_7	6	64	48	21	0	0	20	17	58
10	PZ10_Bujnicki_8	6	65	48	25	0	0	19	15	59
11	PZ10_Bujnicki_9	6	62	45	26	0	0	16	14	56
12	PZ10_Chen_1	6	50	37	3	0	0	24	17	44
13	PZ10_Das_1	4	65	47	29	0	0	14	18	61
14	PZ10_Das_2	4	64	49	30	0	0	14	16	60
15	PZ10_Das_3	4	62	46	29	0	0	14	15	58
16	PZ10_Das_4	4	62	47	30	0	0	13	15	58

17	PZ10_Das_5	3	64	47	29	0	0	14	18	61
18	PZ10_Dokholyan_1	4	52	46	16	0	0	22	10	48
19	PZ10_Dokholyan_10	4	48	46	13	0	0	24	7	44
20	PZ10_Dokholyan_2	5	52	45	14	0	0	23	10	47
21	PZ10_Dokholyan_3	5	54	47	17	0	0	22	10	49
22	PZ10_Dokholyan_4	7	49	47	14	0	0	23	5	42
23	PZ10_Dokholyan_5	6	49	45	17	0	0	21	5	43
24	PZ10_Dokholyan_6	5	52	47	14	0	0	23	10	47
25	PZ10_Dokholyan_7	6	52	47	15	0	0	23	8	46
26	PZ10_Dokholyan_8	5	52	47	17	0	0	22	8	47
27	PZ10_Dokholyan_9	5	54	48	13	1	0	27	8	49
	Average	5.15	58.07	46.37	20.52	0.04	0.00	19.30	13.07	52.93
	Standard deviation	1.17	6.00	2.20	6.77	0.19	0.00	4.34	4.21	6.26
	Median	5.00	61.00	47.00	21.00	0.00	0.00	20.00	15.00	55.00

Table S58. X3DNA report on structures in Puzzle 11.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					Total
					Right-handed		Left-handed	Other		
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ11_Adamiak_1	2	22	20	6	0	0	11	3	20
2	PZ11_Adamiak_10	1	25	21	7	0	0	13	4	24
3	PZ11_Adamiak_2	3	21	20	6	0	0	11	1	18
4	PZ11_Adamiak_3	1	25	22	6	0	0	13	5	24
5	PZ11_Adamiak_4	2	20	19	7	0	0	9	2	18
6	PZ11_Adamiak_5	1	23	22	4	0	0	14	4	22
7	PZ11_Adamiak_6	1	24	19	7	0	0	11	5	23
8	PZ11_Adamiak_7	1	24	21	6	0	0	12	5	23
9	PZ11_Adamiak_8	1	25	18	5	0	0	15	4	24
10	PZ11_Adamiak_9	1	25	20	6	0	0	15	3	24
11	PZ11_Bujnicki_1	1	24	22	6	0	0	12	5	23

12	PZ11_Bujnicki_10	1	24	22	6	0	0	12	5	23
13	PZ11_Bujnicki_2	3	21	20	9	0	0	4	5	18
14	PZ11_Bujnicki_3	1	23	23	11	0	0	6	5	22
15	PZ11_Bujnicki_4	1	23	22	0	2	0	16	4	22
16	PZ11_Bujnicki_5	1	24	23	5	0	0	13	5	23
17	PZ11_Bujnicki_6	1	24	24	9	0	0	8	6	23
18	PZ11_Bujnicki_7	1	23	23	8	0	0	9	5	22
19	PZ11_Bujnicki_8	1	24	23	7	0	0	12	4	23
20	PZ11_Bujnicki_9	1	24	24	9	0	0	9	5	23
21	PZ11_Chen_1	1	23	21	8	0	0	9	5	22
22	PZ11_Chen_10	1	25	24	8	0	0	9	7	24
23	PZ11_Chen_2	1	23	22	9	0	0	8	5	22
24	PZ11_Chen_3	1	24	21	9	0	0	8	6	23
25	PZ11_Chen_4	1	23	21	6	0	0	10	6	22
26	PZ11_Chen_5	1	23	22	15	0	0	2	5	22
27	PZ11_Chen_6	1	25	23	7	0	0	12	5	24
28	PZ11_Chen_7	1	24	23	8	0	0	9	6	23
29	PZ11_Chen_8	1	24	23	8	0	0	10	5	23
30	PZ11_Chen_9	1	24	23	9	0	0	9	5	23
31	PZ11_Das_1	1	24	21	10	0	0	9	4	23
32	PZ11_Das_10	2	24	22	8	0	0	10	4	22
33	PZ11_Das_2	1	24	21	9	0	0	10	4	23
34	PZ11_Das_3	1	25	22	10	0	0	9	5	24
35	PZ11_Das_4	1	24	22	11	0	0	8	4	23
36	PZ11_Das_5	1	25	19	8	0	0	12	4	24
37	PZ11_Das_6	1	24	21	8	0	0	10	5	23
38	PZ11_Das_7	1	24	20	9	0	0	10	4	23
39	PZ11_Das_8	2	24	22	10	0	0	8	4	22
40	PZ11_Das_9	2	22	20	8	0	0	9	3	20
41	PZ11_Ding_1	1	21	18	4	0	0	10	6	20
42	PZ11_Ding_10	2	18	15	0	0	0	12	4	16
43	PZ11_Ding_2	2	23	20	3	0	0	13	5	21
44	PZ11_Ding_3	3	20	19	3	0	0	12	2	17

45	PZ11_Ding_4	2	20	18	1	0	0	14	3	18
46	PZ11_Ding_5	2	15	14	0	0	0	11	2	13
47	PZ11_Ding_6	2	19	18	4	0	0	9	4	17
48	PZ11_Ding_7	2	22	21	2	0	0	13	5	20
49	PZ11_Ding_8	1	20	19	1	0	0	12	6	19
50	PZ11_Ding_9	2	20	18	3	0	0	9	6	18
51	PZ11_Xiao_1	2	25	20	1	0	0	20	2	23
52	PZ11_Xiao_2	2	23	18	1	0	0	16	4	21
53	PZ11_Xiao_3	2	25	19	3	0	0	17	3	23
54	PZ11_refstructure	1	24	22	3	0	0	16	4	23
	Average	1.39	22.98	20.74	6.24	0.04	0.00	10.93	4.39	21.59
	Standard deviation	0.60	2.06	2.12	3.28	0.27	0.00	3.15	1.22	2.45
	Median	1.00	24.00	21.00	7.00	0.00	0.00	10.50	5.00	23.00

Table S59. X3DNA report on structures in Puzzle 12.

			Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
No.	3D RNA model	#Helices	#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ12_refstructure	4	46	38	19	0	0	17	6	42
2	PZ12_Adamiak_1	4	42	36	16	0	0	16	6	38
3	PZ12_Adamiak_2	4	42	36	14	0	0	18	6	38
4	PZ12_Adamiak_3	4	44	37	17	0	0	16	7	40
5	PZ12_Bujnicki_1	6	40	35	11	0	0	20	3	34
6	PZ12_Bujnicki_10	4	44	39	14	0	0	20	6	40
7	PZ12_Bujnicki_2	5	44	37	1	0	0	32	6	39
8	PZ12_Bujnicki_3	4	45	37	10	0	0	24	7	41
9	PZ12_Bujnicki_4	5	45	39	12	0	0	21	7	40
10	PZ12_Bujnicki_5	5	43	39	12	0	0	20	6	38
11	PZ12_Bujnicki_6	5	47	38	10	0	0	21	11	42

12	PZ12_Bujnicki_7	3	43	38	13	0	0	21	6	40
13	PZ12_Bujnicki_8	4	44	40	10	0	0	23	7	40
14	PZ12_Bujnicki_9	5	46	41	9	0	0	24	8	41
15	PZ12_Chen_1	6	42	36	14	0	0	19	3	36
16	PZ12_Chen_10	7	40	38	20	0	0	10	3	33
17	PZ12_Chen_2	5	40	35	13	0	0	16	6	35
18	PZ12_Chen_3	6	40	37	20	0	0	9	5	34
19	PZ12_Chen_4	6	38	35	20	0	0	8	4	32
20	PZ12_Chen_5	7	40	35	23	0	0	7	3	33
21	PZ12_Chen_6	5	39	36	19	0	0	8	7	34
22	PZ12_Chen_7	7	37	35	19	0	0	10	1	30
23	PZ12_Chen_8	6	38	35	18	0	0	12	2	32
24	PZ12_Chen_9	6	39	35	19	0	0	10	4	33
25	PZ12_Das_1	4	44	38	24	0	0	10	6	40
26	PZ12_Das_10	6	44	38	26	0	0	9	3	38
27	PZ12_Das_2	4	43	38	24	0	0	10	5	39
28	PZ12_Das_3	4	46	40	23	0	0	12	7	42
29	PZ12_Das_4	4	44	38	25	0	0	8	7	40
30	PZ12_Das_5	4	41	37	23	0	0	9	5	37
31	PZ12_Das_6	5	44	39	23	0	0	11	5	39
32	PZ12_Das_7	4	44	38	21	0	0	14	5	40
33	PZ12_Das_8	4	45	39	25	0	0	10	6	41
34	PZ12_Das_9	4	45	38	24	0	0	12	5	41
35	PZ12_Ding_1	4	38	38	19	0	0	10	5	34
36	PZ12_Ding_10	4	39	38	14	0	0	15	6	35
37	PZ12_Ding_11	4	40	38	23	0	0	8	5	36
38	PZ12_Ding_12	4	39	38	18	0	0	12	5	35
39	PZ12_Ding_2	4	40	38	18	0	0	12	6	36
40	PZ12_Ding_3	4	40	36	16	0	0	14	6	36
41	PZ12_Ding_4	4	41	38	16	0	0	15	6	37
42	PZ12_Ding_5	4	40	38	16	0	0	14	6	36
43	PZ12_Ding_6	4	38	38	13	0	0	16	5	34
44	PZ12_Ding_7	4	40	38	14	0	0	17	5	36

45	PZ12_Ding_8	5	39	38	16	0	0	14	4	34
46	PZ12_Ding_9	4	39	38	12	0	0	18	5	35
47	PZ12_Weeks_1	5	45	40	20	0	0	13	7	40
48	PZ12_Weeks_2	4	44	41	17	0	0	15	8	40
49	PZ12_Weeks_3	7	40	38	14	0	0	16	3	33
50	PZ12_Xiao_1	8	32	27	6	0	0	17	1	24
51	PZ12_Xiao_2	8	32	28	7	0	0	16	1	24
52	PZ12_Xiao_3	7	32	28	4	0	0	20	1	25
	Average	4.88	41.27	37.04	16.42	0.00	0.00	14.79	5.17	36.38
	Standard deviation	1.22	3.49	2.79	5.72	0.00	0.00	5.21	1.98	4.31
	Median	4.00	41.00	38.00	16.50	0.00	0.00	14.50	5.50	36.50

Table S60. X3DNA report on structures in Puzzle 13.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps						Total
					Right-handed		Left-handed	Other			
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone		
1	PZ13_refstructure	2	26	21	14	0	0	7	3	24	
2	PZ13_Adamiak_1	3	21	19	13	0	0	3	2	18	
3	PZ13_Bujnicki_1	2	24	21	7	0	0	11	4	22	
4	PZ13_Bujnicki_10	4	25	25	15	0	0	4	2	21	
5	PZ13_Bujnicki_2	2	24	21	10	0	0	8	4	22	
6	PZ13_Bujnicki_3	3	25	23	15	0	0	3	4	22	
7	PZ13_Bujnicki_4	2	23	21	10	0	0	8	3	21	
8	PZ13_Bujnicki_5	3	23	22	14	0	0	2	4	20	
9	PZ13_Bujnicki_6	4	23	21	12	0	0	6	1	19	
10	PZ13_Bujnicki_7	2	24	21	14	0	0	5	3	22	
11	PZ13_Bujnicki_8	3	24	22	14	0	0	4	3	21	
12	PZ13_Bujnicki_9	3	22	21	11	0	0	6	2	19	
13	PZ13_Chen_1	4	23	20	8	0	0	10	1	19	
14	PZ13_Chen_2	4	22	19	0	0	0	17	1	18	

15	PZ13_Chen_3	3	20	19	11	0	0	5	1	17
16	PZ13_Chen_4	4	24	20	7	0	0	11	2	20
17	PZ13_Chen_5	3	20	19	5	0	0	11	1	17
18	PZ13_Chen_6	4	25	20	11	0	0	9	1	21
19	PZ13_Chen_7	4	19	18	6	0	0	9	0	15
20	PZ13_Chen_8	4	19	18	10	0	0	5	0	15
21	PZ13_Chen_9	4	21	18	12	0	0	4	1	17
22	PZ13_Das_1	3	25	21	14	0	0	4	4	22
23	PZ13_Das_10	4	24	21	14	0	0	3	3	20
24	PZ13_Das_2	3	22	19	14	0	0	4	1	19
25	PZ13_Das_3	4	22	19	13	0	0	5	0	18
26	PZ13_Das_4	2	23	20	14	0	0	4	3	21
27	PZ13_Das_5	3	24	20	15	0	0	3	3	21
28	PZ13_Das_6	4	22	20	12	0	0	5	1	18
29	PZ13_Das_7	3	23	20	14	0	0	4	2	20
30	PZ13_Das_8	4	25	20	16	0	0	5	0	21
31	PZ13_Das_9	3	22	19	12	0	0	6	1	19
32	PZ13_Ding_1	3	21	19	4	0	0	11	3	18
33	PZ13_Ding_10	4	21	20	12	0	0	5	0	17
34	PZ13_Ding_2	3	22	20	6	0	0	12	1	19
35	PZ13_Ding_3	3	24	20	7	0	0	13	1	21
36	PZ13_Ding_4	4	20	19	4	0	0	12	0	16
37	PZ13_Ding_5	2	22	20	10	0	0	7	3	20
38	PZ13_Ding_6	4	21	19	7	0	0	10	0	17
39	PZ13_Ding_7	3	22	20	9	0	0	8	2	19
40	PZ13_Ding_8	3	24	20	7	0	0	11	3	21
41	PZ13_Ding_9	3	23	20	10	0	0	8	2	20
42	PZ13_Dokholyan_1	5	22	18	7	0	0	10	0	17
43	PZ13_Dokholyan_2	3	21	18	9	0	0	9	0	18
44	PZ13_Dokholyan_3	3	18	14	5	0	0	8	2	15
45	PZ13_Dokholyan_4	2	14	13	3	0	0	7	2	12
46	PZ13_Dokholyan_5	3	18	17	5	0	0	9	1	15
47	PZ13_Xiao_1	2	12	9	4	0	0	4	2	10

48	PZ13_Xiao_10	4	18	15	3	0	0	11	0	14
49	PZ13_Xiao_2	2	6	4	0	0	0	4	0	4
50	PZ13_Xiao_3	1	5	2	1	0	0	2	1	4
51	PZ13_Xiao_4	2	19	17	4	0	0	9	4	17
52	PZ13_Xiao_5	3	21	18	8	0	0	10	0	18
53	PZ13_Xiao_6	3	15	13	3	0	0	8	1	12
54	PZ13_Xiao_7	5	16	15	4	0	0	7	0	11
55	PZ13_Xiao_8	3	19	17	3	0	0	11	2	16
56	PZ13_Xiao_9	3	16	13	4	0	0	9	0	13
	Average	3.14	20.88	18.36	8.86	0.00	0.00	7.25	1.63	17.73
	Standard deviation	0.84	4.19	4.03	4.45	0.00	0.00	3.27	1.33	4.03
	Median	3.00	22.00	19.50	9.50	0.00	0.00	7.00	1.00	18.50

Table S61. X3DNA report on structures in Puzzle 14a.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					Total
					Right-handed		Left-handed	Other		
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ14_refstructure_bound	2	22	17	10	0	0	7	3	20
2	PZ14_AdamiakPostExp_1	2	21	16	11	0	0	6	2	19
3	PZ14_AdamiakPostExp_2	2	19	16	4	0	0	10	3	17
4	PZ14_AdamiakPreExp_1	2	21	16	10	0	0	7	2	19
5	PZ14_AdamiakPreExp_2	3	21	16	6	0	0	9	3	18
6	PZ14_BujnickiPostExp_1	2	19	16	9	0	0	6	2	17
7	PZ14_BujnickiPostExp_2	3	20	18	12	0	0	3	2	17
8	PZ14_BujnickiPostExp_3	4	24	21	11	0	0	5	4	20
9	PZ14_BujnickiPostExp_4	4	23	19	12	0	0	7	0	19
10	PZ14_BujnickiPostExp_5	2	20	16	10	0	0	6	2	18
11	PZ14_BujnickiPreExp_4	2	26	17	13	0	0	8	3	24
12	PZ14_BujnickiPreExp_5	2	27	17	11	0	0	11	3	25
13	PZ14_BujnickiPreExp_6	2	23	18	10	0	0	8	3	21

14	PZ14_BujnickiPreExp_7	4	23	23	9	0	0	7	3	19
15	PZ14_ChenPostExp_1	2	20	17	9	0	0	5	4	18
16	PZ14_ChenPostExp_10	3	19	16	12	0	0	3	1	16
17	PZ14_ChenPostExp_2	2	18	16	10	0	0	5	1	16
18	PZ14_ChenPostExp_3	3	20	16	13	0	0	3	1	17
19	PZ14_ChenPostExp_4	3	20	16	12	0	0	4	1	17
20	PZ14_ChenPostExp_5	3	17	16	13	0	0	1	0	14
21	PZ14_ChenPostExp_6	3	17	16	11	0	0	3	0	14
22	PZ14_ChenPostExp_7	2	18	16	13	0	0	2	1	16
23	PZ14_ChenPostExp_8	2	20	16	13	0	0	2	3	18
24	PZ14_ChenPostExp_9	3	17	16	13	0	0	1	0	14
25	PZ14_DasPostExp_1	3	25	16	9	0	0	12	1	22
26	PZ14_DasPostExp_10	2	25	17	9	0	0	11	3	23
27	PZ14_DasPostExp_2	2	25	17	9	0	0	11	3	23
28	PZ14_DasPostExp_3	2	25	16	9	0	0	12	2	23
29	PZ14_DasPostExp_4	2	24	16	10	0	0	10	2	22
30	PZ14_DasPostExp_5	2	23	16	10	0	0	8	3	21
31	PZ14_DasPostExp_6	2	25	17	9	0	0	10	4	23
32	PZ14_DasPostExp_7	2	24	17	10	0	0	10	2	22
33	PZ14_DasPostExp_8	1	24	17	9	0	0	9	5	23
34	PZ14_DasPostExp_9	3	23	16	10	0	0	9	1	20
35	PZ14_DasPreExp_1	2	25	17	9	0	0	10	4	23
36	PZ14_DasPreExp_10	3	23	16	10	0	0	9	1	20
37	PZ14_DasPreExp_2	2	24	17	10	0	0	10	2	22
38	PZ14_DasPreExp_3	1	24	17	9	0	0	9	5	23
39	PZ14_DasPreExp_4	4	26	17	8	0	0	13	1	22
40	PZ14_DasPreExp_5	2	25	17	9	0	0	11	3	23
41	PZ14_DasPreExp_6	2	26	17	9	0	0	12	3	24
42	PZ14_DasPreExp_7	2	24	16	9	0	0	11	2	22
43	PZ14_DasPreExp_8	2	24	17	10	0	0	10	2	22
44	PZ14_DasPreExp_9	2	24	17	10	0	0	10	2	22
45	PZ14_DingPostExp_1	2	18	16	8	0	0	7	1	16
46	PZ14_DingPostExp_10	2	17	16	5	0	0	9	1	15

47	PZ14_DingPostExp_2	2	21	16	10	0	0	6	3	19
48	PZ14_DingPostExp_3	2	18	16	7	0	0	6	3	16
49	PZ14_DingPostExp_4	2	16	16	10	0	0	3	1	14
50	PZ14_DingPostExp_5	2	19	16	7	0	0	6	4	17
51	PZ14_DingPostExp_6	1	23	16	7	0	0	10	5	22
52	PZ14_DingPostExp_7	2	18	16	7	0	0	7	2	16
53	PZ14_DingPostExp_8	2	19	16	9	0	0	5	3	17
54	PZ14_DingPostExp_9	2	19	16	4	0	0	10	3	17
55	PZ14_DingPreExp_1	2	16	16	7	0	0	6	1	14
56	PZ14_DingPreExp_2	3	17	16	5	0	0	8	1	14
57	PZ14_DingPreExp_3	2	19	17	10	0	0	4	3	17
58	PZ14_DingPreExp_4	2	16	16	6	0	0	7	1	14
59	PZ14_DingPreExp_5	2	19	16	9	0	0	5	3	17
60	PZ14_DingPreExp_6	2	20	16	8	0	0	7	3	18
61	PZ14_DingPreExp_7	2	17	16	9	0	0	4	2	15
62	PZ14_DingPreExp_8	3	18	16	2	0	0	11	2	15
	Average	2.29	21.18	16.60	9.26	0.00	0.00	7.37	2.26	18.89
	Standard deviation	0.66	3.12	1.19	2.33	0.00	0.00	3.06	1.24	3.21
	Median	2.00	21.00	16.00	9.00	0.00	0.00	7.00	2.00	18.50

Table S62. X3DNA report on structures in Puzzle 14b.

			Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
No.	3D RNA model	#Helices	#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ14_refstructure_free	2	21	17	9	0	0	8	2	19
2	PZ14_BujnickiPostExp_1	3	22	19	12	0	0	5	2	19
3	PZ14_BujnickiPostExp_2	2	23	17	12	0	0	5	4	21
4	PZ14_BujnickiPostExp_3	5	23	22	11	0	0	6	1	18
5	PZ14_BujnickiPostExp_4	2	20	17	10	0	0	6	2	18
6	PZ14_BujnickiPreExp_1	2	21	17	12	0	0	5	2	19
7	PZ14_BujnickiPreExp_2	2	21	17	11	0	0	6	2	19
8	PZ14_BujnickiPreExp_3	3	21	17	11	0	0	6	1	18
9	PZ14_BujnickiPreExp_4	4	23	22	13	0	0	5	1	19
10	PZ14_ChenPostExp_1	2	20	16	9	0	0	5	4	18
11	PZ14_ChenPostExp_10	3	19	17	12	0	0	2	2	16
12	PZ14_ChenPostExp_2	3	18	16	10	0	0	5	0	15
13	PZ14_ChenPostExp_3	3	20	16	13	0	0	3	1	17
14	PZ14_ChenPostExp_4	3	20	16	12	0	0	4	1	17
15	PZ14_ChenPostExp_5	3	17	16	13	0	0	1	0	14
16	PZ14_ChenPostExp_6	3	17	16	11	0	0	3	0	14
17	PZ14_ChenPostExp_7	2	18	17	13	0	0	1	2	16
18	PZ14_ChenPostExp_8	3	20	16	13	0	0	2	2	17
19	PZ14_ChenPostExp_9	3	17	16	13	0	0	1	0	14
20	PZ14_DasPostExp_1	2	22	17	7	0	0	11	2	20
21	PZ14_DasPostExp_10	2	25	17	10	0	0	11	2	23
22	PZ14_DasPostExp_2	2	24	16	9	0	0	11	2	22
23	PZ14_DasPostExp_3	2	25	18	9	0	0	12	2	23
24	PZ14_DasPostExp_4	2	25	17	9	0	0	12	2	23
25	PZ14_DasPostExp_5	2	25	16	9	0	0	12	2	23
26	PZ14_DasPostExp_6	2	25	17	9	0	0	12	2	23

27	PZ14_DasPostExp_7	2	23	17	9	0	0	10	2	21
28	PZ14_DasPostExp_8	2	23	17	9	0	0	10	2	21
29	PZ14_DasPostExp_9	2	25	17	10	0	0	11	2	23
30	PZ14_DasPreExp_1	2	25	17	9	0	0	12	2	23
31	PZ14_DasPreExp_10	2	25	17	10	0	0	11	2	23
32	PZ14_DasPreExp_2	2	23	17	9	0	0	10	2	21
33	PZ14_DasPreExp_3	2	25	17	8	0	0	13	2	23
34	PZ14_DasPreExp_4	2	23	17	9	0	0	10	2	21
35	PZ14_DasPreExp_5	2	25	17	10	0	0	11	2	23
36	PZ14_DasPreExp_6	2	22	17	7	0	0	11	2	20
37	PZ14_DasPreExp_7	2	24	17	9	0	0	11	2	22
38	PZ14_DasPreExp_8	2	23	17	9	0	0	10	2	21
39	PZ14_DasPreExp_9	2	23	17	9	0	0	10	2	21
40	PZ14_DingPostExp_1	2	20	17	11	0	0	4	3	18
41	PZ14_DingPostExp_10	2	17	17	9	0	0	5	1	15
42	PZ14_DingPostExp_2	2	19	16	7	0	0	6	4	17
43	PZ14_DingPostExp_3	2	20	18	8	0	0	7	3	18
44	PZ14_DingPostExp_4	2	17	17	10	0	0	4	1	15
45	PZ14_DingPostExp_5	2	17	17	7	0	0	7	1	15
46	PZ14_DingPostExp_6	2	19	17	7	0	0	9	1	17
47	PZ14_DingPostExp_7	3	21	17	10	0	0	5	3	18
48	PZ14_DingPostExp_8	2	19	17	6	0	0	9	2	17
49	PZ14_DingPostExp_9	2	17	17	5	0	0	9	1	15
50	PZ14_DingPreExp_1	2	19	17	10	0	0	5	2	17
51	PZ14_DingPreExp_2	2	18	17	10	0	0	4	2	16
52	PZ14_DingPreExp_3	2	18	17	7	0	0	8	1	16
53	PZ14_DingPreExp_4	2	21	17	6	0	0	11	2	19
	Average	2.30	21.19	17.06	9.66	0.00	0.00	7.42	1.81	18.89
	Standard deviation	0.61	2.74	1.13	2.00	0.00	0.00	3.48	0.88	2.89
	Median	2.00	21.00	17.00	9.00	0.00	0.00	7.00	2.00	19.00

Table S63. X3DNA report on structures in Puzzle 15.

			Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
No.	3D RNA model	#Helices	#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ15_3dRNA2_1	3	23	22	7	0	0	11	2	20
2	PZ15_3dRNA2_10	3	23	22	5	0	0	13	2	20
3	PZ15_3dRNA2_2	3	23	22	7	0	0	11	2	20
4	PZ15_3dRNA2_3	3	23	22	7	0	0	11	2	20
5	PZ15_3dRNA2_4	3	23	22	6	0	0	12	2	20
6	PZ15_3dRNA2_5	3	23	22	7	0	0	11	2	20
7	PZ15_3dRNA2_6	3	23	22	7	0	0	11	2	20
8	PZ15_3dRNA2_7	3	23	22	6	0	0	12	2	20
9	PZ15_3dRNA2_8	3	23	22	5	0	0	13	2	20
10	PZ15_3dRNA2_9	3	23	22	6	0	0	12	2	20
11	PZ15_Adamiak_1	3	24	24	12	0	0	7	2	21
12	PZ15_Adamiak_10	3	27	25	18	0	0	1	5	24
13	PZ15_Adamiak_2	2	28	24	18	0	0	3	5	26
14	PZ15_Adamiak_3	2	29	24	17	0	0	3	7	27
15	PZ15_Adamiak_4	3	25	25	19	0	0	0	3	22
16	PZ15_Adamiak_5	3	26	25	19	0	0	0	4	23
17	PZ15_Adamiak_6	2	26	24	17	0	0	3	4	24
18	PZ15_Adamiak_7	2	25	25	19	0	0	0	4	23
19	PZ15_Adamiak_8	2	28	25	16	0	0	4	6	26
20	PZ15_Adamiak_9	3	23	23	15	0	0	4	1	20
21	PZ15_Chen_1	2	26	23	16	0	0	4	4	24
22	PZ15_Chen_10	3	25	22	16	0	0	2	4	22
23	PZ15_Chen_2	3	24	23	18	0	0	1	2	21
24	PZ15_Chen_3	2	28	24	16	0	0	5	5	26
25	PZ15_Chen_4	2	26	22	9	0	0	11	4	24
26	PZ15_Chen_5	3	24	22	18	0	0	1	2	21

27	PZ15_Chen_6	4	24	22	13	0	0	5	2	20
28	PZ15_Chen_7	5	22	21	15	0	0	2	0	17
29	PZ15_Chen_8	2	24	21	14	0	0	3	5	22
30	PZ15_Chen_9	4	22	19	6	0	0	10	2	18
31	PZ15_FARFAR1_1	3	27	23	19	0	0	4	1	24
32	PZ15_FARFAR1_10	2	28	23	19	0	0	4	3	26
33	PZ15_FARFAR1_2	3	25	23	19	0	0	2	1	22
34	PZ15_FARFAR1_3	2	25	24	19	0	0	1	3	23
35	PZ15_FARFAR1_4	3	29	23	20	0	0	4	2	26
36	PZ15_FARFAR1_5	2	27	23	19	0	0	3	3	25
37	PZ15_FARFAR1_6	3	25	23	19	0	0	1	2	22
38	PZ15_FARFAR1_7	2	27	23	19	0	0	3	3	25
39	PZ15_FARFAR1_8	3	29	24	19	0	0	6	1	26
40	PZ15_FARFAR1_9	2	27	23	19	0	0	4	2	25
41	PZ15_FARFAR2_1	2	28	24	20	0	0	2	4	26
42	PZ15_FARFAR2_10	2	27	24	19	0	0	3	3	25
43	PZ15_FARFAR2_2	3	28	24	19	0	0	5	1	25
44	PZ15_FARFAR2_3	2	29	24	21	0	0	4	2	27
45	PZ15_FARFAR2_4	4	26	24	19	0	0	2	1	22
46	PZ15_FARFAR2_5	2	27	24	19	0	0	4	2	25
47	PZ15_FARFAR2_6	3	29	24	18	0	0	6	2	26
48	PZ15_FARFAR2_7	3	27	24	20	0	0	3	1	24
49	PZ15_FARFAR2_8	2	28	24	19	0	0	4	3	26
50	PZ15_FARFAR2_9	3	29	24	19	0	0	4	3	26
51	PZ15_RNAComposer1_1	2	28	24	18	0	0	3	5	26
52	PZ15_RNAComposer1_2	2	29	24	17	0	0	3	7	27
53	PZ15_RNAComposer2_1	3	25	25	19	0	0	0	3	22
54	PZ15_RNAComposer2_2	3	26	25	19	0	0	0	4	23
55	PZ15_SimRNA1_1	3	27	25	8	0	0	12	4	24
56	PZ15_SimRNA1_10	3	29	24	14	0	0	10	2	26
57	PZ15_SimRNA1_2	2	26	23	6	0	0	14	4	24
58	PZ15_SimRNA1_3	2	27	25	6	0	0	11	8	25
59	PZ15_SimRNA1_4	4	27	22	9	0	0	11	3	23

60	PZ15_SimRNA1_5	3	27	23	9	0	0	12	3	24
61	PZ15_SimRNA1_6	1	26	24	6	0	0	11	8	25
62	PZ15_SimRNA1_7	2	24	22	9	0	0	8	5	22
63	PZ15_SimRNA1_8	2	28	23	11	0	0	12	3	26
64	PZ15_SimRNA1_9	4	27	23	11	0	0	11	1	23
65	PZ15_SimRNA2_1	2	26	24	10	0	0	12	2	24
66	PZ15_SimRNA2_10	2	26	24	6	0	0	16	2	24
67	PZ15_SimRNA2_2	2	27	24	13	0	0	9	3	25
68	PZ15_SimRNA2_3	2	28	24	10	0	0	13	3	26
69	PZ15_SimRNA2_4	3	26	24	7	0	0	15	1	23
70	PZ15_SimRNA2_5	2	29	25	11	0	0	13	3	27
71	PZ15_SimRNA2_6	3	28	24	11	0	0	13	1	25
72	PZ15_SimRNA2_7	2	29	24	11	0	0	12	4	27
73	PZ15_SimRNA2_8	3	29	24	10	0	0	14	2	26
74	PZ15_SimRNA2_9	2	28	23	7	0	0	17	2	26
75	PZ15_refstructure	2	21	17	13	0	0	2	4	19
	Average	2.63	26.08	23.25	13.72	0.00	0.00	6.79	2.95	23.45
	Standard deviation	0.69	2.17	1.38	5.26	0.00	0.00	4.86	1.65	2.51
	Median	3.00	26.00	24.00	15.00	0.00	0.00	5.00	3.00	24.00

Table S64. X3DNA report on structures in Puzzle 17.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ17_refstructure	2	23	19	8	0	0	9	4	21
2	PZ17_Adamiak_1	5	23	21	6	0	0	12	0	18
3	PZ17_Adamiak_2	5	22	21	6	0	0	10	1	17
4	PZ17_Adamiak_3	5	22	20	7	0	0	10	0	17
5	PZ17_Bujnicki_1	2	23	23	15	0	0	2	4	21
6	PZ17_Bujnicki_10	2	23	21	4	0	0	13	4	21

7	PZ17_Bujnicki_2	2	23	21	4	0	0	13	4	21
8	PZ17_Bujnicki_3	2	22	21	6	0	0	10	4	20
9	PZ17_Bujnicki_4	2	22	21	9	0	0	7	4	20
10	PZ17_Bujnicki_5	2	22	22	11	0	0	5	4	20
11	PZ17_Bujnicki_6	2	23	21	5	1	0	11	4	21
12	PZ17_Bujnicki_7	3	20	20	12	0	0	4	1	17
13	PZ17_Bujnicki_8	3	21	19	11	0	0	5	2	18
14	PZ17_Bujnicki_9	2	23	23	15	0	0	2	4	21
15	PZ17_Chen_1	2	19	18	5	0	0	10	2	17
16	PZ17_Chen_10	1	24	16	5	0	0	14	4	23
17	PZ17_Chen_2	2	22	20	5	0	0	12	3	20
18	PZ17_Chen_3	3	16	16	3	0	0	9	1	13
19	PZ17_Chen_4	1	20	17	6	0	0	9	4	19
20	PZ17_Chen_5	6	21	19	5	0	0	9	1	15
21	PZ17_Chen_6	3	20	17	2	0	0	11	4	17
22	PZ17_Chen_7	3	19	19	12	0	0	2	2	16
23	PZ17_Chen_8	2	19	18	12	0	0	3	2	17
24	PZ17_Chen_9	3	23	20	7	0	0	7	6	20
25	PZ17_Das_1	2	23	20	15	0	0	3	3	21
26	PZ17_Das_10	4	23	21	14	0	0	3	2	19
27	PZ17_Das_2	3	23	20	15	0	0	3	2	20
28	PZ17_Das_3	3	20	19	12	0	0	3	2	17
29	PZ17_Das_4	2	22	21	14	0	0	3	3	20
30	PZ17_Das_5	2	21	21	14	0	0	2	3	19
31	PZ17_Das_6	2	21	21	15	0	0	1	3	19
32	PZ17_Das_7	4	23	19	14	0	0	3	2	19
33	PZ17_Das_8	2	22	21	15	0	0	1	4	20
34	PZ17_Das_9	4	24	20	15	0	0	2	3	20
35	PZ17_DasExtraInfo_1	2	22	21	14	0	0	3	3	20
36	PZ17_DasExtraInfo_2	2	23	21	14	0	0	4	3	21
37	PZ17_DasExtraInfo_3	2	22	21	15	0	0	2	3	20
38	PZ17_Ding_1	1	19	19	9	0	0	6	3	18
39	PZ17_Ding_10	4	19	19	6	0	0	8	1	15

40	PZ17_Ding_2	1	19	19	3	0	0	12	3	18
41	PZ17_Ding_3	1	19	19	7	0	0	8	3	18
42	PZ17_Ding_4	1	20	18	10	0	0	5	4	19
43	PZ17_Ding_5	1	19	18	9	0	0	6	3	18
44	PZ17_Ding_6	4	22	20	5	0	0	11	2	18
45	PZ17_Ding_7	3	21	20	8	0	0	6	4	18
46	PZ17_Ding_8	4	23	20	8	0	0	8	3	19
47	PZ17_Ding_9	2	22	21	7	0	0	8	5	20
48	PZ17_Dohkolyan_1	2	17	17	8	0	0	6	1	15
49	PZ17_Dohkolyan_2	3	20	17	4	0	0	10	3	17
50	PZ17_Dohkolyan_3	3	22	20	8	0	0	9	2	19
51	PZ17_Major_1	3	24	19	1	0	0	18	2	21
52	PZ17_Major_10	2	13	6	0	0	0	5	6	11
53	PZ17_Major_2	4	25	24	1	0	0	18	2	21
54	PZ17_Major_3	3	25	23	1	0	0	18	3	22
55	PZ17_Major_4	3	25	24	1	1	0	17	3	22
56	PZ17_Major_5	3	24	21	0	1	0	17	3	21
57	PZ17_Major_6	3	16	12	0	0	0	10	3	13
58	PZ17_Major_7	4	12	8	0	0	0	8	0	8
59	PZ17_Major_8	3	16	9	0	0	0	9	4	13
60	PZ17_Major_9	2	8	5	1	0	0	4	1	6
61	PZ17_RNAComposer1_1	2	18	17	10	0	0	5	1	16
62	PZ17_RNAComposer1_10	2	17	16	7	0	0	7	1	15
63	PZ17_RNAComposer1_2	1	24	17	3	0	0	18	2	23
64	PZ17_RNAComposer1_3	1	19	14	7	0	0	8	3	18
65	PZ17_RNAComposer1_4	2	17	16	7	0	0	7	1	15
66	PZ17_RNAComposer1_5	1	21	16	6	0	0	10	4	20
67	PZ17_RNAComposer1_6	3	17	15	8	0	0	6	0	14
68	PZ17_RNAComposer1_7	2	22	17	5	0	0	12	3	20
69	PZ17_RNAComposer1_8	3	17	15	8	0	0	6	0	14
70	PZ17_RNAComposer1_9	2	16	16	7	0	0	6	1	14
71	PZ17_RNAComposer2_1	5	22	21	6	0	0	11	0	17
72	PZ17_RNAComposer2_10	3	15	15	6	0	0	6	0	12

73	PZ17_RNAComposer2_2	5	22	21	8	0	0	9	0	17
74	PZ17_RNAComposer2_3	4	19	13	0	0	0	11	4	15
75	PZ17_RNAComposer2_4	4	21	20	6	0	0	10	1	17
76	PZ17_RNAComposer2_5	4	21	20	6	0	0	10	1	17
77	PZ17_RNAComposer2_6	5	21	20	6	0	0	10	0	16
78	PZ17_RNAComposer2_7	5	19	19	8	0	0	6	0	14
79	PZ17_RNAComposer2_8	4	21	18	6	0	0	10	1	17
80	PZ17_RNAComposer2_9	3	15	14	6	0	0	6	0	12
81	PZ17_SimRNA1_1	1	22	19	8	0	0	8	5	21
82	PZ17_SimRNA1_2	2	22	19	11	0	0	4	5	20
83	PZ17_SimRNA1_3	3	22	19	9	0	0	7	3	19
84	PZ17_SimRNA1_4	3	21	19	9	0	0	6	3	18
85	PZ17_SimRNA1_5	3	20	19	10	0	0	5	2	17
86	PZ17_SimRNA1_6	2	22	19	11	0	0	5	4	20
87	PZ17_SimRNA1_7	1	24	20	9	0	0	7	7	23
88	PZ17_SimRNA1_8	1	21	19	8	0	0	7	5	20
89	PZ17_SimRNA1_9	2	20	19	5	0	0	9	4	18
90	PZ17_SimRNA2_1	3	23	22	13	0	0	4	3	20
91	PZ17_SimRNA2_2	3	25	24	12	0	0	6	4	22
92	PZ17_SimRNA2_3	2	22	21	10	0	0	7	3	20
93	PZ17_SimRNA2_4	4	26	24	9	0	0	9	4	22
94	PZ17_SimRNA2_5	2	23	21	10	0	0	7	4	21
95	PZ17_SimRNA2_6	3	23	20	8	0	0	9	3	20
96	PZ17_SimRNA2_7	2	22	22	11	0	0	6	3	20
97	PZ17_SimRNA2_8	2	24	20	9	0	0	8	5	22
98	PZ17_SimRNA2_9	2	24	22	8	0	0	8	6	22
99	PZ17_Xiao_1	3	15	12	1	0	0	8	3	12
100	PZ17_Xiao_10	3	12	9	1	0	0	6	2	9
101	PZ17_Xiao_2	4	15	12	1	0	0	9	1	11
102	PZ17_Xiao_3	2	15	11	1	0	0	4	8	13
103	PZ17_Xiao_4	4	11	6	0	0	0	2	5	7
104	PZ17_Xiao_5	3	12	10	3	0	0	4	2	9
105	PZ17_Xiao_6	3	14	10	0	0	0	8	3	11

106	PZ17_Xiao_7	3	12	9	0	0	0	5	4	9
107	PZ17_Xiao_8	4	11	7	1	0	0	2	4	7
108	PZ17_Xiao_9	3	13	10	0	0	0	6	4	10
	Average	2.71	20.13	17.97	7.11	0.03	0.00	7.49	2.79	17.42
	Standard deviation	1.12	3.69	4.26	4.48	0.17	0.00	3.89	1.64	3.91
	Median	3.00	21.00	19.00	7.00	0.00	0.00	7.00	3.00	18.00

Table S65. X3DNA report on structures in Puzzle 18.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					Total
					Right-handed		Left-handed	Other		
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ18_refstructure	2	29	25	12	0	0	9	6	27
2	PZ18_3dRNA_1	2	29	25	4	0	0	20	3	27
3	PZ18_3dRNA_2	3	29	25	4	0	0	20	2	26
4	PZ18_3dRNA_3	3	27	24	5	0	0	17	2	24
5	PZ18_3dRNA_4	2	28	25	1	0	0	22	3	26
6	PZ18_3dRNA_5	2	29	25	2	0	0	22	3	27
7	PZ18_Chén_1	2	28	27	0	1	0	21	4	26
8	PZ18_Chén_2	2	28	25	1	1	0	20	4	26
9	PZ18_Chén_3	2	29	25	4	0	0	20	3	27
10	PZ18_Chén_4	2	28	24	2	0	0	20	4	26
11	PZ18_Chén_5	3	29	25	20	0	0	4	2	26
12	PZ18_Das_1	2	31	25	11	0	0	12	6	29
13	PZ18_Das_2	2	30	25	11	0	0	11	6	28
14	PZ18_Das_3	2	30	25	11	0	0	11	6	28
15	PZ18_Das_4	2	30	26	11	0	0	13	4	28
16	PZ18_Das_5	4	26	21	8	0	0	11	3	22
17	PZ18_Ding_1	2	30	26	9	0	0	14	5	28
18	PZ18_Ding_2	2	27	26	11	0	0	11	3	25

19	PZ18_Ding_3	2	29	26	10	0	0	12	5	27
20	PZ18_Ding_4	1	27	23	9	0	0	12	5	26
21	PZ18_Ding_5	2	28	26	10	0	0	13	3	26
22	PZ18_Dokholyan_1	3	27	26	9	0	0	12	3	24
23	PZ18_Dokholyan_2	4	28	26	8	0	0	14	2	24
24	PZ18_Dokholyan_3	4	27	26	7	0	0	13	3	23
25	PZ18_FARFAR_1	2	30	26	18	0	0	7	3	28
26	PZ18_FARFAR_10	3	30	26	18	0	0	6	3	27
27	PZ18_FARFAR_2	2	30	26	18	0	0	7	3	28
28	PZ18_FARFAR_3	2	30	26	18	0	0	7	3	28
29	PZ18_FARFAR_4	2	29	26	18	0	0	6	3	27
30	PZ18_FARFAR_5	2	30	26	18	0	0	7	3	28
31	PZ18_FARFAR_6	2	29	26	18	0	0	6	3	27
32	PZ18_FARFAR_7	2	30	26	18	0	0	6	4	28
33	PZ18_FARFAR_8	2	30	26	18	0	0	7	3	28
34	PZ18_FARFAR_9	3	28	26	18	0	0	5	2	25
35	PZ18_Lee_1	3	30	27	14	0	0	11	2	27
36	PZ18_Lee_2	2	28	26	13	0	0	9	4	26
37	PZ18_Lee_3	2	25	23	7	0	0	10	6	23
38	PZ18_Lee_4	2	26	26	15	0	0	6	3	24
39	PZ18_Lee_5	2	25	25	15	0	0	5	3	23
40	PZ18_LeeServer_1	2	29	25	14	0	0	10	3	27
41	PZ18_LeeServer_2	3	26	25	10	0	0	10	3	23
42	PZ18_LeeServer_3	3	24	22	5	0	0	13	3	21
43	PZ18_LeeServer_4	3	27	26	14	0	0	7	3	24
44	PZ18_LeeServer_5	2	26	25	15	0	0	5	4	24
45	PZ18_RNAComposer_1	2	29	26	15	0	0	9	3	27
46	PZ18_RNAComposer_2	3	28	23	11	0	0	10	4	25
47	PZ18_RNAComposer_3	3	29	26	13	0	0	10	3	26
48	PZ18_RNAComposer_4	3	29	26	13	0	0	11	2	26
49	PZ18_RNAComposer_5	4	28	25	11	0	0	12	1	24
50	PZ18_SimRNA_1	1	29	24	9	0	0	11	8	28
51	PZ18_SimRNA_2	2	28	26	9	0	0	13	4	26

52	PZ18_SimRNA_3	2	29	26	8	0	0	15	4	27
53	PZ18_YagoubAli_1	3	29	26	15	0	0	9	2	26
	Average	2.38	28.36	25.28	11.06	0.04	0.00	11.40	3.49	25.98
	Standard deviation	0.69	1.53	1.17	5.33	0.19	0.00	4.87	1.32	1.82
	Median	2.00	29.00	26.00	11.00	0.00	0.00	11.00	3.00	26.00

Table S66. X3DNA report on structures in Puzzle 19.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ19_refstructure	2	27	23	12	0	0	6	7	25
2	PZ19_3dRNA_1	3	24	22	1	0	0	17	3	21
3	PZ19_3dRNA_2	2	24	22	1	0	0	16	5	22
4	PZ19_3dRNA_3	3	25	21	2	2	0	13	5	22
5	PZ19_3dRNA_4	2	24	21	1	0	0	17	4	22
6	PZ19_3dRNA_5	3	23	22	1	0	0	15	4	20
7	PZ19_Adamiak_1	2	28	24	14	0	0	9	3	26
8	PZ19_Adamiak_2	2	25	21	12	0	0	9	2	23
9	PZ19_Adamiak_3	3	24	19	11	0	0	6	4	21
10	PZ19_Adamiak_4	2	27	21	13	0	0	8	4	25
11	PZ19_Adamiak_5	3	24	19	10	0	0	7	4	21
12	PZ19_Bujnicki_1	2	27	25	15	0	0	5	5	25
13	PZ19_Bujnicki_2	2	27	25	16	0	0	4	5	25
14	PZ19_Bujnicki_3	2	25	24	11	0	0	6	6	23
15	PZ19_Bujnicki_4	2	27	25	10	0	0	10	5	25
16	PZ19_Bujnicki_5	2	27	26	16	0	0	4	5	25
17	PZ19_Chén_1	2	24	22	11	1	0	5	5	22
18	PZ19_Chén_2	2	24	21	5	0	0	12	5	22
19	PZ19_Chén_3	2	23	20	6	0	0	11	4	21
20	PZ19_Chén_4	3	24	23	8	0	0	10	3	21

21	PZ19_Chen_5	1	21	17	0	2	0	13	5	20
22	PZ19_Das_1	4	25	24	16	0	0	1	4	21
23	PZ19_Das_2	2	26	21	15	0	0	4	5	24
24	PZ19_Das_3	3	24	20	16	0	0	1	4	21
25	PZ19_Das_4	3	22	20	16	0	0	1	2	19
26	PZ19_Das_5	2	27	24	14	0	0	7	4	25
27	PZ19_Ding_1	2	26	23	10	0	0	9	5	24
28	PZ19_Ding_2	3	23	22	11	0	0	7	2	20
29	PZ19_Ding_3	2	24	23	11	0	0	8	3	22
30	PZ19_Ding_4	3	20	16	0	0	0	15	2	17
31	PZ19_Ding_5	4	18	14	0	0	0	10	4	14
32	PZ19_Dokholyan_1	3	22	22	10	0	0	7	2	19
33	PZ19_FARFAR_1	2	26	20	12	0	0	9	3	24
34	PZ19_FARFAR_10	3	26	20	5	0	0	14	4	23
35	PZ19_FARFAR_2	2	26	20	11	0	0	11	2	24
36	PZ19_FARFAR_3	2	27	20	12	0	0	10	3	25
37	PZ19_FARFAR_4	2	25	21	11	0	0	7	5	23
38	PZ19_FARFAR_5	2	26	20	11	0	0	9	4	24
39	PZ19_FARFAR_6	1	25	21	11	0	0	9	4	24
40	PZ19_FARFAR_7	1	25	20	12	0	0	8	4	24
41	PZ19_FARFAR_8	2	26	20	11	0	0	10	3	24
42	PZ19_FARFAR_9	2	27	20	12	0	0	10	3	25
43	PZ19_LeeServer_1	3	24	22	0	0	0	19	2	21
44	PZ19_LeeServer_2	2	24	22	0	0	0	17	5	22
45	PZ19_LeeServer_3	2	28	24	0	0	0	22	4	26
46	PZ19_LeeServer_4	3	20	17	7	0	0	9	1	17
47	PZ19_LeeServer_5	3	18	17	9	0	0	5	1	15
48	PZ19_RNAComposer_1	2	25	21	10	0	0	9	4	23
49	PZ19_RNAComposer_2	2	26	23	5	0	0	15	4	24
50	PZ19_RNAComposer_3	2	27	24	7	0	0	14	4	25
51	PZ19_RNAComposer_4	3	26	24	10	0	0	10	3	23
52	PZ19_RNAComposer_5	3	25	23	9	0	0	10	3	22
53	PZ19_SimRNA_1	2	26	25	11	0	0	7	6	24

54	PZ19_SimRNA_2	3	25	23	11	0	0	6	5	22
55	PZ19_SimRNA_3	4	25	25	11	0	0	7	3	21
	Average	2.38	24.71	21.53	8.96	0.09	0.00	9.45	3.82	22.33
	Standard deviation	0.68	2.23	2.47	5.00	0.40	0.00	4.50	1.26	2.60
	Median	2.00	25.00	22.00	11.00	0.00	0.00	9.00	4.00	23.00

Table S67. X3DNA report on structures in Puzzle 20.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ20_Adamiak_1	2	30	25	14	0	0	10	4	28
2	PZ20_Adamiak_2	3	29	25	11	0	0	11	4	26
3	PZ20_Adamiak_3	2	30	25	14	0	0	10	4	28
4	PZ20_Adamiak_4	2	30	25	14	0	0	10	4	28
5	PZ20_Adamiak_5	2	30	25	9	0	0	15	4	28
6	PZ20_Bujnicki_1	2	29	23	16	0	0	4	7	27
7	PZ20_Bujnicki_2	2	29	23	16	0	0	4	7	27
8	PZ20_Bujnicki_3	4	28	23	15	0	0	5	4	24
9	PZ20_Bujnicki_4	2	27	23	12	0	0	6	7	25
10	PZ20_Bujnicki_5	2	27	23	8	0	0	12	5	25
11	PZ20_Das_1	4	26	21	16	0	0	2	4	22
12	PZ20_Das_2	2	28	23	15	0	0	5	6	26
13	PZ20_Das_3	4	30	24	16	0	0	6	4	26
14	PZ20_Das_4	4	26	22	16	0	0	1	5	22
15	PZ20_Das_5	5	24	21	16	0	0	1	2	19
16	PZ20_FARFAR_1	2	30	26	17	0	0	7	4	28
17	PZ20_FARFAR_10	2	30	26	17	0	0	7	4	28
18	PZ20_FARFAR_2	2	30	25	17	0	0	7	4	28
19	PZ20_FARFAR_3	2	29	26	17	0	0	7	3	27
20	PZ20_FARFAR_4	2	30	26	18	0	0	6	4	28

21	PZ20_FARFAR_5	2	30	26	17	0	0	7	4	28
22	PZ20_FARFAR_6	2	31	25	17	0	0	8	4	29
23	PZ20_FARFAR_7	2	31	26	17	0	0	8	4	29
24	PZ20_FARFAR_8	2	30	27	16	0	0	6	6	28
25	PZ20_FARFAR_9	2	31	25	18	0	0	7	4	29
26	PZ20_RNAComposer_1	2	30	24	11	0	0	13	4	28
27	PZ20_RNAComposer_2	2	29	25	13	0	0	9	5	27
28	PZ20_RNAComposer_3	4	27	24	13	0	0	7	3	23
29	PZ20_RNAComposer_4	2	28	24	10	0	0	11	5	26
30	PZ20_RNAComposer_5	3	28	23	13	0	0	9	3	25
31	PZ20_SimRNA_1	2	28	24	1	0	0	17	8	26
32	PZ20_SimRNA_2	2	25	21	9	0	0	7	7	23
33	PZ20_SimRNA_3	2	27	26	8	0	0	6	11	25
34	PZ20_SimRNA_4	3	26	25	12	0	0	6	5	23
35	PZ20_SimRNA_5	1	26	23	10	0	0	6	9	25
36	PZ20_Xiao3_1	4	20	16	4	0	0	10	2	16
37	PZ20_Xiao3_2	3	18	13	3	0	0	11	1	15
38	PZ20_Xiao3_3	3	21	13	3	0	0	11	4	18
39	PZ20_Xiao3_4	4	20	15	2	0	0	10	4	16
40	PZ20_Xiao3_5	4	21	17	2	0	0	11	4	17
41	PZ20_refstructure	2	30	24	17	0	0	4	7	28
	Average	2.56	27.54	23.07	12.44	0.00	0.00	7.80	4.73	24.98
	Standard deviation	0.92	3.34	3.49	5.04	0.00	0.00	3.44	1.91	3.93
	Median	2.00	29.00	24.00	14.00	0.00	0.00	7.00	4.00	26.00

Table S68. X3DNA report on structures in Puzzle 21.

			Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
No.	3D RNA model	#Helices	#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ21_3dRNA_1	1	4	4	3	0	0	0	0	3
2	PZ21_3dRNA_2	1	5	4	0	0	0	3	1	4
3	PZ21_3dRNA_3	1	4	4	0	0	0	3	0	3
4	PZ21_3dRNA_4	2	12	9	0	0	0	9	1	10
5	PZ21_3dRNA_5	2	15	11	0	0	0	11	2	13
6	PZ21_Adamiak_1	2	12	12	4	0	0	5	1	10
7	PZ21_Adamiak_2	2	12	12	6	0	0	3	1	10
8	PZ21_Adamiak_3	2	11	11	5	0	0	4	0	9
9	PZ21_Adamiak_4	2	12	11	6	0	0	3	1	10
10	PZ21_Adamiak_5	2	11	11	6	0	0	3	0	9
11	PZ21_Bujnicki_1	2	13	10	3	0	0	6	2	11
12	PZ21_Bujnicki_2	1	13	11	8	0	0	2	2	12
13	PZ21_Bujnicki_3	2	17	15	2	0	0	10	3	15
14	PZ21_Bujnicki_4	1	12	11	9	0	0	1	1	11
15	PZ21_Bujnicki_5	1	10	9	2	0	0	4	3	9
16	PZ21_ChenHighLig_1	1	13	11	3	0	0	8	1	12
17	PZ21_ChenHighLig_2	1	13	11	6	0	0	5	1	12
18	PZ21_ChenHighLig_3	2	13	11	7	0	0	2	2	11
19	PZ21_ChenHighLig_4	1	13	10	5	0	0	4	3	12
20	PZ21_ChenHighLig_5	2	14	11	2	0	0	9	1	12
21	PZ21_ChenLowLig_1	1	13	11	3	0	0	8	1	12
22	PZ21_ChenLowLig_2	1	13	11	6	0	0	5	1	12
23	PZ21_ChenLowLig_3	2	13	11	7	0	0	2	2	11
24	PZ21_ChenLowLig_4	1	13	10	5	0	0	4	3	12
25	PZ21_ChenLowLig_5	2	14	11	2	0	0	9	1	12
26	PZ21_Das_1	1	13	11	10	0	0	1	1	12

27	PZ21_Das_2	1	12	11	10	0	0	0	1	11
28	PZ21_Das_3	1	13	11	8	0	0	2	2	12
29	PZ21_Das_4	2	13	12	9	0	0	0	2	11
30	PZ21_Das_5	1	13	11	9	0	0	1	2	12
31	PZ21_DasLORES_1	1	13	11	9	0	0	1	2	12
32	PZ21_DasLORES_2	1	13	11	10	0	0	1	1	12
33	PZ21_DasLORES_3	2	15	13	9	0	0	0	4	13
34	PZ21_DasLORES_4	1	12	12	9	0	0	0	2	11
35	PZ21_DasLORES_5	2	15	12	9	0	0	1	3	13
36	PZ21_FARFAR_1	2	16	12	8	0	0	3	3	14
37	PZ21_FARFAR_10	2	17	12	8	0	0	3	4	15
38	PZ21_FARFAR_2	3	17	12	8	0	0	4	2	14
39	PZ21_FARFAR_3	1	17	11	9	0	0	5	2	16
40	PZ21_FARFAR_4	2	16	12	9	0	0	2	3	14
41	PZ21_FARFAR_5	1	15	12	8	0	0	3	3	14
42	PZ21_FARFAR_6	2	16	11	9	0	0	3	2	14
43	PZ21_FARFAR_7	2	17	12	9	0	0	3	3	15
44	PZ21_FARFAR_8	1	15	12	8	0	0	2	4	14
45	PZ21_FARFAR_9	1	17	11	8	0	0	6	2	16
46	PZ21_RNAComposer_1	2	13	8	6	0	0	2	3	11
47	PZ21_RNAComposer_2	1	12	9	7	0	0	2	2	11
48	PZ21_RNAComposer_3	2	11	11	3	0	0	6	0	9
49	PZ21_RNAComposer_4	2	11	11	1	0	0	8	0	9
50	PZ21_RNAComposer_5	3	14	11	8	0	0	2	1	11
51	PZ21_Sanbonmatsu_1	3	11	10	8	0	0	0	0	8
52	PZ21_Sanbonmatsu_2	3	11	10	8	0	0	0	0	8
53	PZ21_Sanbonmatsu_3	2	13	12	9	0	0	0	2	11
54	PZ21_Sanbonmatsu_4	2	13	12	9	0	0	0	2	11
55	PZ21_SimRNA_1	2	16	15	5	0	0	6	3	14
56	PZ21_SimRNA_2	1	17	16	4	0	0	8	4	16
57	PZ21_SimRNA_3	2	17	14	10	0	0	3	2	15
58	PZ21_SimRNA_4	1	17	16	8	0	0	4	4	16
59	PZ21_SimRNA_5	2	17	14	10	0	0	3	2	15

60	PZ21_refstructure	2	13	12	6	0	0	2	3	11
	Average	1.63	13.27	11.10	6.30	0.00	0.00	3.50	1.83	11.63
	Standard deviation	0.61	2.86	2.22	3.00	0.00	0.00	2.85	1.15	2.80
	Median	2.00	13.00	11.00	7.50	0.00	0.00	3.00	2.00	12.00

Table S69. X3DNA report on structures in Puzzle 24.

No.	3D RNA model	#Helices	Base pairs		Dinucleotide steps					
					Right-handed		Left-handed	Other		Total
			#all bps	#canonical / wobble bps	#A-RNA	#B-RNA	#Z-RNA	#Unclassified steps	#Steps without a continuous backbone	
1	PZ24_refstructure	3	49	46	32	0	0	11	3	46
2	PZ24_3dRNA_1	4	40	35	19	0	0	15	2	36
3	PZ24_3dRNA_2	4	40	36	22	0	0	13	1	36
4	PZ24_3dRNA_3	4	45	39	22	0	0	17	2	41
5	PZ24_3dRNA_4	3	43	39	26	0	0	12	2	40
6	PZ24_3dRNA_5	3	44	39	23	0	0	16	2	41
7	PZ24_Adamiak_1	4	46	42	18	1	0	19	4	42
8	PZ24_Adamiak_2	4	46	42	14	0	0	24	4	42
9	PZ24_Adamiak_3	4	46	43	20	0	0	20	2	42
10	PZ24_Adamiak_4	4	46	44	23	0	0	17	2	42
11	PZ24_Adamiak_5	4	46	44	28	0	0	12	2	42
12	PZ24_Bujnicki_1	3	47	42	15	0	0	24	5	44
13	PZ24_Bujnicki_2	3	48	46	23	0	0	16	6	45
14	PZ24_Bujnicki_3	3	47	44	23	0	0	16	5	44
15	PZ24_Bujnicki_4	4	49	46	19	0	0	21	5	45
16	PZ24_Bujnicki_5	3	49	46	29	0	0	11	6	46
17	PZ24_Das_1	3	50	45	31	0	0	11	5	47
18	PZ24_Das_10	3	50	45	30	0	0	12	5	47
19	PZ24_Das_2	3	50	45	31	0	0	11	5	47
20	PZ24_Das_3	3	50	45	32	0	0	10	5	47
21	PZ24_Das_4	3	50	45	33	0	0	9	5	47

22	PZ24_Das_5	3	50	45	31	0	0	11	5	47
23	PZ24_Das_6	3	50	45	28	0	0	14	5	47
24	PZ24_Das_7	3	50	45	30	0	0	12	5	47
25	PZ24_Das_8	3	50	45	31	0	0	11	5	47
26	PZ24_Das_9	3	50	45	29	0	0	13	5	47
27	PZ24_DasTFN_1	4	50	44	27	0	0	17	2	46
28	PZ24_DasTFN_10	3	50	43	29	0	0	13	5	47
29	PZ24_DasTFN_2	3	50	45	25	0	0	19	3	47
30	PZ24_DasTFN_3	3	50	44	29	0	0	15	3	47
31	PZ24_DasTFN_4	2	51	44	23	0	0	22	4	49
32	PZ24_DasTFN_5	2	49	44	30	0	0	13	4	47
33	PZ24_DasTFN_6	4	50	44	25	0	0	19	2	46
34	PZ24_DasTFN_7	3	50	44	24	0	0	19	4	47
35	PZ24_DasTFN_8	3	51	46	25	0	0	20	3	48
36	PZ24_DasTFN_9	3	51	45	25	0	0	19	4	48
37	PZ24_Ding_1	3	26	23	11	0	0	7	5	23
38	PZ24_Ding_10	3	31	24	11	0	0	10	7	28
39	PZ24_Ding_2	4	30	23	12	0	0	9	5	26
40	PZ24_Ding_3	3	31	24	9	0	0	12	7	28
41	PZ24_Ding_4	3	30	25	15	0	0	8	4	27
42	PZ24_Ding_5	5	30	24	12	0	0	8	5	25
43	PZ24_Ding_6	2	28	25	8	0	0	11	7	26
44	PZ24_Ding_7	3	29	25	11	0	0	10	5	26
45	PZ24_Ding_8	4	26	22	10	0	0	10	2	22
46	PZ24_Ding_9	3	26	23	10	0	0	8	5	23
47	PZ24_FARFAR2_1	3	50	44	29	0	0	15	3	47
48	PZ24_FARFAR2_10	3	49	45	27	0	0	15	4	46
49	PZ24_FARFAR2_2	2	52	45	31	0	0	13	6	50
50	PZ24_FARFAR2_3	3	50	44	28	0	0	15	4	47
51	PZ24_FARFAR2_4	3	50	43	28	0	0	15	4	47
52	PZ24_FARFAR2_5	4	49	44	31	0	0	12	2	45
53	PZ24_FARFAR2_6	3	51	45	25	0	0	19	4	48
54	PZ24_FARFAR2_7	3	49	44	32	0	0	9	5	46

55	PZ24_FARFAR2_8	3	48	44	28	0	0	13	4	45
56	PZ24_FARFAR2_9	3	49	44	28	0	0	15	3	46
57	PZ24_iFoldRNA_1	3	45	43	11	0	0	26	5	42
58	PZ24_iFoldRNA_2	3	45	42	9	0	0	29	4	42
59	PZ24_iFoldRNA_3	4	42	39	11	1	0	21	5	38
60	PZ24_iFoldRNA_4	3	45	37	11	0	0	25	6	42
61	PZ24_iFoldRNA_5	7	40	36	3	2	0	26	2	33
62	PZ24_Kollmann_1	8	40	36	21	0	0	10	1	32
63	PZ24_Kollmann_10	7	43	36	17	0	0	13	6	36
64	PZ24_Kollmann_2	6	42	34	19	0	0	9	8	36
65	PZ24_Kollmann_3	6	37	30	19	0	0	6	6	31
66	PZ24_Kollmann_4	7	37	32	22	0	0	4	4	30
67	PZ24_Kollmann_5	5	43	41	22	0	0	10	6	38
68	PZ24_Kollmann_6	6	46	39	23	0	0	9	8	40
69	PZ24_Kollmann_7	8	43	36	18	0	0	12	5	35
70	PZ24_Kollmann_8	6	39	32	21	0	0	7	5	33
71	PZ24_Kollmann_9	5	40	35	17	0	0	12	6	35
72	PZ24_RNAComposer_1	4	47	44	19	0	0	21	3	43
73	PZ24_RNAComposer_2	4	48	43	17	0	0	24	3	44
74	PZ24_RNAComposer_3	3	43	41	23	0	0	14	3	40
75	PZ24_RNAComposer_4	3	44	42	26	0	0	12	3	41
76	PZ24_RNAComposer_5	4	44	42	20	0	0	17	3	40
77	PZ24_SimRNA_1	3	46	43	17	0	0	17	9	43
78	PZ24_SimRNA_2	2	43	41	17	0	0	13	11	41
79	PZ24_SimRNA_3	4	42	41	23	0	0	10	5	38
80	PZ24_SimRNA_4	6	44	44	11	0	0	22	5	38
81	PZ24_SimRNA_5	4	42	40	20	0	0	14	4	38
82	PZ24_Vfold3D_1	4	47	44	15	1	0	25	2	43
83	PZ24_Vfold3D_2	4	46	45	15	0	0	25	2	42
84	PZ24_Vfold3D_3	5	47	45	10	0	0	30	2	42
85	PZ24_Vfold3D_4	4	48	47	9	3	0	30	2	44
86	PZ24_Vfold3D_5	3	46	45	11	1	0	28	3	43
87	PZ24_VfoldLA_1	4	43	39	10	0	0	23	6	39

88	PZ24_VfoldLA_2	4	44	41	12	0	0	15	13	40
89	PZ24_VfoldLA_3	5	44	40	10	0	0	17	12	39
90	PZ24_VfoldLA_4	4	44	42	14	0	0	18	8	40
91	PZ24_VfoldLA_5	6	42	40	10	0	0	14	12	36
	Average	3.78	44.37	40.03	20.58	0.10	0.00	15.34	4.57	40.59
	Standard deviation	1.28	6.57	6.75	7.64	0.42	0.00	5.87	2.32	6.98
	Median	3.00	46.00	43.00	22.00	0.00	0.00	14.00	5.00	42.00

MolProbity reports:

(a) Clash score is the number of serious steric overlaps ($> 0.4 \text{ \AA}$) per 1000 atoms.

(b) 100th percentile is the best among structures of comparable resolution; 0th percentile is the worst. For clashscore the comparative set of structures was selected in 2004, for MolProbity score in 2006.

(c) RNA backbone was recently shown to be rotameric. Outliers are RNA suites that don't fall into recognized rotamers.

Table S70. MolProbity report on the reference structures.

No.	3D RNA model	(a) Clash score	(b) Rank-ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outliers	#Probably wrong sugar puckers	(c) #Bad back-bone conformations	Total
1	PZ01_refstructure	2.03	99	5	34	0	0	1	2	42
2	PZ02_refstructure	29.34	16	7	2	0	0	1	25	35
3	PZ03_refstructure	0.73	99	0	4	0	0	2	14	20
4	PZ04_refstructure	26.15	19	0	31	0	2	10	21	64
5	PZ05_refstructure	7.95	82	0	6	0	2	1	28	37
6	PZ06_refstructure	9.74	73	0	0	0	0	3	33	36
7	PZ07_refstructure	3.02	98	0	3	0	0	0	21	24
8	PZ08_refstructure	7.04	86	1	10	0	0	3	13	27
9	PZ09_refstructure	4.39	95	0	2	0	0	0	8	10
10	PZ10_refstructure	4.17	96	0	0	0	0	2	29	31
11	PZ11_refstructure	0.00	100	1	1	0	0	5	12	19
12	PZ12_refstructure	11.35	65	0	0	0	0	2	23	25
13	PZ13_refstructure	0.00	100	0	0	0	0	0	4	4
14	PZ14_refstructure_bound	4.56	95	1	0	0	0	0	10	11
15	PZ14_refstructure_free	13.38	56	0	0	0	0	1	13	14
16	PZ15_refstructure	0.91	99	1	0	0	0	0	5	6
17	PZ17_refstructure	15.59	47	0	3	0	0	1	11	15
18	PZ18_refstructure	3.48	97	0	0	0	0	0	7	7
19	PZ19_refstructure	2.50	99	1	6	0	0	1	6	14
20	PZ20_refstructure	0.46	99	0	0	0	0	0	5	5
21	PZ21_refstructure	20.29	31	10	2	0	0	0	16	28
22	PZ24_refstructure	0.28	99	0	0	0	0	1	10	11

	Average	7.61	79.55	1.23	4.73	0.00	0.18	1.55	14.36	22.05
	Standard deviation	8.54	28.01	2.64	9.37	0.00	0.59	2.28	8.96	14.77
	Median	4.28	95.50	0.00	1.50	0.00	0.00	1.00	12.50	19.50

Table S71. MolProbity report on structures in Puzzle 01.

No.	3D RNA model	(a) Clash score	(b) Ranking	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outliers	#Probably wrong sugar puckers	(c) #Bad backbone conformations	Total
1	PZ01_Das_1	0.00	100	0	0	0	0	0	3	3
2	PZ01_Das_4	0.00	100	0	0	0	0	0	3	3
3	PZ01_Das_2	0.68	99	0	2	0	0	0	3	5
4	PZ01_Das_3	0.00	100	0	1	0	0	0	4	5
5	PZ01_Das_5	0.00	100	0	4	0	0	0	5	9
6	PZ01_Chen_1	0.00	100	2	17	0	0	0	2	21
7	PZ01_Bujnicki_1	0.00	100	0	18	1	0	2	3	24
8	PZ01_refstructure	2.03	99	5	34	0	0	1	2	42
9	PZ01_Dokholyan_1	26.33	19	3	51	0	0	0	6	60
10	PZ01_Bujnicki_3	47.30	5	33	50	0	0	0	0	83
11	PZ01_Bujnicki_5	65.72	1	29	52	0	0	1	2	84
12	PZ01_Bujnicki_4	69.11	1	30	61	0	0	0	1	92
13	PZ01_Santalucia_1	25.00	22	65	26	0	0	1	8	100
14	PZ01_Bujnicki_2	60.09	2	42	74	0	2	1	4	123
15	PZ01_Major_1	55.48	3	84	276	0	0	7	25	392
	Average	23.45	56.73	19.53	44.40	0.07	0.13	0.87	4.73	69.73
	Standard deviation	28.15	47.96	26.98	68.70	0.26	0.52	1.81	5.95	98.12
	Median	2.03	99.00	3.00	26.00	0.00	0.00	0.00	3.00	42.00

Table S72. MolProbity report on structures in Puzzle 02.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar pucker- ers	(c) #Bad back- bone confor- mations	Total
1	PZ02_Das_1	14.23	53	0	0	0	0	1	23	24
2	PZ02_Das_2	17.33	40	0	1	0	0	1	26	28
3	PZ02_Das_4	16.71	43	1	1	0	0	1	26	29
4	PZ02_Das_3	17.33	40	0	0	0	0	2	31	33
5	PZ02_refstructure	29.34	16	7	2	0	0	1	25	35
6	PZ02_Das_5	17.95	38	2	3	0	0	1	29	35
7	PZ02_Santalucia_1	18.29	37	36	22	0	0	0	2	60
8	PZ02_Bujnicki_3	0.31	99	0	71	0	0	3	17	91
9	PZ02_Bujnicki_2	12.69	60	0	71	0	0	3	25	99
10	PZ02_Dokholyan_1	12.07	62	6	98	0	0	4	34	142
11	PZ02_Bujnicki_1	10.83	67	4	103	1	4	6	43	161
12	PZ02_Wildauer_1	153.39	0	23	63	0	0	15	68	169
13	PZ02_Chen_1	21.05	30	22	135	2	3	5	28	195
14	PZ02_Major_1	125.58	0	140	182	0	12	0	64	398
	Average	33.36	41.79	17.21	53.71	0.21	1.36	3.07	31.50	107.07
	Standard deviation	45.73	26.48	37.07	59.30	0.58	3.32	3.89	17.19	103.03
	Median	17.33	40.00	3.00	42.50	0.00	0.00	1.50	27.00	75.50

Table S73. MolProbity report on structures in Puzzle 03.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar pucker- ers	(c) #Bad back- bone confor- mations	Total
1	PZ03_Das_1	0.00	100	1	3	0	0	1	5	10
2	PZ03_Das_2	0.74	99	1	2	0	0	0	9	12
3	PZ03_Das_3	1.10	99	0	4	0	0	0	12	16
4	PZ03_Das_5	1.10	99	2	2	0	0	2	10	16
5	PZ03_Das_4	2.21	99	1	6	0	0	2	11	20
6	PZ03_refstructure	0.73	99	0	4	0	0	2	14	20
7	PZ03_Bujnicki_2	3.68	97	0	38	0	0	1	7	46
8	PZ03_Chen_1	0.00	100	1	74	0	0	2	22	99
9	PZ03_Bujnicki_1	9.20	75	1	82	0	0	2	19	104
10	PZ03_Dokholyan_2	32.01	13	1	108	0	0	7	30	146
11	PZ03_Dokholyan_1	32.74	13	1	113	0	0	8	28	150
12	PZ03_Major_2	76.16	0	167	546	1	1	35	62	812
13	PZ03_Major_1	61.83	2	176	617	0	3	24	65	885
	Average	17.04	68.85	27.08	123.00	0.08	0.31	6.62	22.62	179.69
	Standard deviation	25.90	43.55	64.13	208.22	0.28	0.85	10.67	19.72	301.51
	Median	2.21	99.00	1.00	38.00	0.00	0.00	2.00	14.00	46.00

Table S74. MolProbity report on structures in Puzzle 04.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar pucker- ers	(c) #Bad back- bone confor- mations	Total
1	PZ04_Das_1	8.60	79	1	7	0	0	0	3	11
2	PZ04_Das_2	8.60	79	1	7	0	0	0	3	11
3	PZ04_Das_3	8.60	79	1	7	0	0	0	3	11
4	PZ04_Das_4	8.60	79	1	7	0	0	0	3	11
5	PZ04_Das_5	8.60	79	1	7	0	0	0	3	11

6	PZ04_Adamiak_3	18.44	36	0	0	0	0	8	45	53
7	PZ04_Adamiak_2	19.91	33	0	0	0	0	8	46	54
8	PZ04_refstructure	26.15	19	0	31	0	2	10	21	64
9	PZ04_Adamiak_1	17.70	39	0	2	0	0	8	59	69
10	PZ04_Adamiak_5	69.08	1	0	0	0	0	7	68	75
11	PZ04_Santalucia_1	33.19	13	30	23	0	3	5	22	83
12	PZ04_Adamiak_4	69.08	1	0	0	0	0	8	79	87
13	PZ04_Bujnicki_3	22.13	27	29	49	0	1	8	27	114
14	PZ04_Bujnicki_4	25.82	20	29	45	0	1	10	29	114
15	PZ04_Bujnicki_5	21.15	30	29	49	0	1	9	27	115
16	PZ04_Bujnicki_2	25.82	20	30	46	0	1	10	29	116
17	PZ04_Dokholyan_1	12.54	60	0	75	1	3	10	27	116
18	PZ04_Dokholyan_2	12.54	60	0	75	1	3	10	27	116
19	PZ04_Bujnicki_1	20.90	30	31	52	0	1	8	26	118
20	PZ04_Mikolajczak_1	29.53	16	31	59	0	4	14	30	138
21	PZ04_Chen_1	1.97	99	1	106	0	0	9	23	139
22	PZ04_Chen_4	3.45	97	1	119	0	1	9	20	150
23	PZ04_Chen_6	2.46	99	1	122	0	1	9	19	152
24	PZ04_Major_1	0.49	99	0	108	1	0	8	35	152
25	PZ04_Chen_10	1.97	99	1	124	0	1	9	19	154
26	PZ04_Chen_8	3.46	97	2	126	0	0	9	21	158
27	PZ04_Chen_2	2.22	99	1	132	0	1	9	20	163
28	PZ04_Chen_7	2.96	98	1	130	0	1	10	22	164
29	PZ04_Chen_3	2.46	99	2	136	0	1	9	20	168
30	PZ04_Chen_9	1.98	99	4	141	0	1	9	19	174
31	PZ04_Chen_5	2.71	98	8	150	0	1	9	19	187
	Average	15.91	60.74	7.61	62.42	0.10	0.90	7.48	26.26	104.77
	Standard deviation	17.19	35.91	12.31	53.46	0.30	1.08	3.61	17.87	55.12
	Median	8.60	79.00	1.00	49.00	0.00	1.00	9.00	22.00	116.00

Table S75. MolProbity report on structures in Puzzle 05.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahe- dral geome- try outliers	#Probably wrong sugar puckers	(c) #Bad back- bone confor- mations	Total
1	PZ05_refstructure	7.95	82	0	6	0	2	1	28	37
2	PZ05_Adamiak_1	16.56	43	0	2	0	0	6	45	53
3	PZ05_Bujnicki_1	1.49	99	0	45	0	10	0	35	90
4	PZ05_Chen_6	0.33	99	0	23	5	0	16	46	90
5	PZ05_Chen_7	0.00	100	0	29	5	0	14	47	95
6	PZ05_Das_2	9.93	72	10	50	0	0	2	33	95
7	PZ05_Bujnicki_4	1.32	99	0	42	0	13	3	40	98
8	PZ05_Bujnicki_5	0.99	99	0	52	0	9	2	41	104
9	PZ05_Das_1	11.75	64	13	46	0	0	6	44	109
10	PZ05_Bujnicki_3	6.13	90	0	53	0	10	2	47	112
11	PZ05_Chen_3	11.42	65	24	40	4	2	10	43	123
12	PZ05_Bujnicki_2	2.65	98	0	67	0	19	1	44	131
13	PZ05_Chen_1	5.63	92	10	53	5	5	14	47	134
14	PZ05_Chen_4	9.11	76	20	53	5	6	15	49	148
15	PZ05_Chen_5	14.24	53	28	54	6	10	14	41	153
16	PZ05_Chen_2	8.94	77	21	58	5	6	18	56	164
17	PZ05_Dokholyan_3	10.43	69	0	242	0	0	7	57	306
18	PZ05_Dokholyan_5	10.93	67	0	242	0	0	13	64	319
19	PZ05_Xiao_1	0.00	100	23	206	2	2	16	72	321
20	PZ05_Dokholyan_2	11.26	66	0	251	0	0	13	59	323
21	PZ05_Dokholyan_4	11.26	66	0	251	0	0	13	59	323
22	PZ05_Dokholyan_1	9.77	73	0	270	0	0	13	58	341
23	PZ05_Dokholyan_6	14.24	53	4	284	0	1	14	50	353
24	PZ05_Dokholyan_7	10.76	68	11	284	0	0	14	55	364
25	PZ05_Dokholyan_8	11.59	64	7	315	0	0	18	67	407
26	PZ05_Xiao_2	0.17	99	57	270	2	3	29	82	443
	Average	7.65	78.19	8.77	126.46	1.50	3.77	10.54	50.35	201.38
	Standard deviation	5.14	17.46	13.47	111.25	2.25	5.14	7.04	12.29	125.48
	Median	9.44	74.50	0.00	53.50	0.00	1.50	13.00	47.00	141.00

Table S76. MolProbity report on structures in Puzzle 06.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar pucker- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ06_refstructure	9.74	73	0	0	0	0	3	33	36
2	PZ06_Bujnicki_1	0.55	99	0	33	0	9	1	19	62
3	PZ06_Bujnicki_3	1.10	99	0	32	0	7	1	26	66
4	PZ06_Bujnicki_4	1.83	99	0	31	0	8	0	30	69
5	PZ06_Das_5	14.67	51	7	24	0	0	2	41	74
6	PZ06_Bujnicki_2	1.28	99	0	40	0	9	1	25	75
7	PZ06_Das_8	15.22	48	7	24	0	0	3	41	75
8	PZ06_Das_9	20.54	31	11	29	0	0	4	33	77
9	PZ06_Das_10	23.67	23	13	26	0	0	4	38	81
10	PZ06_Das_2	20.55	31	12	31	0	0	3	35	81
11	PZ06_Das_4	27.88	17	12	37	0	0	4	37	90
12	PZ06_Das_1	28.99	16	12	37	0	0	5	37	91
13	PZ06_Das_6	29.72	16	13	40	0	0	5	37	95
14	PZ06_Das_7	15.96	46	10	29	0	0	5	56	100
15	PZ06_Das_3	18.71	36	10	27	0	0	4	60	101
16	PZ06_Chen_6	2.20	99	9	73	0	1	6	52	141
17	PZ06_Chen_1	0.37	99	1	63	0	0	18	69	151
18	PZ06_Chen_7	9.90	72	18	57	0	5	8	70	158
19	PZ06_Major_4	0.92	99	0	90	4	0	13	57	164
20	PZ06_Major_6	0.73	99	1	94	3	0	16	50	164
21	PZ06_Chen_4	1.83	99	5	97	0	0	8	57	167
22	PZ06_Major_1	0.73	99	0	89	4	0	16	61	170
23	PZ06_Chen_2	0.18	99	2	70	0	0	12	93	177
24	PZ06_Major_3	0.92	99	0	104	5	0	16	53	178
25	PZ06_Major_7	1.10	99	0	114	4	0	13	54	185
26	PZ06_Major_2	0.55	99	0	102	7	0	17	62	188
27	PZ06_Chen_3	0.55	99	8	83	0	0	12	96	199

28	PZ06_Major_5	0.73	99	0	129	5	0	18	59	211
29	PZ06_Chen_5	17.43	40	34	150	0	6	15	57	262
30	PZ06_Dokholyan_5	10.46	69	5	240	0	0	9	47	301
31	PZ06_Dokholyan_2	9.36	75	2	248	0	0	12	51	313
32	PZ06_Dokholyan_1	11.01	67	5	246	0	0	10	54	315
33	PZ06_Dokholyan_3	9.17	76	3	259	0	0	9	46	317
34	PZ06_Dokholyan_6	14.68	51	0	255	0	0	17	59	331
35	PZ06_Dokholyan_4	9.54	74	7	278	0	0	9	58	352
	Average	9.51	71.31	5.91	93.74	0.91	1.29	8.54	50.09	160.49
	Standard deviation	9.42	30.31	7.14	81.82	1.93	2.87	5.73	16.93	90.67
	Median	9.36	75.00	5.00	70.00	0.00	0.00	8.00	52.00	158.00

Table S77. MolProbity report on structures in Puzzle 07.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar pucker- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ07_refstructure	3.02	98	0	3	0	0	0	21	24
2	PZ07_Adamiak_5	9.91	72	0	0	0	0	1	46	47
3	PZ07_Adamiak_4	14.61	51	0	1	0	0	3	45	49
4	PZ07_Adamiak_1	14.44	52	0	0	0	0	2	59	61
5	PZ07_Adamiak_2	14.95	50	0	0	0	0	4	57	61
6	PZ07_Adamiak_3	17.64	39	0	0	0	0	5	56	61
7	PZ07_Das_5	7.39	85	1	8	0	0	4	48	61
8	PZ07_Das_8	7.73	83	4	14	0	0	6	41	65
9	PZ07_Das_7	13.29	57	4	13	0	0	6	54	77
10	PZ07_Das_2	7.89	82	6	21	0	1	6	45	79
11	PZ07_Das_3	8.40	80	3	21	0	0	6	49	79
12	PZ07_Das_1	11.25	66	4	21	0	0	8	47	80
13	PZ07_Das_6	10.58	68	4	16	0	1	6	57	84
14	PZ07_Bujnicki_4	1.01	99	0	45	7	1	9	24	86
15	PZ07_Bujnicki_5	1.01	99	0	48	7	1	9	24	89
16	PZ07_Das_4	9.57	74	7	23	0	2	8	57	97

17	PZ07_Bujnicki_7	1.01	99	0	61	5	0	9	31	106
18	PZ07_Bujnicki_3	0.50	99	1	56	9	0	14	30	110
19	PZ07_Bujnicki_2	0.34	99	0	69	6	4	10	25	114
20	PZ07_Bujnicki_1	1.01	99	0	71	7	3	9	25	115
21	PZ07_Bujnicki_6	0.50	99	1	63	10	0	15	34	123
22	PZ07_Chen_8	55.32	3	89	167	0	0	6	26	288
23	PZ07_Chen_9	64.15	1	90	167	0	0	6	26	289
24	PZ07_Chen_10	47.47	4	91	169	0	0	7	24	291
25	PZ07_Dokholyan_2	8.73	78	0	231	0	0	6	56	293
26	PZ07_Chen_5	61.90	2	96	177	0	0	4	25	302
27	PZ07_Chen_3	53.52	3	97	181	0	0	6	23	307
28	PZ07_Chen_6	60.76	2	96	179	0	0	5	27	307
29	PZ07_Chen_2	59.79	2	88	178	0	0	10	32	308
30	PZ07_Chen_7	71.32	1	86	185	0	0	10	31	312
31	PZ07_Chen_4	65.65	1	96	191	0	0	7	23	317
32	PZ07_Dokholyan_1	7.05	86	0	253	1	0	9	61	324
33	PZ07_Ding_10	11.25	66	9	280	0	0	7	46	342
34	PZ07_Ding_8	13.77	55	5	278	0	0	8	57	348
35	PZ07_Ding_4	14.28	52	7	274	0	0	12	59	352
36	PZ07_Ding_3	15.45	48	4	287	0	0	14	54	359
37	PZ07_Ding_9	11.08	66	10	275	0	0	12	64	361
38	PZ07_Ding_1	14.61	51	8	286	0	1	17	51	363
39	PZ07_Ding_5	11.76	64	5	284	0	0	13	63	365
40	PZ07_Ding_6	10.92	67	8	282	0	0	12	68	370
41	PZ07_Ding_7	12.26	62	6	291	0	0	12	61	370
42	PZ07_Ding_2	10.92	67	6	304	0	0	8	60	378
43	PZ07_Chen_1	0.00	100	281	349	3	0	22	91	746
44	PZ07_Major_4	0.00	100	61	577	4	5	25	91	763
45	PZ07_Major_7	0.00	100	61	595	2	7	26	89	780
46	PZ07_Major_5	0.00	100	60	603	2	6	24	89	784
47	PZ07_Major_8	0.00	100	55	643	0	7	23	116	844
48	PZ07_Major_6	0.00	100	91	641	1	6	33	100	872
49	PZ07_Major_1	0.00	100	62	669	2	8	29	116	886

50	PZ07_Major_9	0.00	100	84	683	2	12	33	110	924
51	PZ07_Major_3	0.00	100	90	680	3	12	36	105	926
52	PZ07_Major_10	0.00	100	95	700	2	10	33	111	951
53	PZ07_Major_2	0.00	100	91	715	3	15	29	115	968
	Average	15.81	66.62	37.04	232.60	1.43	1.92	12.15	55.57	340.72
	Standard deviation	21.08	34.59	52.27	229.65	2.58	3.69	9.31	28.35	293.59
	Median	9.91	72.00	6.00	179.00	0.00	0.00	9.00	54.00	307.00

Table S78. MolProbity report on structures in Puzzle 08.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar puck- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ08_refstructure	7.04	86	1	10	0	0	3	13	27
2	PZ08_Adamiak_1	10.25	70	0	0	0	0	1	19	20
3	PZ08_Adamiak_2	11.21	66	0	0	0	0	1	24	25
4	PZ08_Bujnicki_1	8.47	79	14	146	2	3	8	23	196
5	PZ08_Bujnicki_10	9.38	74	14	133	8	1	16	25	197
6	PZ08_Bujnicki_2	12.81	59	16	225	0	6	8	26	281
7	PZ08_Bujnicki_3	29.32	16	20	180	0	5	6	22	233
8	PZ08_Bujnicki_4	26.06	20	13	183	1	2	6	20	225
9	PZ08_Bujnicki_5	18.89	35	17	180	1	3	7	25	233
10	PZ08_Bujnicki_6	11.85	63	12	150	3	2	9	24	200
11	PZ08_Bujnicki_7	0.96	99	0	36	8	0	9	20	73
12	PZ08_Bujnicki_8	5.76	91	7	92	7	2	10	19	137
13	PZ08_Bujnicki_9	4.80	94	8	72	2	0	10	22	114
14	PZ08_Chen_1	38.45	9	25	87	1	2	0	41	156
15	PZ08_Chen_10	24.90	22	11	50	2	0	0	40	103
16	PZ08_Chen_2	24.90	22	3	37	0	0	0	34	74
17	PZ08_Chen_3	30.55	15	8	59	0	1	0	37	105
18	PZ08_Chen_4	27.54	18	5	55	0	0	0	37	97
19	PZ08_Chen_5	30.55	15	5	53	0	0	0	29	87
20	PZ08_Chen_6	37.34	9	133	205	0	1	0	52	391

21	PZ08_Chen_7	63.37	1	45	117	0	4	0	39	205
22	PZ08_Chen_8	34.70	11	164	181	1	0	0	46	392
23	PZ08_Chen_9	29.80	16	167	236	1	0	0	50	454
24	PZ08_Das_1	14.41	52	1	4	0	0	1	13	19
25	PZ08_Das_2	12.81	59	1	4	0	0	1	15	21
26	PZ08_Das_3	13.77	55	2	5	0	0	0	16	23
27	PZ08_Das_4	7.36	85	1	5	0	0	1	23	30
28	PZ08_Das_5	7.68	83	1	5	0	0	3	28	37
29	PZ08_Das_6	5.44	92	0	5	0	0	0	27	32
30	PZ08_Ding_1	14.09	53	4	148	0	0	14	33	199
31	PZ08_Ding_10	12.49	61	2	152	0	0	12	35	201
32	PZ08_Ding_2	17.61	40	2	160	0	0	6	35	203
33	PZ08_Ding_3	14.41	52	4	164	0	0	11	31	210
34	PZ08_Ding_4	10.89	67	1	154	0	0	5	29	189
35	PZ08_Ding_5	12.17	62	2	141	0	0	8	36	187
36	PZ08_Ding_6	7.36	85	3	147	0	0	9	29	188
37	PZ08_Ding_7	11.21	66	4	147	0	0	7	30	188
38	PZ08_Ding_8	13.77	55	3	137	0	0	11	32	183
39	PZ08_Ding_9	13.45	56	4	162	0	0	6	33	205
40	PZ08_Dokholyan_1	7.36	85	0	130	0	0	5	22	157
41	PZ08_Dokholyan_2	11.53	65	0	136	0	0	4	30	170
42	PZ08_Dokholyan_3	6.40	89	0	119	0	0	6	31	156
43	PZ08_Dokholyan_4	9.61	73	0	127	0	0	3	31	161
	Average	16.81	54.07	16.81	105.56	0.86	0.74	4.81	28.98	157.77
	Standard deviation	12.06	28.70	39.36	70.10	2.02	1.47	4.51	9.14	102.08
	Median	12.81	59.00	4.00	130.00	0.00	0.00	5.00	29.00	170.00

Table S79. MolProbity report on structures in Puzzle 09.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar pucker- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ09_refstructure	4.39	95	0	2	0	0	0	8	10
2	PZ09_Das_8	2.20	99	0	3	0	0	0	11	14
3	PZ09_Das_2	2.20	99	2	6	1	0	0	6	15
4	PZ09_Chen_2	26.42	19	6	6	0	0	0	5	17
5	PZ09_Das_6	9.22	75	1	1	0	0	1	14	17
6	PZ09_Das_9	3.07	98	1	5	0	0	1	12	19
7	PZ09_Das_4	3.51	97	2	5	1	0	0	12	20
8	PZ09_Das_7	9.22	75	1	1	0	0	4	14	20
9	PZ09_Das_5	4.83	94	2	6	1	0	1	11	21
10	PZ09_Das_1	4.83	94	2	7	1	0	0	12	22
11	PZ09_Das_3	15.81	46	2	8	1	0	2	10	23
12	PZ09_Chen_4	23.76	23	6	8	0	1	2	8	25
13	PZ09_Chen_5	33.01	13	7	10	0	0	8	17	42
14	PZ09_Chen_3	29.49	16	8	27	0	1	2	8	46
15	PZ09_Chen_1	34.73	11	10	38	0	0	0	4	52
16	PZ09_Chen_7	18.08	37	11	36	0	0	0	5	52
17	PZ09_Chen_8	65.82	1	15	52	0	0	0	4	71
18	PZ09_Bujnicki_3	1.32	99	0	26	12	0	18	31	87
19	PZ09_Bujnicki_4	1.32	99	0	26	12	0	18	31	87
20	PZ09_Bujnicki_5	1.32	99	0	26	12	0	18	31	87
21	PZ09_Chen_6	64.62	1	20	66	0	0	1	9	96
22	PZ09_Dokholyan_4	4.83	94	0	88	0	0	3	20	111
23	PZ09_Ding_5	14.05	53	2	99	0	0	1	17	119
24	PZ09_Dokholyan_1	7.91	82	0	96	0	0	7	28	131
25	PZ09_Dokholyan_3	6.59	89	0	103	0	0	8	24	135
26	PZ09_Ding_10	8.78	78	2	109	0	0	4	22	137
27	PZ09_Ding_9	10.54	68	6	109	0	1	2	19	137
28	PZ09_Ding_6	10.54	68	1	116	0	0	4	21	142

29	PZ09_Ding_7	9.66	73	2	111	0	0	6	24	143
30	PZ09_Dokholyan_2	7.03	86	0	120	0	0	4	20	144
31	PZ09_Ding_8	14.05	53	5	123	0	0	3	16	147
32	PZ09_Ding_4	12.30	61	5	114	0	0	7	22	148
33	PZ09_Ding_1	14.93	50	2	120	0	0	6	22	150
34	PZ09_Ding_3	10.54	68	6	123	0	0	4	17	150
35	PZ09_Ding_2	14.05	53	3	126	0	0	8	26	163
	Average	14.43	64.74	3.71	54.91	1.17	0.09	4.09	16.03	80.00
	Standard deviation	15.48	32.08	4.60	49.20	3.38	0.28	5.05	8.11	54.89
	Median	9.66	73.00	2.00	36.00	0.00	0.00	2.00	16.00	87.00

Table S80. MolProbity report on structures in Puzzle 10.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar puck- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ10_refstructure	4.17	96	0	0	0	0	2	29	31
2	PZ10_Das_5	13.24	57	5	27	0	0	6	40	78
3	PZ10_Das_2	13.61	55	7	32	0	0	6	39	84
4	PZ10_Das_3	13.79	55	8	31	0	0	6	41	86
5	PZ10_Das_4	12.34	61	8	30	0	0	8	40	86
6	PZ10_Das_1	14.15	53	6	34	0	1	9	46	96
7	PZ10_Bujnicki_4	0.29	99	0	94	23	1	24	54	196
8	PZ10_Bujnicki_1	1.17	99	0	98	26	0	27	56	207
9	PZ10_Bujnicki_7	1.58	99	0	116	22	0	21	51	210
10	PZ10_Bujnicki_2	1.75	99	0	99	24	1	28	59	211
11	PZ10_Bujnicki_5	1.46	99	2	109	23	1	26	51	212
12	PZ10_Bujnicki_6	1.46	99	1	108	24	1	25	57	216
13	PZ10_Bujnicki_3	0.29	99	2	88	32	0	33	64	219
14	PZ10_Bujnicki_8	2.34	99	0	128	18	2	21	53	222
15	PZ10_Bujnicki_9	0.32	99	0	117	24	1	25	62	229
16	PZ10_Bujnicki_10	0.00	100	1	123	30	1	30	68	253
17	PZ10_Chen_1	9.08	77	36	146	2	5	21	79	289

18	PZ10_Dokholyan_2	11.61	64	8	249	0	0	16	61	334
19	PZ10_Dokholyan_3	9.98	71	12	265	0	0	14	56	347
20	PZ10_Dokholyan_5	11.79	64	3	272	0	0	11	62	348
21	PZ10_Dokholyan_9	13.43	56	7	270	0	0	14	69	360
22	PZ10_Dokholyan_7	8.71	78	10	279	0	0	19	53	361
23	PZ10_Dokholyan_1	14.70	51	9	293	0	0	12	48	362
24	PZ10_Dokholyan_8	12.70	60	7	303	0	0	8	46	364
25	PZ10_Dokholyan_4	12.34	61	8	292	0	1	13	54	368
26	PZ10_Dokholyan_6	9.25	75	6	301	1	0	16	63	387
27	PZ10_Dokholyan_10	15.06	49	5	300	1	0	18	65	389
	Average	7.80	76.81	5.59	155.70	9.26	0.56	17.00	54.30	242.41
	Standard deviation	5.71	19.87	7.13	105.64	12.22	1.05	8.48	11.02	111.51
	Median	9.25	75.00	5.00	117.00	0.00	0.00	16.00	54.00	222.00

Table S81. MolProbity report on structures in Puzzle 11.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar pucker- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ11_Adamiak_3	6.59	89	0	0	0	0	0	9	9
2	PZ11_Adamiak_9	10.97	67	0	0	0	0	1	9	10
3	PZ11_Adamiak_5	6.58	89	0	0	0	0	1	11	12
4	PZ11_Adamiak_4	10.42	69	0	0	0	0	1	12	13
5	PZ11_Chén_10	8.23	81	0	1	0	0	0	12	13
6	PZ11_Chén_6	17.55	40	1	5	0	0	1	6	13
7	PZ11_Chén_7	12.61	60	1	4	0	0	2	7	14
8	PZ11_Chén_8	9.87	72	0	1	0	0	1	12	14
9	PZ11_Adamiak_1	8.23	81	0	0	0	0	0	15	15
10	PZ11_Adamiak_6	10.97	67	0	0	0	0	3	12	15
11	PZ11_Adamiak_2	9.87	72	0	0	0	0	3	13	16
12	PZ11_Das_10	10.42	69	0	0	0	0	2	14	16
13	PZ11_Adamiak_10	9.33	75	0	0	0	0	0	18	18
14	PZ11_Adamiak_8	9.33	75	0	0	0	0	2	16	18

15	PZ11_Adamiak_7	7.13	86	0	0	0	0	1	18	19
16	PZ11_refstructure	0.00	100	1	1	0	0	5	12	19
17	PZ11_Chén_9	14.80	50	1	5	0	0	2	12	20
18	PZ11_Das_2	12.07	62	3	7	0	0	2	8	20
19	PZ11_Das_3	8.78	78	2	5	0	0	2	12	21
20	PZ11_Das_5	10.97	67	2	3	0	0	3	13	21
21	PZ11_Das_7	9.33	75	4	6	0	0	2	9	21
22	PZ11_Das_8	7.68	83	2	5	0	0	2	12	21
23	PZ11_Das_1	8.23	81	3	5	0	0	3	11	22
24	PZ11_Das_9	12.07	62	0	2	0	0	3	17	22
25	PZ11_Bujnicki_5	0.00	100	0	18	2	0	1	3	24
26	PZ11_Bujnicki_8	0.00	100	0	13	3	0	1	7	24
27	PZ11_Bujnicki_1	0.55	99	0	13	2	0	4	8	27
28	PZ11_Bujnicki_7	1.10	99	0	21	2	0	1	5	29
29	PZ11_Das_6	8.78	78	2	7	0	0	3	17	29
30	PZ11_Das_4	10.42	69	2	7	0	1	5	17	32
31	PZ11_Bujnicki_2	0.00	100	0	16	3	0	4	10	33
32	PZ11_Bujnicki_6	0.55	99	0	23	3	0	1	7	34
33	PZ11_Bujnicki_9	1.10	99	0	20	4	0	2	10	36
34	PZ11_Bujnicki_3	0.00	100	0	17	5	0	7	13	42
35	PZ11_Chén_4	0.55	99	0	20	0	0	5	20	45
36	PZ11_Chén_1	1.10	99	1	24	0	0	2	19	46
37	PZ11_Chén_3	1.10	99	2	21	0	0	3	21	47
38	PZ11_Bujnicki_10	0.00	100	0	20	7	0	7	14	48
39	PZ11_Xiao_3	1.10	99	1	40	0	0	1	10	52
40	PZ11_Chén_2	2.74	98	1	27	0	0	5	20	53
41	PZ11_Chén_5	0.55	99	3	30	0	0	3	18	54
42	PZ11_Xiao_2	1.10	99	1	40	0	0	2	14	57
43	PZ11_Xiao_1	4.39	95	1	47	0	0	5	19	72
44	PZ11_Ding_3	13.17	57	3	78	0	0	3	15	99
45	PZ11_Ding_1	11.52	65	2	82	0	0	6	18	108
46	PZ11_Ding_10	13.71	55	3	85	0	0	5	17	110
47	PZ11_Ding_9	9.87	72	0	93	0	0	3	17	113

48	PZ11_Ding_6	10.97	67	0	94	0	0	5	17	116
49	PZ11_Ding_8	9.87	72	1	88	0	0	5	23	117
50	PZ11_Ding_7	14.26	53	2	100	0	0	6	15	123
51	PZ11_Ding_2	14.26	53	2	94	0	0	6	24	126
52	PZ11_Ding_4	9.87	72	2	98	0	0	7	25	132
53	PZ11_Ding_5	12.62	60	1	100	0	0	7	26	134
54	PZ11_Bujnicki_4	2.78	98	57	205	5	0	13	27	307
	Average	7.22	79.70	1.98	29.46	0.67	0.02	3.15	14.19	49.46
	Standard deviation	5.09	17.00	7.71	41.35	1.57	0.14	2.44	5.44	52.21
	Median	8.78	78.00	1.00	13.00	0.00	0.00	3.00	13.50	28.00

Table S82. MolProbity report on structures in Puzzle 12.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar pucker- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ12_Adamiak_3	9.15	76	0	0	0	0	0	18	18
2	PZ12_Bujnicki_7	18.55	36	0	3	0	1	0	18	22
3	PZ12_Adamiak_2	7.91	82	0	0	0	0	0	24	24
4	PZ12_refstructure	11.35	65	0	0	0	0	2	23	25
5	PZ12_Bujnicki_10	27.94	17	0	0	0	0	2	23	25
6	PZ12_Bujnicki_8	33.14	13	0	2	0	1	2	22	27
7	PZ12_Bujnicki_4	22.01	27	0	3	0	1	0	24	28
8	PZ12_Bujnicki_6	21.51	29	0	0	0	0	1	27	28
9	PZ12_Bujnicki_9	25.72	20	0	6	0	0	2	20	28
10	PZ12_Bujnicki_1	25.22	21	0	0	0	0	2	32	34
11	PZ12_Adamiak_1	10.14	71	0	0	0	0	3	32	35
12	PZ12_Bujnicki_3	27.94	17	0	2	0	1	3	29	35
13	PZ12_Bujnicki_5	28.19	17	0	6	0	0	3	27	36
14	PZ12_Das_8	2.97	98	0	2	0	0	1	37	40
15	PZ12_Das_10	3.22	97	1	8	0	0	2	31	42
16	PZ12_Das_9	3.46	97	0	10	0	0	1	32	43
17	PZ12_Das_5	8.65	79	0	2	0	0	3	45	50

18	PZ12_Das_1	8.16	81	1	7	0	1	3	43	55
19	PZ12_Das_2	10.14	71	1	11	0	0	2	43	57
20	PZ12_Das_3	11.62	64	0	7	0	1	1	52	61
21	PZ12_Das_6	8.65	79	2	11	0	0	3	47	63
22	PZ12_Das_4	7.91	82	4	8	0	0	5	51	68
23	PZ12_Das_7	12.61	60	2	15	0	0	4	54	75
24	PZ12_Bujnicki_2	11.13	66	0	4	0	0	5	75	84
25	PZ12_Chen_1	0.00	100	3	44	0	1	8	45	101
26	PZ12_Chen_3	0.00	100	12	61	0	1	10	26	110
27	PZ12_Chen_2	0.00	100	2	47	2	1	10	52	114
28	PZ12_Chen_4	0.00	100	17	64	0	1	11	36	129
29	PZ12_Chen_7	0.00	100	12	72	1	3	12	31	131
30	PZ12_Weeks_1	6.68	88	0	105	0	0	4	23	132
31	PZ12_Chen_6	0.00	100	23	72	0	1	12	32	140
32	PZ12_Weeks_2	9.64	73	0	107	0	0	4	31	142
33	PZ12_Weeks_3	8.16	81	0	113	0	0	6	36	155
34	PZ12_Chen_5	0.00	100	20	91	0	2	12	31	156
35	PZ12_Chen_9	0.00	100	33	90	2	2	13	40	180
36	PZ12_Chen_8	0.00	100	39	126	0	4	15	33	217
37	PZ12_Chen_10	0.00	100	48	117	3	6	12	35	221
38	PZ12_Ding_3	16.33	44	5	181	0	0	7	48	241
39	PZ12_Ding_6	15.33	48	3	190	0	0	11	40	244
40	PZ12_Ding_10	12.12	62	6	202	0	1	9	32	250
41	PZ12_Ding_5	9.39	74	6	196	0	0	9	40	251
42	PZ12_Ding_7	10.14	71	5	200	1	0	7	40	253
43	PZ12_Ding_1	14.84	50	6	205	0	0	8	38	257
44	PZ12_Ding_11	11.38	65	5	202	0	0	11	43	261
45	PZ12_Ding_4	13.11	57	4	207	0	0	14	40	265
46	PZ12_Ding_12	12.61	60	8	216	0	0	10	42	276
47	PZ12_Ding_2	11.87	63	6	204	0	0	12	56	278
48	PZ12_Ding_9	12.86	59	5	214	0	0	15	45	279
49	PZ12_Ding_8	13.85	54	9	219	0	0	10	42	280
50	PZ12_Xiao_3	20.05	32	29	224	6	5	29	63	356

51	PZ12_Xiao_1	45.04	5	72	312	3	8	28	66	489
52	PZ12_Xiao_2	50.45	4	72	301	6	6	38	70	493
	Average	12.52	64.52	8.87	86.33	0.46	0.92	7.63	38.17	142.38
	Standard deviation	11.11	29.56	16.57	94.02	1.32	1.78	7.60	13.08	119.52
	Median	10.64	68.50	2.00	54.00	0.00	0.00	5.50	36.50	112.00

Table S83. MolProbity report on structures in Puzzle 13.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry out- liers	#Probably wrong sugar puck- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ13_refstructure	0.00	100	0	0	0	0	0	4	4
2	PZ13_Adamiak_1	6.07	90	0	0	0	0	2	15	17
3	PZ13_Das_2	4.34	96	0	2	0	0	1	16	19
4	PZ13_Das_4	8.68	78	0	5	0	0	2	18	25
5	PZ13_Das_9	11.71	64	0	0	0	0	3	22	25
6	PZ13_Das_1	5.21	93	0	5	0	0	2	19	26
7	PZ13_Das_10	5.64	92	0	3	0	0	2	21	26
8	PZ13_Das_6	8.68	78	0	1	0	0	1	25	27
9	PZ13_Das_8	4.77	94	1	2	0	0	3	23	29
10	PZ13_Das_7	10.85	67	0	3	0	1	4	25	33
11	PZ13_Das_5	15.18	49	0	7	0	0	6	28	41
12	PZ13_Das_3	6.07	90	2	7	6	1	4	25	45
13	PZ13_Chén_6	0.00	100	6	27	1	0	4	26	64
14	PZ13_Bujnicki_8	1.74	99	0	49	1	0	5	14	69
15	PZ13_Chén_1	0.00	100	1	28	2	0	12	38	81
16	PZ13_Chén_3	1.74	99	4	34	2	0	10	33	83
17	PZ13_Bujnicki_10	3.04	98	0	64	5	1	7	21	98
18	PZ13_Chén_4	0.00	100	4	47	2	0	11	37	101
19	PZ13_Dokholyan_3	11.28	66	0	76	0	0	4	21	101
20	PZ13_Dokholyan_2	10.41	69	0	90	0	0	2	18	110
21	PZ13_Bujnicki_9	1.74	99	1	79	5	0	10	18	113
22	PZ13_Ding_10	11.28	66	3	89	0	0	5	20	117

23	PZ13_Chen_8	2.17	99	8	64	1	0	8	38	119
24	PZ13_Chen_7	0.43	99	3	62	1	0	11	45	122
25	PZ13_Ding_7	18.22	37	2	97	0	0	4	22	125
26	PZ13_Ding_4	10.41	69	1	103	0	0	2	20	126
27	PZ13_Chen_5	0.43	99	8	62	4	0	9	45	128
28	PZ13_Ding_5	13.02	58	4	99	0	0	5	20	128
29	PZ13_Ding_1	13.45	56	2	107	0	0	2	18	129
30	PZ13_Chen_9	0.43	99	25	57	4	0	8	36	130
31	PZ13_Bujnicki_6	6.51	89	0	118	0	0	2	11	131
32	PZ13_Chen_2	0.43	99	10	55	5	0	15	49	134
33	PZ13_Ding_9	10.85	67	2	109	0	0	9	21	141
34	PZ13_Ding_6	12.15	62	5	118	0	0	1	18	142
35	PZ13_Ding_3	13.02	58	3	116	0	0	4	21	144
36	PZ13_Ding_8	6.94	87	3	115	0	0	4	23	145
37	PZ13_Dokholyan_1	13.88	54	0	109	0	0	4	32	145
38	PZ13_Dokholyan_4	13.45	56	0	109	2	0	11	31	153
39	PZ13_Xiao_8	1.30	99	4	103	3	0	12	31	153
40	PZ13_Dokholyan_5	14.75	50	0	108	0	0	11	35	154
41	PZ13_Xiao_9	2.17	99	4	100	3	0	14	33	154
42	PZ13_Xiao_10	1.30	99	0	105	2	0	12	36	155
43	PZ13_Xiao_6	1.74	99	1	101	3	0	12	39	156
44	PZ13_Ding_2	19.09	35	6	125	0	0	6	22	159
45	PZ13_Bujnicki_7	12.15	62	5	178	0	3	5	16	207
46	PZ13_Bujnicki_2	20.39	31	6	179	0	4	7	22	218
47	PZ13_Bujnicki_5	9.11	76	11	176	0	5	7	20	219
48	PZ13_Bujnicki_3	22.13	27	10	191	0	3	2	22	228
49	PZ13_Bujnicki_4	41.25	7	20	230	0	5	4	13	272
50	PZ13_Xiao_4	0.00	100	77	175	3	0	6	14	275
51	PZ13_Xiao_1	4.42	95	68	191	3	0	6	24	292
52	PZ13_Xiao_7	32.13	13	37	196	3	3	19	38	296
53	PZ13_Bujnicki_1	37.38	9	23	251	0	9	10	25	318
54	PZ13_Xiao_5	26.46	19	96	190	4	1	10	21	322
55	PZ13_Xiao_2	27.74	17	82	217	6	1	8	28	342

56	PZ13_Xiao_3	16.29	44	93	217	6	3	10	33	362
	Average	9.89	72.43	11.45	91.98	1.38	0.71	6.43	25.16	137.11
	Standard deviation	9.55	28.37	23.92	69.71	1.92	1.70	4.21	9.26	90.06
	Median	8.68	78.00	2.50	98.00	0.00	0.00	5.50	22.00	128.50

Table S84. MolProbity report on structures in Puzzle 14a.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry out- liers	#Probably wrong sugar pucker- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ14_AdamiakPostExp_1	6.08	90	0	0	0	0	0	8	8
2	PZ14_AdamiakPreExp_1	5.57	92	0	0	0	0	0	8	8
3	PZ14_refstructure_bound	4.56	95	1	0	0	0	0	10	11
4	PZ14_AdamiakPreExp_2	8.61	79	0	0	0	0	1	11	12
5	PZ14_AdamiakPostExp_2	14.69	51	0	0	0	0	0	14	14
6	PZ14_DasPostExp_10	5.57	92	0	0	0	0	2	12	14
7	PZ14_DasPreExp_5	5.57	92	0	0	0	0	2	12	14
8	PZ14_DasPostExp_9	6.08	90	0	1	0	0	0	14	15
9	PZ14_DasPreExp_10	6.08	90	0	1	0	0	0	14	15
10	PZ14_DasPostExp_3	14.18	53	1	3	0	0	2	12	18
11	PZ14_DasPostExp_4	5.07	93	0	2	0	0	1	16	19
12	PZ14_DasPreExp_8	6.59	89	0	7	0	0	1	11	19
13	PZ14_DasPreExp_9	6.08	90	0	5	0	0	1	13	19
14	PZ14_DasPostExp_5	6.08	90	0	4	0	0	0	16	20
15	PZ14_DasPostExp_7	2.53	98	0	5	0	0	1	14	20
16	PZ14_DasPreExp_2	2.53	98	0	5	0	0	1	14	20
17	PZ14_DasPreExp_7	12.16	62	1	2	0	0	1	16	20
18	PZ14_DasPostExp_2	8.61	79	0	0	0	0	1	21	22
19	PZ14_DasPreExp_6	11.65	64	0	1	0	0	3	18	22
20	PZ14_DasPostExp_6	7.09	86	0	3	0	0	2	19	24
21	PZ14_DasPreExp_1	7.09	86	0	3	0	0	2	19	24
22	PZ14_DasPostExp_1	12.16	62	0	4	0	0	3	19	26
23	PZ14_BujnickiPreExp_4	11.65	64	1	6	2	0	3	16	28

24	PZ14_ChenPostExp_1	0.00	100	0	8	0	0	4	16	28
25	PZ14_DasPostExp_8	11.66	64	0	6	0	0	2	21	29
26	PZ14_DasPreExp_3	11.66	64	0	6	0	0	2	21	29
27	PZ14_DasPreExp_4	13.68	55	0	6	0	0	1	26	33
28	PZ14_BujnickiPreExp_5	0.00	100	0	13	2	0	3	17	35
29	PZ14_ChenPostExp_2	0.00	100	0	16	0	0	2	23	41
30	PZ14_ChenPostExp_4	0.00	100	0	18	0	0	2	24	44
31	PZ14_ChenPostExp_5	0.00	100	1	18	1	0	2	24	46
32	PZ14_ChenPostExp_8	0.00	100	2	27	0	0	5	16	50
33	PZ14_BujnickiPreExp_6	11.35	65	0	23	5	0	8	19	55
34	PZ14_ChenPostExp_9	0.00	100	6	27	0	1	3	20	57
35	PZ14_ChenPostExp_10	0.00	100	12	25	0	0	4	17	58
36	PZ14_ChenPostExp_7	0.00	100	12	28	0	0	3	20	63
37	PZ14_ChenPostExp_6	0.00	100	7	35	0	0	5	17	64
38	PZ14_BujnickiPostExp_3	12.66	60	2	46	9	0	10	21	88
39	PZ14_ChenPostExp_3	0.00	100	22	45	0	0	5	18	90
40	PZ14_BujnickiPreExp_7	8.61	79	0	52	10	0	12	25	99
41	PZ14_DingPreExp_3	16.21	45	5	85	0	0	3	18	111
42	PZ14_DingPostExp_3	10.64	68	6	88	0	0	2	20	116
43	PZ14_DingPreExp_5	12.66	60	1	96	0	0	4	15	116
44	PZ14_DingPostExp_4	15.70	47	7	93	0	0	2	17	119
45	PZ14_DingPreExp_2	16.21	45	7	90	0	0	3	19	119
46	PZ14_DingPostExp_7	20.77	30	6	94	0	0	3	18	121
47	PZ14_DingPostExp_5	21.28	29	5	93	0	0	4	20	122
48	PZ14_DingPreExp_4	17.73	39	5	98	0	0	3	16	122
49	PZ14_DingPostExp_6	17.22	41	6	100	0	0	3	14	123
50	PZ14_DingPostExp_10	13.68	55	4	94	0	0	4	24	126
51	PZ14_DingPreExp_7	16.21	45	3	106	0	0	2	20	131
52	PZ14_DingPreExp_8	13.68	55	4	95	0	0	8	25	132
53	PZ14_DingPostExp_9	11.14	66	0	107	0	0	3	23	133
54	PZ14_DingPostExp_2	13.68	55	4	109	0	1	5	17	136
55	PZ14_DingPreExp_6	8.61	79	2	108	0	0	5	21	136
56	PZ14_DingPostExp_1	11.14	66	1	107	0	0	5	25	138

57	PZ14_DingPreExp_1	13.68	55	4	110	0	0	4	24	142
58	PZ14_DingPostExp_8	16.20	45	5	125	0	0	1	15	146
59	PZ14_BujnickiPostExp_1	22.88	25	27	103	5	1	9	21	166
60	PZ14_BujnickiPostExp_5	23.30	24	20	92	12	3	16	31	174
61	PZ14_BujnickiPostExp_4	28.40	17	36	148	2	4	6	16	212
62	PZ14_BujnickiPostExp_2	29.38	16	31	149	5	0	10	23	218
	Average	9.94	70.63	4.15	44.21	0.85	0.16	3.31	17.97	70.65
	Standard deviation	7.22	24.80	7.66	47.26	2.46	0.66	3.09	4.66	56.97
	Median	10.89	67.00	1.00	20.50	0.00	0.00	3.00	18.00	48.00

Table S85. MolProbity report on structures in Puzzle 14b.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry out- liers	#Probably wrong sugar pucker- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ14_DasPostExp_5	5.58	92	0	2	0	0	2	9	13
2	PZ14_refstructure_free	13.38	56	0	0	0	0	1	13	14
3	PZ14_DasPostExp_7	5.58	92	0	5	0	0	1	11	17
4	PZ14_DasPreExp_2	5.58	92	0	5	0	0	1	11	17
5	PZ14_DasPreExp_7	5.58	92	0	2	0	0	2	15	19
6	PZ14_DasPostExp_3	5.58	92	1	2	0	0	0	17	20
7	PZ14_DasPostExp_4	6.60	89	0	2	0	0	2	16	20
8	PZ14_DasPostExp_6	16.24	45	1	1	0	0	4	14	20
9	PZ14_DasPreExp_1	16.24	45	1	1	0	0	4	14	20
10	PZ14_DasPreExp_9	4.57	95	0	8	0	0	1	12	21
11	PZ14_DasPreExp_8	4.57	95	0	7	0	0	1	14	22
12	PZ14_DasPostExp_10	6.09	90	0	1	0	0	2	20	23
13	PZ14_DasPreExp_5	6.09	90	0	1	0	0	2	20	23
14	PZ14_DasPostExp_9	6.60	89	1	8	0	1	2	12	24
15	PZ14_DasPreExp_10	6.60	89	1	8	0	1	2	12	24
16	PZ14_DasPostExp_8	12.20	62	1	5	0	0	1	18	25
17	PZ14_DasPreExp_4	12.20	62	1	5	0	0	1	18	25
18	PZ14_DasPreExp_3	8.63	79	0	0	0	0	2	24	26

19	PZ14_DasPostExp_2	10.66	68	0	2	0	1	2	22	27
20	PZ14_DasPostExp_1	10.15	71	1	4	0	1	4	24	34
21	PZ14_DasPreExp_6	10.15	71	1	4	0	1	4	24	34
22	PZ14_ChenPostExp_1	0.00	100	7	29	0	5	5	16	62
23	PZ14_BujnickiPreExp_4	7.61	83	0	31	6	1	7	20	65
24	PZ14_ChenPostExp_2	0.00	100	5	34	0	2	2	23	66
25	PZ14_BujnickiPreExp_2	12.12	62	0	27	10	0	10	21	68
26	PZ14_BujnickiPostExp_1	14.74	50	4	38	4	0	7	16	69
27	PZ14_BujnickiPreExp_3	11.11	66	1	29	9	0	11	24	74
28	PZ14_ChenPostExp_4	0.00	100	8	37	0	6	2	23	76
29	PZ14_ChenPostExp_8	0.00	100	9	44	0	4	5	16	78
30	PZ14_ChenPostExp_9	0.00	100	12	44	0	7	2	19	84
31	PZ14_ChenPostExp_5	0.00	100	11	42	1	5	2	24	85
32	PZ14_ChenPostExp_6	0.00	100	14	53	0	2	5	18	92
33	PZ14_ChenPostExp_10	0.00	100	22	46	0	5	4	18	95
34	PZ14_ChenPostExp_7	0.00	100	18	49	0	7	4	20	98
35	PZ14_BujnickiPostExp_2	22.85	25	10	70	5	0	6	12	103
36	PZ14_DingPostExp_1	14.21	53	3	83	0	0	3	16	105
37	PZ14_DingPostExp_2	15.23	48	5	87	0	0	0	15	107
38	PZ14_ChenPostExp_3	0.00	100	29	54	0	6	5	18	112
39	PZ14_DingPreExp_4	16.75	43	5	91	0	0	1	17	114
40	PZ14_BujnickiPostExp_3	12.70	60	21	71	3	0	5	16	116
41	PZ14_DingPostExp_5	7.61	83	5	100	0	0	1	11	117
42	PZ14_DingPostExp_6	13.20	57	3	94	0	0	3	18	118
43	PZ14_DingPostExp_3	15.23	48	4	97	0	0	3	19	123
44	PZ14_DingPreExp_1	11.68	64	5	99	0	0	5	18	127
45	PZ14_DingPostExp_9	11.17	66	4	103	0	0	5	22	134
46	PZ14_DingPostExp_4	13.71	55	6	108	1	0	5	23	143
47	PZ14_DingPostExp_7	9.64	73	4	120	0	0	3	16	143
48	PZ14_DingPreExp_2	11.17	66	4	109	0	0	8	24	145
49	PZ14_DingPreExp_3	13.71	55	7	106	0	0	8	24	145
50	PZ14_BujnickiPreExp_1	4.04	96	5	95	9	2	11	25	147
51	PZ14_DingPostExp_10	11.68	64	1	122	0	0	5	22	150

52	PZ14_DingPostExp_8	14.21	53	6	109	0	0	8	29	152
53	PZ14_BujnickiPostExp_4	23.86	23	20	101	13	3	16	31	184
	Average	8.81	74.51	5.04	45.19	1.15	1.13	3.92	18.38	74.81
	Standard deviation	6.00	21.47	6.62	42.04	2.94	2.06	3.18	4.86	49.58
	Median	9.64	73.00	3.00	37.00	0.00	0.00	3.00	18.00	74.00

Table S86. MolProbity report on structures in Puzzle 15.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry out- liers	#Probably wrong sugar pucker- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ15_Adamiak_10	8.64	79	0	0	0	0	0	6	6
2	PZ15_Adamiak_3	5.46	92	0	0	0	0	0	6	6
3	PZ15_RNAComposer1_2	5.46	92	0	0	0	0	0	6	6
4	PZ15_refstructure	0.91	99	1	0	0	0	0	5	6
5	PZ15_Adamiak_2	6.37	89	0	0	0	0	0	7	7
6	PZ15_RNAComposer1_1	5.91	91	0	0	0	0	0	7	7
7	PZ15_Adamiak_1	26.39	19	0	0	0	0	0	11	11
8	PZ15_Adamiak_4	10.92	67	0	0	0	0	0	11	11
9	PZ15_Adamiak_5	10.46	69	0	0	0	0	0	11	11
10	PZ15_Adamiak_8	12.74	60	0	1	0	0	1	9	11
11	PZ15_Adamiak_9	11.83	64	0	0	0	0	0	11	11
12	PZ15_RNAComposer2_1	10.46	69	0	0	0	0	0	11	11
13	PZ15_RNAComposer2_2	9.55	74	0	0	0	0	0	11	11
14	PZ15_Adamiak_7	9.55	74	0	0	0	0	0	13	13
15	PZ15_Adamiak_6	10.46	69	0	0	0	0	1	13	14
16	PZ15_FARFAR2_10	7.73	83	0	4	0	0	0	11	15
17	PZ15_FARFAR2_6	7.28	85	0	2	0	0	1	13	16
18	PZ15_FARFAR2_2	7.28	85	0	2	0	0	0	15	17
19	PZ15_FARFAR2_3	9.10	77	0	6	0	0	2	9	17
20	PZ15_FARFAR2_1	10.46	69	1	5	0	0	1	11	18
21	PZ15_FARFAR2_7	10.46	69	1	2	0	0	1	15	19
22	PZ15_FARFAR2_8	5.00	94	0	2	0	0	0	17	19

23	PZ15_FARFAR2_9	9.10	77	1	4	0	1	4	10	20
24	PZ15_FARFAR2_5	9.55	74	0	2	0	0	2	17	21
25	PZ15_FARFAR2_4	12.74	60	0	1	0	0	0	24	25
26	PZ15_Chen_3	0.45	99	0	17	0	0	2	13	32
27	PZ15_Chen_2	0.00	100	2	17	0	0	5	19	43
28	PZ15_Chen_1	0.45	99	4	24	0	0	4	22	54
29	PZ15_Chen_6	0.46	99	9	42	0	0	5	24	80
30	PZ15_Chen_4	0.00	100	4	39	0	0	7	36	86
31	PZ15_Chen_5	0.00	100	11	56	0	1	5	23	96
32	PZ15_Chen_9	0.91	99	13	60	3	0	8	42	126
33	PZ15_Chen_10	0.91	99	30	66	2	3	8	22	131
34	PZ15_Chen_7	3.64	97	25	70	0	0	10	26	131
35	PZ15_Chen_8	1.36	99	27	63	1	1	11	32	135
36	PZ15_SimRNA2_10	72.86	1	53	158	0	2	4	17	234
37	PZ15_SimRNA2_2	73.18	0	60	153	0	1	4	18	236
38	PZ15_SimRNA1_7	70.55	1	68	149	0	4	3	19	243
39	PZ15_SimRNA1_1	94.72	0	67	160	1	2	3	18	251
40	PZ15_SimRNA2_7	81.09	0	65	160	2	3	4	21	255
41	PZ15_3dRNA2_9	34.56	11	18	163	20	9	15	32	257
42	PZ15_3dRNA2_10	34.11	11	21	163	20	9	14	32	259
43	PZ15_SimRNA1_3	78.53	0	70	164	1	2	2	21	260
44	PZ15_3dRNA2_1	35.02	11	22	164	20	9	14	32	261
45	PZ15_SimRNA2_1	38.25	9	67	175	2	0	2	15	261
46	PZ15_SimRNA2_9	84.58	0	66	164	1	5	5	20	261
47	PZ15_3dRNA2_2	33.65	12	22	165	20	9	15	31	262
48	PZ15_3dRNA2_8	34.56	11	20	168	20	9	14	32	263
49	PZ15_SimRNA1_8	68.27	1	78	158	1	2	3	22	264
50	PZ15_3dRNA2_7	32.74	13	23	168	21	8	14	31	265
51	PZ15_SimRNA1_5	85.23	0	69	168	2	1	1	26	267
52	PZ15_3dRNA2_4	32.74	13	24	171	20	9	14	31	269
53	PZ15_3dRNA2_3	32.74	13	24	176	21	8	15	31	275
54	PZ15_3dRNA2_5	32.29	13	25	176	21	7	16	31	276
55	PZ15_SimRNA2_6	78.82	0	80	169	1	3	4	20	277

56	PZ15_3dRNA2_6	31.83	14	25	177	21	8	15	32	278
57	PZ15_SimRNA2_5	80.15	0	74	182	0	2	5	15	278
58	PZ15_SimRNA1_6	97.77	0	74	177	1	4	6	17	279
59	PZ15_SimRNA2_3	85.12	0	78	174	1	3	2	22	280
60	PZ15_SimRNA1_2	96.00	0	66	182	0	7	4	23	282
61	PZ15_SimRNA2_4	63.21	1	67	190	0	5	5	16	283
62	PZ15_SimRNA1_10	107.22	0	67	176	1	4	11	26	285
63	PZ15_SimRNA2_8	59.49	2	73	178	2	4	6	25	288
64	PZ15_SimRNA1_4	88.76	0	78	181	1	2	5	23	290
65	PZ15_SimRNA1_9	64.78	1	71	198	1	1	2	22	295
66	PZ15_FARFAR1_1	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 128.024 > 50: distance: 1553 - 1554: 126.362								
67	PZ15_FARFAR1_10	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 110.638 > 50: distance: 1553 - 1554: 110.120								
68	PZ15_FARFAR1_2	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 110.873 > 50: distance: 1553 - 1554: 110.360								
69	PZ15_FARFAR1_3	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 111.621 > 50: distance: 1553 - 1554: 111.175								
70	PZ15_FARFAR1_4	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 123.221 > 50: distance: 1553 - 1554: 121.354								
71	PZ15_FARFAR1_5	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 123.078 > 50: distance: 1553 - 1554: 122.427								
72	PZ15_FARFAR1_6	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 119.902 > 50: distance: 1553 - 1554: 118.260								
73	PZ15_FARFAR1_7	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 126.282 > 50: distance: 1553 - 1554: 124.545								
74	PZ15_FARFAR1_8	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 134.966 > 50: distance: 1553 - 1554: 133.430								
75	PZ15_FARFAR1_9	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 120.129 > 50: distance: 1553 - 1554: 118.685								
	Average	33.00	46.29	26.83	86.03	3.51	2.28	4.69	19.38	142.72
	Standard deviation	33.25	41.10	30.23	80.64	7.29	3.11	5.07	8.75	120.96
	Median	12.74	60.00	18.00	63.00	0.00	1.00	3.00	19.00	131.00

Table S87. MolProbity report on structures in Puzzle 17.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry out- liers	#Probably wrong sugar puckers:	(c) #Bad back- bone confor- mations	Total
1	PZ17_RNAComposer1_3	9.55	74	0	0	0	0	1	7	8
2	PZ17_RNAComposer1_5	15.08	49	0	0	0	0	1	9	10
3	PZ17_RNAComposer2_2	9.55	74	0	0	0	0	0	12	12
4	PZ17_RNAComposer2_5	12.56	60	0	0	0	0	0	12	12

5	PZ17_RNAComposer2_4	9.55	74	0	0	0	0	0	14	14
6	PZ17_refstructure	15.59	47	0	3	0	0	1	11	15
7	PZ17_RNAComposer2_1	6.53	89	0	0	0	0	0	15	15
8	PZ17_RNAComposer1_10	11.06	66	0	0	0	0	2	14	16
9	PZ17_RNAComposer2_6	16.59	43	0	0	0	0	0	16	16
10	PZ17_Das_1	3.02	98	0	6	0	0	0	11	17
11	PZ17_Das_4	6.53	89	0	1	0	0	2	14	17
12	PZ17_Das_9	6.53	89	0	1	0	0	3	13	17
13	PZ17_RNAComposer1_1	10.55	68	0	0	0	0	1	16	17
14	PZ17_RNAComposer1_4	10.55	68	0	0	0	0	1	16	17
15	PZ17_RNAComposer2_8	11.06	66	0	0	0	0	0	17	17
16	PZ17_RNAComposer2_9	11.06	66	0	0	0	0	1	16	17
17	PZ17_Das_6	4.02	96	0	4	0	0	1	13	18
18	PZ17_RNAComposer1_7	12.56	60	0	0	0	0	1	17	18
19	PZ17_RNAComposer1_8	12.56	60	0	0	0	0	2	16	18
20	PZ17_RNAComposer2_7	13.07	58	0	0	0	0	0	18	18
21	PZ17_Das_5	8.54	79	0	1	0	0	3	15	19
22	PZ17_DasExtraInfo_1	10.05	71	0	2	0	0	0	17	19
23	PZ17_Das_8	7.04	86	0	4	0	0	1	15	20
24	PZ17_RNAComposer2_10	10.05	71	0	0	0	0	1	19	20
25	PZ17_Das_7	13.07	58	0	4	0	0	4	14	22
26	PZ17_RNAComposer1_2	8.04	82	0	0	0	0	2	20	22
27	PZ17_RNAComposer1_9	8.54	79	0	0	0	0	2	20	22
28	PZ17_Adamiak_2	15.58	47	0	1	0	0	2	20	23
29	PZ17_DasExtraInfo_3	12.06	62	1	3	0	0	2	18	24
30	PZ17_Das_2	7.04	86	0	1	0	0	5	19	25
31	PZ17_RNAComposer1_6	16.58	43	0	0	0	0	2	23	25
32	PZ17_Das_3	10.05	71	1	1	0	0	2	22	26
33	PZ17_Adamiak_3	11.06	66	0	0	0	0	1	26	27
34	PZ17_DasExtraInfo_2	9.05	77	1	5	1	0	1	19	27
35	PZ17_Adamiak_1	10.55	68	0	0	0	0	1	27	28
36	PZ17_Bujnicki_4	0.00	100	0	17	1	0	2	10	30
37	PZ17_Bujnicki_8	0.00	100	0	18	0	0	2	10	30

38	PZ17_Bujnicki_3	0.00	100	0	15	1	0	2	13	31
39	PZ17_Das_10	13.57	56	0	3	0	0	1	27	31
40	PZ17_Bujnicki_10	0.00	100	0	15	1	0	4	13	33
41	PZ17_Bujnicki_2	0.00	100	0	15	1	0	4	13	33
42	PZ17_Bujnicki_7	1.01	99	0	23	0	0	3	7	33
43	PZ17_Bujnicki_6	0.00	100	0	21	0	0	1	13	35
44	PZ17_Chen_10	0.50	99	0	12	1	0	4	19	36
45	PZ17_Major_2	0.00	100	1	30	0	0	3	15	49
46	PZ17_Major_5	0.00	100	0	28	0	0	2	22	52
47	PZ17_Major_1	0.50	99	1	33	0	0	5	16	55
48	PZ17_Major_4	0.00	100	0	34	0	0	9	20	63
49	PZ17_Major_3	0.00	100	0	34	3	0	10	23	70
50	PZ17_Chen_3	0.00	100	2	33	2	0	11	35	83
51	PZ17_Ding_1	8.54	79	0	93	0	0	4	13	110
52	PZ17_Ding_5	8.54	79	3	88	0	0	4	20	115
53	PZ17_Ding_8	13.57	56	5	90	0	0	4	17	116
54	PZ17_Major_6	1.01	99	0	67	5	0	13	32	117
55	PZ17_Major_8	0.00	100	1	60	4	0	15	38	118
56	PZ17_Dohkolyan_1	17.59	40	0	93	0	0	7	19	119
57	PZ17_RNAComposer2_3	68.45	1	48	64	0	0	0	8	120
58	PZ17_Ding_6	10.05	71	3	95	0	0	5	19	122
59	PZ17_Ding_9	7.04	86	3	97	0	0	4	18	122
60	PZ17_Dohkolyan_2	22.61	26	0	100	0	0	5	19	124
61	PZ17_Ding_4	10.05	71	3	100	0	0	3	21	127
62	PZ17_Ding_3	9.55	74	3	103	0	0	4	18	128
63	PZ17_Ding_10	8.04	82	5	104	0	0	2	18	129
64	PZ17_Dohkolyan_3	19.60	34	0	102	0	0	4	25	131
65	PZ17_Ding_2	11.06	66	6	96	0	0	7	28	137
66	PZ17_Major_7	2.01	99	1	81	4	0	15	38	139
67	PZ17_Bujnicki_1	3.02	98	1	109	3	4	6	17	140
68	PZ17_Bujnicki_9	3.02	98	1	109	3	4	6	17	140
69	PZ17_Ding_7	8.54	79	3	110	0	0	9	28	150
70	PZ17_Chen_7	4.52	95	35	78	2	1	10	29	155

71	PZ17_Xiao_7	0.50	99	1	73	31	1	24	44	174
72	PZ17_Xiao_2	0.00	100	1	74	36	0	21	43	175
73	PZ17_Xiao_1	12.56	60	11	94	20	0	16	35	176
74	PZ17_Xiao_3	3.02	98	1	77	40	0	23	41	182
75	PZ17_Major_9	13.57	56	8	97	10	3	24	49	191
76	PZ17_SimRNA1_2	109.15	0	53	121	0	2	3	12	191
77	PZ17_Xiao_4	4.02	96	1	88	32	0	30	42	193
78	PZ17_Chen_8	1.51	99	41	108	2	2	14	34	201
79	PZ17_Major_10	15.08	49	8	116	5	4	22	46	201
80	PZ17_Bujnicki_5	5.03	94	6	164	2	5	10	26	213
81	PZ17_SimRNA1_7	140.42	0	61	134	0	1	3	17	216
82	PZ17_SimRNA1_9	141.93	0	61	138	0	2	1	14	216
83	PZ17_SimRNA1_8	121.91	0	54	143	0	3	2	15	217
84	PZ17_Xiao_10	4.52	95	1	94	47	0	28	47	217
85	PZ17_SimRNA1_1	140.48	0	57	140	0	4	4	13	218
86	PZ17_Xiao_5	27.14	18	21	118	23	0	18	38	218
87	PZ17_Chen_2	101.35	0	47	146	0	1	9	17	220
88	PZ17_Chen_6	177.18	0	51	140	0	2	9	18	220
89	PZ17_SimRNA2_4	102.72	0	65	132	1	2	3	17	220
90	PZ17_SimRNA2_2	134.24	0	63	135	0	5	2	16	221
91	PZ17_SimRNA1_5	161.45	0	62	140	0	5	3	15	225
92	PZ17_SimRNA1_3	176.65	0	61	148	0	3	3	13	228
93	PZ17_SimRNA2_7	158.61	0	66	142	1	1	2	17	229
94	PZ17_Chen_9	107.65	0	49	156	0	2	5	18	230
95	PZ17_Chen_1	102.46	0	39	165	0	0	8	22	234
96	PZ17_SimRNA2_9	160.97	0	62	147	1	3	6	16	235
97	PZ17_Xiao_6	30.15	15	22	125	25	1	23	40	236
98	PZ17_SimRNA1_6	139.63	0	67	152	1	2	2	14	238
99	PZ17_Chen_5	156.64	0	49	169	1	0	7	19	245
100	PZ17_Xiao_8	16.08	45	15	119	40	1	27	43	245
101	PZ17_SimRNA2_1	151.48	0	59	170	2	1	2	15	249
102	PZ17_Chen_4	169.44	0	52	169	0	0	11	23	255
103	PZ17_SimRNA2_8	154.46	0	69	160	0	4	3	22	258

104	PZ17_SimRNA2_6	122.29	0	64	166	1	5	4	20	260
105	PZ17_SimRNA2_3	126.88	0	75	152	0	9	2	23	261
106	PZ17_SimRNA2_5	128.01	0	67	162	1	3	7	23	263
107	PZ17_Xiao_9	14.07	53	15	137	39	1	30	45	267
108	PZ17_SimRNA1_4	162.23	0	65	175	0	6	3	21	270
	Average	38.08	58.36	15.72	67.53	3.64	0.86	6.02	20.94	114.71
	Standard deviation	56.18	37.43	24.78	61.21	9.94	1.67	7.29	9.77	91.03
	Median	10.55	68.00	1.00	73.50	0.00	0.00	3.00	18.00	117.50

Table S88. MolProbity report on structures in Puzzle 18.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar puckers:	(c) #Bad back- bone confor- mations	Total
1	PZ18_refstructure	3.48	97	0	0	0	0	0	7	7
2	PZ18_FARFAR_2	5.22	93	0	0	0	0	0	8	8
3	PZ18_FARFAR_10	6.52	89	0	0	0	0	1	8	9
4	PZ18_Lee_4	3.91	96	1	4	0	0	1	3	9
5	PZ18_FARFAR_6	3.91	96	0	0	0	0	0	11	11
6	PZ18_Lee_1	1.74	99	1	3	0	0	2	6	12
7	PZ18_Lee_5	2.17	99	1	5	0	0	1	5	12
8	PZ18_FARFAR_3	10.44	69	1	2	0	0	1	9	13
9	PZ18_FARFAR_4	3.48	97	0	0	0	0	0	13	13
10	PZ18_Lee_2	3.91	96	1	4	0	0	2	6	13
11	PZ18_FARFAR_7	7.39	85	0	2	0	0	1	11	14
12	PZ18_FARFAR_8	3.48	97	0	1	0	0	1	12	14
13	PZ18_LeeServer_1	0.87	99	1	5	0	0	2	6	14
14	PZ18_RNAComposer_1	12.61	60	0	0	0	0	0	14	14
15	PZ18_FARFAR_1	6.52	89	0	1	0	0	1	13	15
16	PZ18_FARFAR_9	1.74	99	1	1	0	0	1	15	18
17	PZ18_RNAComposer_2	10.87	67	0	0	0	0	1	17	18
18	PZ18_RNAComposer_3	10.87	67	0	0	0	0	2	16	18
19	PZ18_RNAComposer_4	10.87	67	0	0	0	0	2	16	18

20	PZ18_Das_2	16.09	45	1	5	0	0	0	13	19
21	PZ18_LeeServer_5	2.17	99	1	6	0	0	2	10	19
22	PZ18_Lee_3	1.74	99	1	7	0	0	1	11	20
23	PZ18_LeeServer_4	4.78	94	1	7	0	0	4	8	20
24	PZ18_RNAComposer_5	13.92	54	0	0	0	0	4	16	20
25	PZ18_Das_3	9.57	74	0	6	0	0	0	15	21
26	PZ18_Das_4	13.05	58	0	6	0	0	1	14	21
27	PZ18_FARFAR_5	8.26	81	0	5	0	0	2	14	21
28	PZ18_Das_1	13.05	58	1	9	0	0	0	15	25
29	PZ18_LeeServer_2	4.35	95	1	11	0	0	5	15	32
30	PZ18_LeeServer_3	3.48	97	1	8	0	1	5	17	32
31	PZ18_Das_5	19.57	34	1	10	0	0	2	21	34
32	PZ18_YagoubAli_1	8.26	81	2	4	0	0	4	26	36
33	PZ18_3dRNA_2	0.43	99	1	42	3	0	5	12	63
34	PZ18_Chen_5	1.31	99	7	34	0	2	3	17	63
35	PZ18_Chen_1	0.43	99	5	40	0	0	7	32	84
36	PZ18_Chen_4	4.78	94	9	45	0	1	3	28	86
37	PZ18_Chen_3	4.78	94	9	56	0	1	5	31	102
38	PZ18_Chen_2	2.17	99	9	51	0	0	11	35	106
39	PZ18_3dRNA_4	0.87	99	1	57	19	1	10	22	110
40	PZ18_Ding_2	10.87	67	3	94	0	0	1	15	113
41	PZ18_Ding_4	8.26	81	4	97	0	1	2	11	115
42	PZ18_Ding_1	10.44	69	6	97	0	0	1	14	118
43	PZ18_Ding_5	9.13	76	2	98	0	0	5	17	122
44	PZ18_Dokholyan_2	14.79	50	1	93	0	0	5	24	123
45	PZ18_3dRNA_5	0.43	99	1	66	16	0	11	31	125
46	PZ18_3dRNA_3	12.61	60	10	83	9	0	9	22	133
47	PZ18_Dokholyan_3	13.48	56	0	94	0	0	8	31	133
48	PZ18_Ding_3	7.83	82	5	108	0	0	5	20	138
49	PZ18_Dokholyan_1	9.57	74	0	108	0	0	5	29	142
50	PZ18_3dRNA_1	11.74	64	9	84	13	0	10	31	147
51	PZ18_SimRNA_1	100.48	0	62	131	1	1	3	17	215
52	PZ18_SimRNA_3	100.78	0	74	133	0	2	4	16	229

53	PZ18_SimRNA_2	87.75	0	67	162	1	3	1	13	247
	Average	12.10	77.19	5.70	35.57	1.17	0.25	3.08	16.21	61.96
	Standard deviation	21.41	25.85	15.63	45.30	3.94	0.62	3.02	7.90	62.93
	Median	7.39	85.00	1.00	7.00	0.00	0.00	2.00	15.00	21.00

Table S89. MolProbity report on structures in Puzzle 19.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry out- liers	#Probably wrong sugar puckers:	(c) #Bad back- bone confor- mations	Total
1	PZ19_Adamiak_4	6.99	87	0	0	0	0	0	4	4
2	PZ19_Adamiak_2	6.99	87	0	0	0	0	0	6	6
3	PZ19_Adamiak_3	7.49	84	0	0	0	0	2	4	6
4	PZ19_RNAComposer_1	6.49	89	0	0	0	0	0	8	8
5	PZ19_Adamiak_1	7.99	82	0	0	0	0	2	8	10
6	PZ19_FARFAR_9	5.99	90	0	1	0	0	2	8	11
7	PZ19_FARFAR_7	6.99	87	0	3	0	0	1	8	12
8	PZ19_RNAComposer_3	11.48	65	0	0	0	0	1	11	12
9	PZ19_LeeServer_5	4.49	95	2	4	0	0	0	7	13
10	PZ19_refstructure	2.50	99	1	6	0	0	1	6	14
11	PZ19_Adamiak_5	5.49	92	0	0	0	0	1	13	14
12	PZ19_RNAComposer_2	9.99	71	0	0	0	0	2	12	14
13	PZ19_FARFAR_1	4.00	96	0	2	0	0	1	12	15
14	PZ19_FARFAR_8	5.00	94	1	2	0	0	2	10	15
15	PZ19_RNAComposer_5	11.48	65	0	0	0	0	4	11	15
16	PZ19_FARFAR_2	7.49	84	0	2	0	0	3	11	16
17	PZ19_RNAComposer_4	12.98	58	0	0	0	0	2	14	16
18	PZ19_FARFAR_3	4.50	95	0	4	0	0	1	12	17
19	PZ19_FARFAR_6	5.00	94	1	3	0	0	3	10	17
20	PZ19_FARFAR_10	7.49	84	1	0	0	0	2	15	18
21	PZ19_FARFAR_5	7.99	82	0	3	0	0	2	13	18
22	PZ19_LeeServer_4	6.49	89	2	7	0	1	2	10	22
23	PZ19_FARFAR_4	10.99	67	0	10	0	0	3	11	24

24	PZ19_Bujnicki_1	1.50	99	0	17	2	0	2	11	32
25	PZ19_Chen_4	0.00	100	5	16	0	0	3	21	45
26	PZ19_Chen_3	0.00	100	1	30	0	0	4	22	57
27	PZ19_Bujnicki_2	4.49	95	0	42	5	0	6	13	66
28	PZ19_Dokholyan_1	6.49	89	0	50	0	0	3	15	68
29	PZ19_Bujnicki_5	1.00	99	0	40	11	1	10	18	80
30	PZ19_Bujnicki_3	3.99	96	0	63	4	0	5	11	83
31	PZ19_Chen_2	0.50	99	8	43	0	0	4	29	84
32	PZ19_LeeServer_3	1.50	99	2	12	49	0	11	17	91
33	PZ19_LeeServer_2	1.00	99	2	7	51	0	12	20	92
34	PZ19_LeeServer_1	1.50	99	2	12	50	0	11	18	93
35	PZ19_Ding_2	10.98	67	1	77	0	0	3	14	95
36	PZ19_Ding_4	12.98	58	2	93	0	0	2	16	113
37	PZ19_Ding_1	8.49	79	5	97	0	0	2	10	114
38	PZ19_Ding_5	8.49	79	3	95	0	1	2	13	114
39	PZ19_Ding_3	7.99	82	5	89	0	0	3	18	115
40	PZ19_Bujnicki_4	4.99	94	1	114	9	2	8	18	152
41	PZ19_Chen_1	18.97	35	22	92	1	1	10	26	152
42	PZ19_3dRNA_5	5.50	92	15	102	11	1	8	30	167
43	PZ19_3dRNA_2	4.00	96	15	94	11	1	14	34	169
44	PZ19_3dRNA_4	4.00	96	16	101	15	1	11	33	177
45	PZ19_3dRNA_1	4.50	95	15	103	12	1	15	33	179
46	PZ19_3dRNA_3	6.00	90	7	102	15	2	14	40	180
47	PZ19_SimRNA_1	108.39	0	52	119	1	1	1	9	183
48	PZ19_Chen_5	19.97	32	41	125	3	5	8	35	217
49	PZ19_SimRNA_2	134.40	0	55	158	0	3	3	17	236
50	PZ19_SimRNA_3	105.68	0	71	148	2	2	5	19	247
51	PZ19_Das_1	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 146.452 > 50: distance: 1298 - 1299: 144.568								
52	PZ19_Das_2	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 104.524 > 50: distance: 1298 - 1299: 103.861								
53	PZ19_Das_3	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 114.045 > 50: distance: 1298 - 1299: 112.953								
54	PZ19_Das_4	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 145.887 > 50: distance: 1298 - 1299: 144.334								
55	PZ19_Das_5	Rejected as unacceptable - Bond distance > max_reasonable_bond_distance: 76.1157 > 50: distance: 1298 - 1299: 75.621								
	Average	13.07	80.10	7.08	41.76	5.04	0.46	4.34	15.68	74.36

	Standard deviation	26.83	25.61	15.38	48.66	12.23	0.95	4.14	8.65	70.88
	Median	6.49	89.00	1.00	12.00	0.00	0.00	3.00	13.00	51.00

Table S90. MolProbity report on structures in Puzzle 20.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar pucker- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ20_FARFAR_2	3.19	97	0	0	0	0	0	4	4
2	PZ20_refstructure	0.46	99	0	0	0	0	0	5	5
3	PZ20_FARFAR_9	2.28	99	0	0	0	0	0	6	6
4	PZ20_RNAComposer_3	10.48	69	0	0	0	0	0	8	8
5	PZ20_RNAComposer_5	9.12	76	0	0	0	0	1	10	11
6	PZ20_Adamiak_2	9.12	76	0	0	0	0	1	11	12
7	PZ20_FARFAR_1	6.84	87	0	0	0	0	0	12	12
8	PZ20_FARFAR_5	5.47	92	0	1	0	0	2	9	12
9	PZ20_FARFAR_3	9.57	74	0	3	0	0	1	9	13
10	PZ20_FARFAR_4	3.65	97	0	4	0	0	0	9	13
11	PZ20_RNAComposer_1	6.84	87	0	0	0	0	1	12	13
12	PZ20_RNAComposer_2	5.47	92	0	0	0	0	0	13	13
13	PZ20_FARFAR_10	6.84	87	0	3	0	0	3	8	14
14	PZ20_Adamiak_1	8.20	81	0	0	0	0	2	13	15
15	PZ20_Adamiak_3	10.48	69	1	0	0	0	2	12	15
16	PZ20_Adamiak_4	7.29	85	0	0	0	0	1	15	16
17	PZ20_Das_3	9.57	74	3	4	0	0	2	7	16
18	PZ20_FARFAR_6	6.84	87	0	3	0	0	2	11	16
19	PZ20_FARFAR_7	8.20	81	0	3	0	1	3	9	16
20	PZ20_FARFAR_8	6.38	89	0	3	0	0	1	13	17
21	PZ20_RNAComposer_4	5.47	92	0	0	0	0	1	16	17
22	PZ20_Adamiak_5	6.84	87	0	0	0	0	2	16	18
23	PZ20_Das_2	15.50	48	1	5	0	0	0	12	18
24	PZ20_Das_1	15.50	48	1	5	0	0	1	15	22
25	PZ20_Das_4	18.23	37	1	3	0	0	1	19	24

26	PZ20_Das_5	28.70	17	1	5	0	0	3	16	25
27	PZ20_Bujnicki_5	0.46	99	0	13	3	0	5	11	32
28	PZ20_Bujnicki_1	21.41	29	23	105	1	0	4	10	143
29	PZ20_Xiao3_5	1.82	99	2	88	34	1	16	34	175
30	PZ20_SimRNA_2	144.49	0	63	139	1	1	4	13	221
31	PZ20_Xiao3_3	39.32	8	27	130	27	0	18	34	236
32	PZ20_SimRNA_5	98.63	0	64	149	0	3	2	20	238
33	PZ20_Xiao3_2	13.70	55	8	133	37	0	19	41	238
34	PZ20_Bujnicki_3	27.37	18	55	158	1	5	6	14	239
35	PZ20_SimRNA_4	102.91	0	79	145	0	3	3	18	248
36	PZ20_Bujnicki_4	37.37	9	41	180	1	6	7	19	254
37	PZ20_SimRNA_1	129.15	0	77	154	0	2	7	19	259
38	PZ20_Bujnicki_2	32.80	13	40	195	1	4	7	14	261
39	PZ20_SimRNA_3	101.32	0	69	169	2	2	4	23	269
40	PZ20_Xiao3_4	13.68	55	9	137	50	0	27	48	271
41	PZ20_Xiao3_1	25.57	20	21	127	53	2	28	51	282
	Average	24.79	59.32	14.29	50.34	5.15	0.73	4.56	16.07	91.15
	Standard deviation	36.05	35.88	24.89	69.80	13.69	1.48	6.95	10.78	109.42
	Median	9.57	74.00	0.00	3.00	0.00	0.00	2.00	13.00	17.00

Table S91. MolProbity report on structures in Puzzle 21.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar puck- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ21_Das_1	17.29	41	0	0	0	0	0	3	3
2	PZ21_RNAComposer_2	9.02	77	0	0	0	0	0	3	3
3	PZ21_Das_2	19.55	34	0	0	0	0	0	4	4
4	PZ21_Das_4	11.28	66	0	3	0	0	0	1	4
5	PZ21_Das_3	15.04	49	0	3	0	0	0	3	6
6	PZ21_RNAComposer_1	15.04	49	0	0	0	0	1	5	6
7	PZ21_RNAComposer_5	6.77	88	0	0	0	0	0	7	7
8	PZ21_Adamiak_3	8.27	81	0	0	0	0	1	7	8

9	PZ21_DasLORES_4	3.01	98	1	0	0	0	0	7	8
10	PZ21_Das_5	14.29	52	0	5	0	0	1	3	9
11	PZ21_Adamiak_4	13.53	56	0	0	0	0	1	9	10
12	PZ21_FARFAR_8	6.02	90	0	1	0	0	2	7	10
13	PZ21_Adamiak_2	10.53	68	0	0	0	0	0	11	11
14	PZ21_Adamiak_5	13.53	56	0	0	0	0	0	11	11
15	PZ21_DasLORES_3	6.77	88	1	2	0	0	0	8	11
16	PZ21_RNAComposer_4	9.02	77	0	0	0	0	0	11	11
17	PZ21_Adamiak_1	12.78	60	0	0	0	0	0	12	12
18	PZ21_DasLORES_2	6.77	88	0	1	0	0	1	10	12
19	PZ21_FARFAR_3	8.27	81	0	1	0	0	2	10	13
20	PZ21_FARFAR_6	4.51	95	0	1	0	0	2	10	13
21	PZ21_DasLORES_5	5.26	93	0	0	0	0	0	14	14
22	PZ21_FARFAR_7	10.53	68	0	2	0	0	2	10	14
23	PZ21_FARFAR_9	2.26	99	0	4	0	0	0	10	14
24	PZ21_RNAComposer_3	18.80	36	0	0	0	0	0	14	14
25	PZ21_FARFAR_5	6.02	90	0	3	0	0	3	9	15
26	PZ21_FARFAR_10	9.77	73	0	1	0	0	3	12	16
27	PZ21_FARFAR_4	7.52	84	0	4	0	0	2	10	16
28	PZ21_Bujnicki_4	0.00	100	0	3	4	0	3	8	18
29	PZ21_FARFAR_2	9.77	73	1	4	0	0	3	10	18
30	PZ21_DasLORES_1	9.77	73	0	4	0	0	2	13	19
31	PZ21_FARFAR_1	9.02	77	0	3	0	0	3	13	19
32	PZ21_Bujnicki_1	0.00	100	0	7	4	0	4	10	25
33	PZ21_refstructure	20.29	31	10	2	0	0	0	16	28
34	PZ21_Bujnicki_3	0.00	100	0	6	6	0	6	13	31
35	PZ21_Bujnicki_5	0.75	99	0	16	4	0	4	11	35
36	PZ21_Sanbonmatsu_2	109.19	0	14	33	12	14	6	16	95
37	PZ21_Sanbonmatsu_4	122.93	0	14	39	8	14	5	16	96
38	PZ21_Sanbonmatsu_1	109.19	0	14	35	12	14	6	16	97
39	PZ21_Sanbonmatsu_3	122.93	0	14	42	8	14	5	16	99
40	PZ21_Bujnicki_2	8.00	82	29	61	0	2	2	6	100
41	PZ21_3dRNA_5	0.75	99	0	54	22	0	10	20	106

42	PZ21_3dRNA_4	0.75	99	1	54	26	0	15	31	127
43	PZ21_ChenHighLig_3	107.92	0	32	88	0	0	1	6	127
44	PZ21_ChenLowLig_3	107.92	0	32	88	0	0	1	6	127
45	PZ21_3dRNA_3	0.00	100	0	66	21	1	14	32	134
46	PZ21_SimRNA_4	117.03	0	38	87	0	2	0	10	137
47	PZ21_SimRNA_2	116.54	0	35	90	0	3	3	9	140
48	PZ21_SimRNA_1	114.95	0	40	101	1	0	1	11	154
49	PZ21_ChenLowLig_1	128.21	0	33	116	0	0	3	8	160
50	PZ21_ChenHighLig_1	128.21	0	33	117	0	0	3	8	161
51	PZ21_ChenHighLig_2	73.04	1	29	120	0	1	2	9	161
52	PZ21_ChenLowLig_2	73.04	1	29	120	0	1	2	9	161
53	PZ21_3dRNA_1	37.65	9	19	79	16	0	18	30	162
54	PZ21_ChenHighLig_5	124.53	0	29	117	0	0	7	15	168
55	PZ21_ChenLowLig_5	123.77	0	29	118	0	0	7	15	169
56	PZ21_SimRNA_3	114.54	0	47	104	1	3	2	12	169
57	PZ21_SimRNA_5	114.54	0	47	104	1	3	2	12	169
58	PZ21_3dRNA_2	46.62	5	21	103	24	0	19	32	199
59	PZ21_ChenLowLig_4	223.48	0	41	128	0	2	12	20	203
60	PZ21_ChenHighLig_4	222.73	0	41	129	0	2	12	20	204
	Average	46.16	49.77	11.23	37.82	2.83	1.27	3.40	11.67	68.22
	Standard deviation	57.90	39.95	15.73	47.05	6.45	3.53	4.53	6.76	69.14
	Median	13.16	58.00	0.00	4.00	0.00	0.00	2.00	10.00	19.00

Table S92. MolProbity report on structures in Puzzle 24.

No.	3D RNA model	(a) Clash score	(b) Rank- ing	#Bad bonds	#Bad angles	#Chiral handedness swaps	#Tetrahedral geometry outli- ers	#Probably wrong sugar pucker- ers:	(c) #Bad back- bone confor- mations	Total
1	PZ24_FARFAR2_2	0.55	99	0	2	0	0	0	3	5
2	PZ24_FARFAR2_5	0.83	99	0	1	0	0	0	4	5
3	PZ24_FARFAR2_4	0.83	99	0	1	0	0	0	5	6
4	PZ24_FARFAR2_8	0.83	99	0	3	0	0	0	4	7
5	PZ24_FARFAR2_3	0.83	99	0	3	0	0	0	5	8

6	PZ24_Das_2	1.94	99	0	0	0	0	0	9	9
7	PZ24_Das_3	1.94	99	0	0	0	0	0	9	9
8	PZ24_Das_4	2.22	99	0	0	0	0	0	9	9
9	PZ24_Das_8	1.94	99	0	0	0	0	0	9	9
10	PZ24_Das_1	1.94	99	0	0	0	0	0	10	10
11	PZ24_Das_5	1.94	99	0	0	0	0	0	10	10
12	PZ24_refstructure	0.28	99	0	0	0	0	1	10	11
13	PZ24_Das_6	2.22	99	0	0	0	0	0	12	12
14	PZ24_RNAComposer_1	8.87	78	0	0	0	0	0	12	12
15	PZ24_Das_9	1.94	99	0	0	0	0	0	13	13
16	PZ24_Das_10	1.94	99	0	1	0	0	0	13	14
17	PZ24_Das_7	1.94	99	0	1	0	0	0	13	14
18	PZ24_DasTFN_3	1.66	99	0	2	0	0	0	12	14
19	PZ24_FARFAR2_1	1.66	99	0	2	0	0	0	12	14
20	PZ24_FARFAR2_7	1.66	99	0	0	0	0	0	15	15
21	PZ24_DasTFN_9	2.22	99	1	3	0	0	0	14	18
22	PZ24_FARFAR2_6	2.22	99	1	3	0	0	0	14	18
23	PZ24_RNAComposer_3	6.10	90	0	0	0	0	0	19	19
24	PZ24_RNAComposer_5	5.82	91	0	0	0	0	0	19	19
25	PZ24_Adamiak_5	11.92	63	0	0	0	0	1	19	20
26	PZ24_RNAComposer_4	8.32	80	0	0	0	0	0	21	21
27	PZ24_FARFAR2_10	3.05	98	0	3	0	0	3	16	22
28	PZ24_FARFAR2_9	1.66	99	0	1	0	0	0	21	22
29	PZ24_Adamiak_1	10.82	67	0	0	0	0	2	21	23
30	PZ24_DasTFN_2	4.99	94	0	4	0	0	2	17	23
31	PZ24_DasTFN_10	0.55	99	0	4	0	0	2	18	24
32	PZ24_Adamiak_4	12.20	62	0	0	0	0	2	24	26
33	PZ24_DasTFN_4	1.94	99	0	2	0	0	2	24	28
34	PZ24_DasTFN_7	5.82	91	1	5	0	0	4	19	29
35	PZ24_Adamiak_3	10.54	68	0	0	0	0	1	29	30
36	PZ24_DasTFN_6	4.16	96	1	6	0	0	5	18	30
37	PZ24_DasTFN_1	3.33	97	1	6	0	0	5	20	32
38	PZ24_DasTFN_5	4.16	96	1	7	0	0	3	21	32

39	PZ24_Adamiak_2	14.42	52	0	0	0	0	5	29	34
40	PZ24_DasTFN_8	5.82	91	0	9	0	1	3	22	35
41	PZ24_RNAComposer_2	11.92	63	0	0	0	0	4	32	36
42	PZ24_3dRNA_4	0.00	100	1	18	0	0	4	25	48
43	PZ24_3dRNA_5	1.11	99	1	23	0	0	6	18	48
44	PZ24_3dRNA_2	0.00	100	1	26	0	0	8	19	54
45	PZ24_Bujnicki_4	0.00	100	0	32	6	0	6	16	60
46	PZ24_Bujnicki_2	0.00	100	0	27	6	0	8	20	61
47	PZ24_3dRNA_1	0.28	99	1	42	0	0	8	16	67
48	PZ24_3dRNA_3	0.00	100	1	39	1	0	12	24	77
49	PZ24_iFoldRNA_1	0.83	99	1	61	0	0	3	15	80
50	PZ24_Bujnicki_3	0.00	100	1	44	9	0	8	25	87
51	PZ24_Bujnicki_1	0.00	100	0	24	17	0	16	34	91
52	PZ24_iFoldRNA_3	2.22	99	1	75	0	0	2	15	93
53	PZ24_iFoldRNA_2	1.67	99	1	79	0	1	3	16	100
54	PZ24_iFoldRNA_5	0.55	99	1	84	0	0	4	16	105
55	PZ24_iFoldRNA_4	1.94	99	1	83	0	1	4	17	106
56	PZ24_Vfold3D_4	0.00	100	6	68	2	0	4	44	124
57	PZ24_Ding_3	13.03	58	0	116	0	0	0	11	127
58	PZ24_Ding_10	8.04	82	0	104	0	0	4	20	128
59	PZ24_Ding_8	9.71	73	0	109	0	0	4	18	131
60	PZ24_Ding_2	10.26	70	0	115	0	0	3	15	133
61	PZ24_Vfold3D_5	0.00	100	9	85	0	1	4	34	133
62	PZ24_Ding_7	10.82	67	0	119	0	0	2	13	134
63	PZ24_Vfold3D_2	0.00	100	6	81	0	0	6	44	137
64	PZ24_Ding_4	12.76	60	0	127	0	0	2	13	142
65	PZ24_Ding_6	11.37	65	0	124	0	0	3	15	142
66	PZ24_Ding_5	9.43	74	0	123	0	0	4	16	143
67	PZ24_Ding_9	9.98	71	0	119	0	0	4	20	143
68	PZ24_Ding_1	7.49	84	0	131	0	0	4	15	150
69	PZ24_Vfold3D_1	0.00	100	11	90	0	1	4	44	150
70	PZ24_Vfold3D_3	0.00	100	27	93	0	1	7	46	174
71	PZ24_Bujnicki_5	0.00	100	2	192	6	1	10	22	233

72	PZ24_Kollmann_2	128.68	0	62	192	1	6	4	21	286
73	PZ24_Kollmann_4	123.19	0	71	216	1	8	5	22	323
74	PZ24_Kollmann_7	117.55	0	67	215	2	6	10	29	329
75	PZ24_Kollmann_6	92.12	0	77	219	0	5	9	25	335
76	PZ24_Kollmann_10	113.64	0	73	233	0	8	8	26	348
77	PZ24_Kollmann_8	114.07	0	75	235	0	7	8	28	353
78	PZ24_Kollmann_5	121.04	0	89	230	0	11	5	26	361
79	PZ24_Kollmann_3	120.66	0	91	236	1	5	7	26	366
80	PZ24_Kollmann_9	104.33	0	85	241	0	8	10	26	370
81	PZ24_Kollmann_1	115.47	0	98	236	0	8	11	29	382
82	PZ24_SimRNA_2	136.29	0	107	243	0	5	3	27	385
83	PZ24_SimRNA_5	96.00	0	120	256	2	4	3	28	413
84	PZ24_SimRNA_3	124.86	0	119	255	0	2	6	32	414
85	PZ24_SimRNA_1	120.70	0	118	273	2	9	5	34	441
86	PZ24_VfoldLA_1	144.71	0	85	308	0	0	9	43	445
87	PZ24_VfoldLA_2	171.09	0	94	334	0	1	13	43	485
88	PZ24_VfoldLA_3	158.98	0	84	350	0	5	14	44	497
89	PZ24_VfoldLA_5	147.87	0	99	341	0	3	8	49	500
90	PZ24_VfoldLA_4	155.67	0	99	342	0	3	15	46	505
91	PZ24_SimRNA_4	99.70	0	129	323	0	9	9	41	511
	Average	30.64	70.88	21.10	85.71	0.62	1.32	4.00	21.29	134.03
	Standard deviation	51.62	39.75	39.03	106.67	2.27	2.68	3.91	10.79	154.52
	Median	3.33	97.00	0.00	27.00	0.00	0.00	3.00	19.00	61.00