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Influence of Na^{+} and Mg^{2+} ions on RNA structures studied with molecular dynamics simulations - Supporting Information

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Table S1. Three numbers, called validation scores (clashscore, backbone, and resolution), that represent the quality of the experimental structure are taken from the Protein Data Bank (PDB, http://www.rcsb.org/pdb/). Also the number of water and ions that are added to each system (Na^+_{CI}/Na^+_{PS}/Mg^{2+}_{CI}/Mg^{2+}_{PS}) to be able to run MD simulations are listed.

	PDB id	clashscore	backbone	resolution (Å)	Water	Mg^{2+}	Na^+	Cl^-
X-ray	helical							
	1D4R	20	0.61	2.0	29700	0/0/26/26	52/137/0/85	0/85/0/85
	1QC0	3	0.71	1.6	20900	0/0/18/18	36/98/0/62	0/62/0/62
	2QEK	1	0.82	1.8	25300	0/0/22/22	44/118/0/74	0/74/0/74
	4K31	18	0.67	1.4	24200	0/0/21/21	42/114/0/72	0/72/0/72
	413D	7	0.81	1.8	14300	0/0/12/12	24/66/0/42	0/42/0/42
	420D	5	0.84	1.9	17600	0/0/15/15	30/90/0/60	0/60/0/60
X-ray	complex folded							
	4B5R	12	0.45	2.5	51700	0/0/47/47	93/260/0/167	0/167/1/168
	4FEJ	5	0.67	1.5	36850	0/0/33/33	66/185/0/119	0/119/0/119
	4FRG	1	0.66	2.9	46200	0/0/42/42	83/218/0/135	0/135/1/136
	4JF2	4	0.68	2.3	41800	0/0/38/38	75/194/0/119	0/119/1/120
	4KQY	19	0.36	3.0	65450	0/0/59/59	118/310/0/192	0/192/0/192
	4P5J	14	0.64	2.0	45640	0/0/41/41	82/220/0/138	0/138/0/138
NMR	helical							
	1A4D	20	0.41		22500	0/0/20/20	40/106/0/66	0/66/0/66
	2D18	0	0.75		18700	0/0/18/18	32/90/0/58	0/58/0/58
	2KYD	0	0.70		17600	0/0/15/15	30/88/0/58	0/58/0/58
	2L2J	0	0.75		23100	0/0/21/21	41/108/0/67	0/67/1/68
	2LPS	0	0.64		18700	0/0/17/17	33/88/0/55	0/55/1/56
	2LV0	0	0.64		13200	0/0/12/12	23/68/0/45	0/45/1/46
NMR	complex folded							
	1YMO	118	0.11		25820	0/0/23/23	46/121/0/75	0/75/0/75
	2ADT	56	0.34		47300	0/0/42/42	84/225/0/141	0/141/0/141
	2LKR	76	0.10		61050	0/0/55/55	110/285/0/175	0/175/0/175
	2MHI	134	0.08		29150	0/0/26/26	52/150/0/98	0/98/0/98
	2MTK	24	0.31		25850	0/0/23/23	46/119/0/73	0/73/0/73
	2M8K	84	0.11		26400	0/0/24/24	47/123/0/76	0/76/1/77

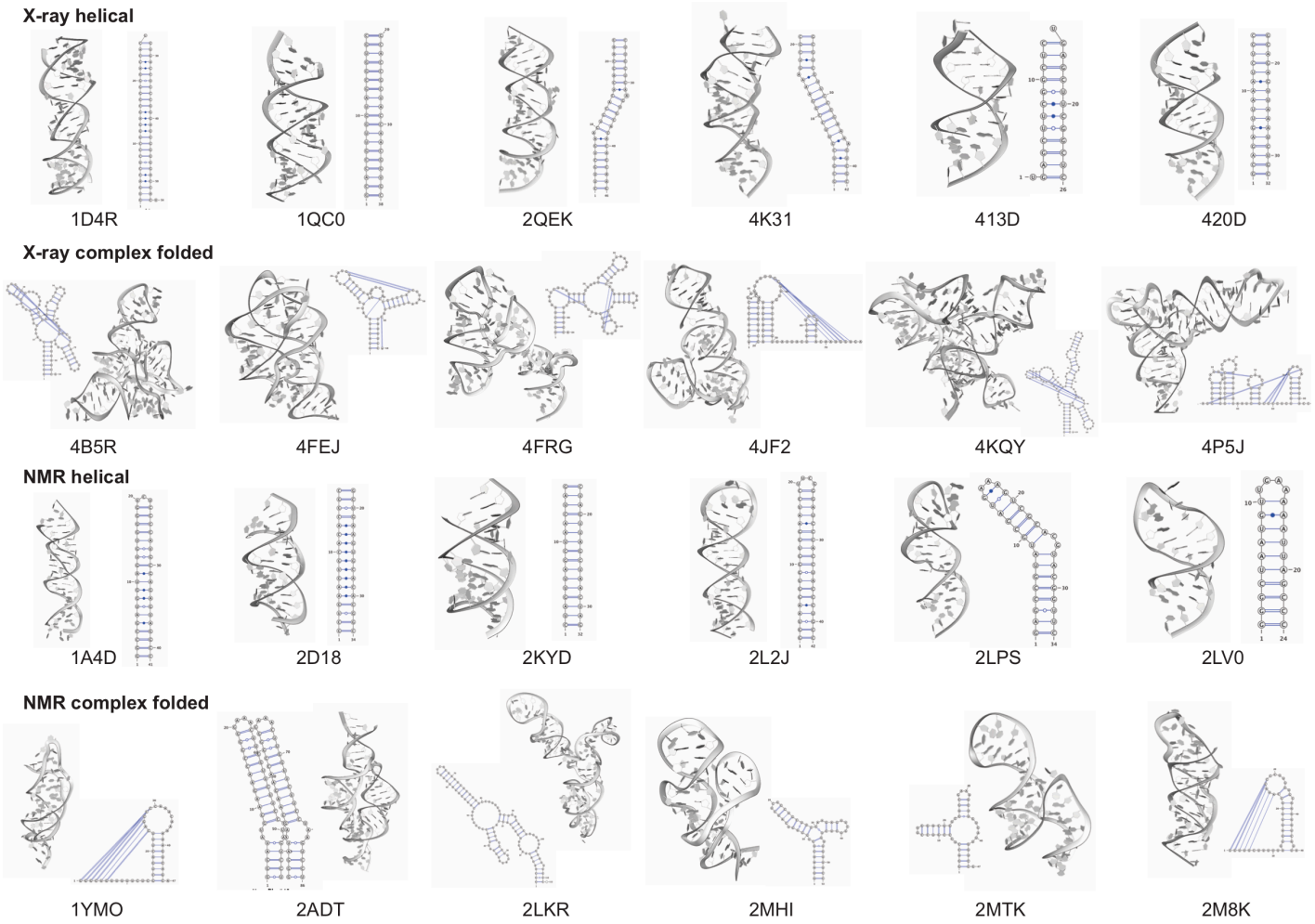

Figure S1. Secondary and three-dimensional structures of each RNA is given. The structures are grouped in the four groups used throughout the manuscript: X-ray helical, X-ray complex folded, NMR helical, NMR complex folded. Secondary structures are obtained using the visualization software VARNA (v3.9) with dot-bracket-notation obtained from x3dna-dssr (v1.7.3). Three-dimensional structures are visualized with BALLView.

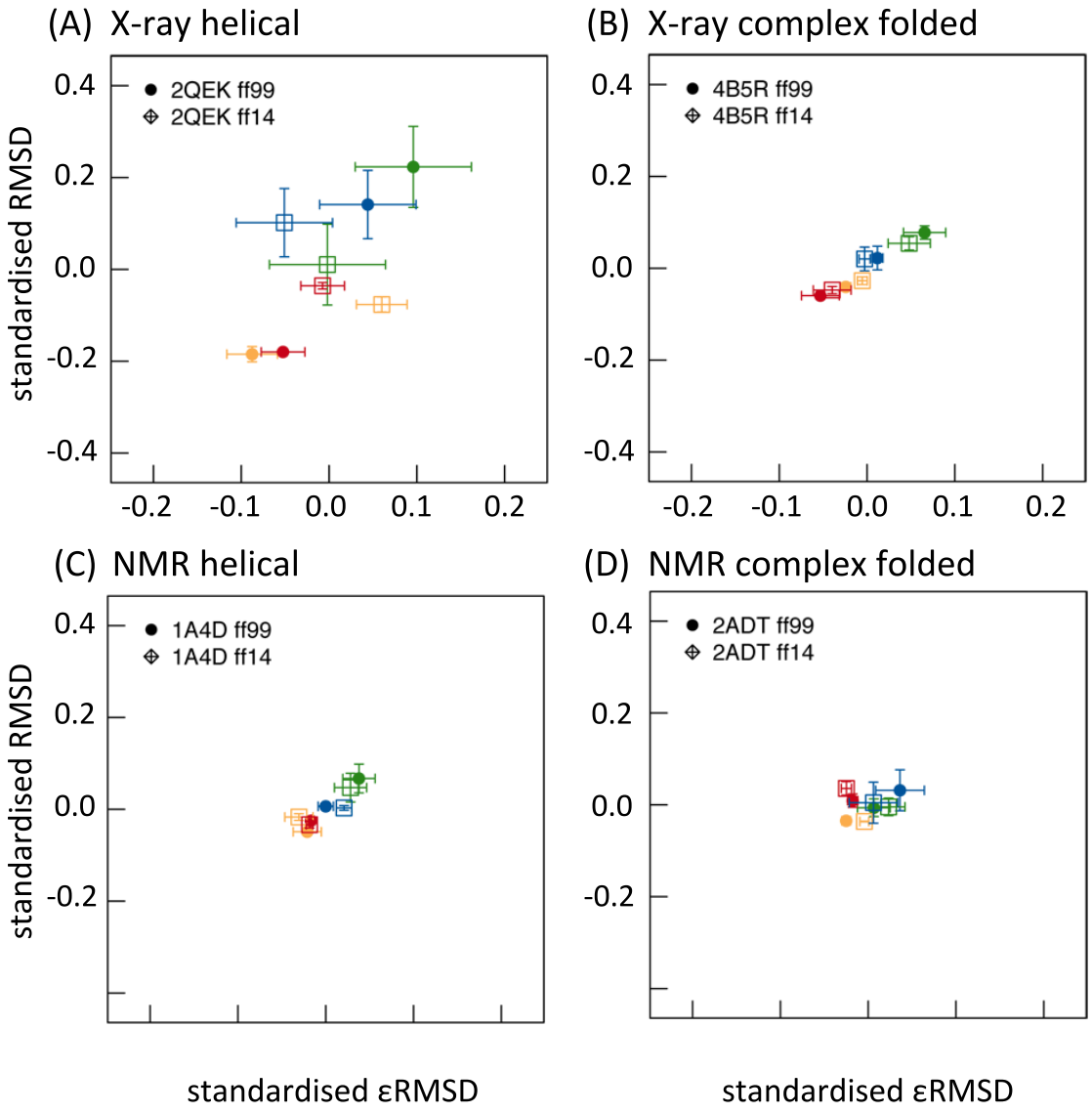

Figure S2. Standardised mean RMSD (nm) values are plotted against standardised mean ϵRMSD values for four RNA structure. RMSD and ϵRMSD values for helical X-ray and NMR as well as for complex folded X-ray and NMR structures are obtained during the production run for each replica and each system. Instead of comparing different RNA structures, we compare here two force fields: ff99 with parameter set parm99 (solid dots) and ff14 with parameter set parmOL combined with parmbsc0 (squares). The four systems are shown in different colors (as in Fig. 1): Na^{+}_{CI} (green), Na^{+}_{PS} (blue), Mg^{2+}_{CI} (orange), Mg^{2+}_{PS} (red).

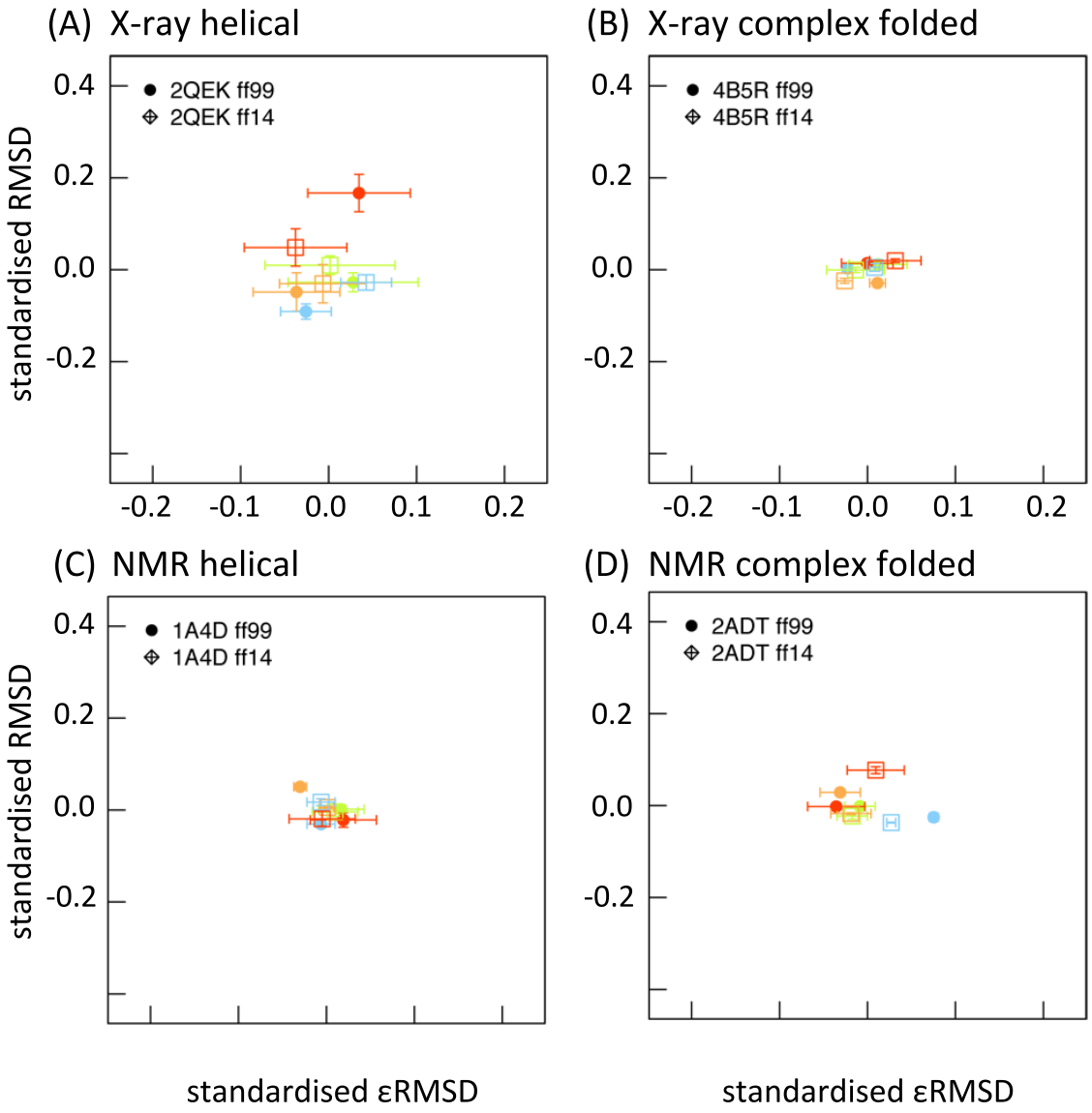

Figure S3. Standardised mean RMSD (nm) values are plotted against standardised mean ϵRMSD values for four RNA structure. RMSD and ϵRMSD values for helical X-ray and NMR as well as for complex folded X-ray and NMR structures are obtained during the production run for each replica and each system. Instead of comparing different RNA structures, we compare here two force fields: ff99 with parameter set parm99 (solid dots) and ff14 with parameter set parmOL combined with parmbsc0 (squares). Here, we also used K^+ instead of Na^+ and indicate this with lighter colors compared to Fig. 1 or Fig. S2. The four systems are shown in different colors: Na^+_{CI} (green), Na^+_{PS} (blue), Mg^{2+}_{CI} (orange), Mg^{2+}_{PS} (red).

Table S2. The average ϵRMSD values with errors and the maximum ϵRMSD value are determined for all three replicas in one system.

	PDB id	Na^+ mean ϵRMSD	max	Na^+ and NaCl mean ϵRMSD	max	Mg^{2+} mean ϵRMSD	max	Mg^{2+} and NaCl mean ϵRMSD	max
X-ray	helical								
	1D4R	0.92±0.12	1.37	0.96±0.12	1.38	0.80±0.10	1.05	0.92±0.10	1.23
	1QC0	0.49±0.04	0.77	0.48±0.04	0.66	0.51±0.06	0.78	0.47±0.04	0.67
	2QEK	0.98±0.11	1.39	0.92±0.07	1.25	0.79±0.05	1.01	0.83±0.04	1.08
	4K31	0.64±0.05	0.85	0.62±0.05	0.88	0.71±0.07	0.98	0.67±0.05	0.96
	413D	0.80±0.07	1.11	0.83±0.12	1.44	0.67±0.08	0.98	0.67±0.09	1.01
	420D	0.69±0.10	1.12	0.63±0.05	0.88	0.60±0.07	1.01	0.56±0.05	0.86
X-ray	complex folded								
	4B5R	0.86±0.03	0.98	0.80±0.05	0.99	0.77±0.04	0.92	0.74±0.06	0.92
	4FEJ	0.98±0.06	1.30	0.93±0.07	1.26	0.84±0.11	1.12	0.75±0.07	1.00
	4FRG	0.79±0.08	1.03	0.76±0.04	0.97	0.74±0.06	0.88	0.70±0.05	0.88
	4JF2	0.88±0.04	1.11	0.83±0.07	1.08	0.78±0.05	0.99	0.77±0.06	1.04
	4KQY	0.91±0.09	1.12	0.86±0.07	1.08	0.86±0.07	1.00	0.78±0.06	0.97
	4P5J	0.78±0.04	0.92	0.85±0.06	1.00	0.72±0.05	0.86	0.83±0.04	0.99
NMR	helical								
	1A4D	0.80±0.06	1.08	0.77±0.06	0.99	0.74±0.06	0.95	0.75±0.06	0.95
	2D18	1.10±0.12	1.44	1.14±0.10	1.56	0.99±0.10	1.26	0.91±0.09	1.24
	2KYD	0.60±0.06	1.07	0.59±0.15	1.15	0.47±0.05	0.72	0.47±0.06	0.86
	2L2J	0.67±0.08	0.99	0.58±0.04	0.82	0.59±0.04	0.79	0.59±0.05	0.84
	2LPS	0.93±0.08	1.27	0.90±0.12	1.22	0.68±0.09	1.00	0.64±0.09	1.02
	2LV0	0.98±0.08	1.30	1.03±0.05	1.29	0.85±0.10	1.31	0.92±0.06	1.17
NMR	complex folded								
	1YMO	1.28±0.04	1.46	1.38±0.08	1.70	1.28±0.04	1.53	1.33±0.05	1.54
	2ADT	0.96±0.03	1.12	0.99±0.03	1.14	0.93±0.03	1.06	0.94±0.02	1.05
	2LKR	1.53±0.04	1.68	1.44±0.04	1.60	1.49±0.05	1.66	1.45±0.03	1.59
	2MHI	1.44±0.04	1.57	1.45±0.07	1.66	1.43±0.04	1.55	1.44±0.05	1.72
	2MTK	1.14±0.07	1.37	1.04±0.03	1.23	1.00±0.05	1.21	0.97±0.05	1.19
	2M8K	1.05±0.05	1.23	1.08±0.04	1.25	1.07±0.04	1.30	1.02±0.06	1.26

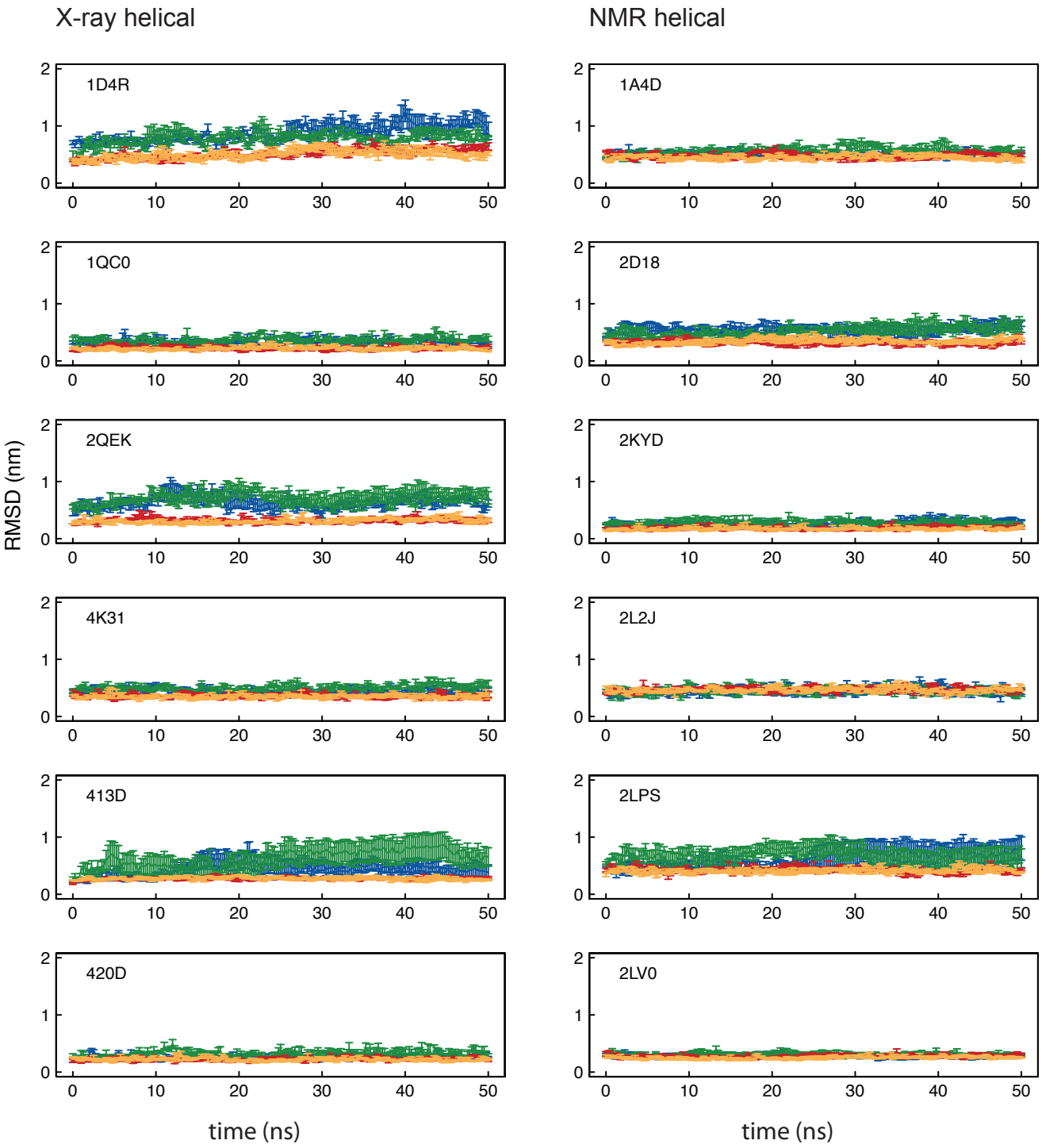

Figure S4. RMSD values are calculated to the original PDB structure over 50 ns production runs for three replicas in each system. The average RMSD and its error are shown for each helical RNA obtained by X-ray or NMR. The four systems are shown in different colors (as in Fig. 1): Na^{+}_{CI} (green), Na^{+}_{PS} (blue), Mg^{2+}_{CI} (orange), Mg^{2+}_{PS} (red).

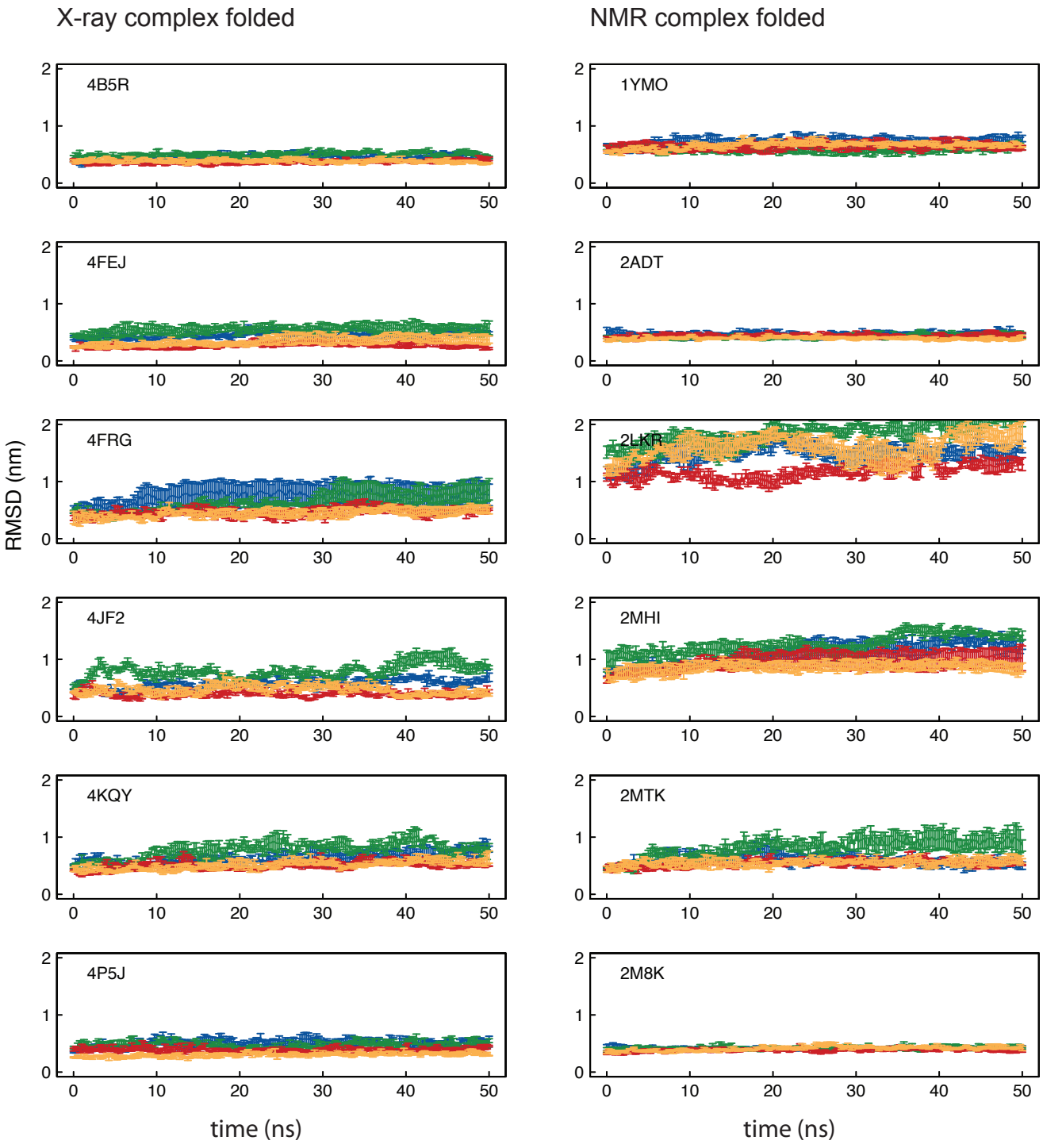

Figure S5. RMSD values are calculated to the original PDB structure over 50 ns production runs for three replicas in each system. The average RMSD and its error are shown for each complex folded RNA obtained by X-ray or NMR. The four systems are shown in different colors (as in Fig. 1): Na^{+}_{CI} (green), Na^{+}_{PS} (blue), Mg^{2+}_{CI} (orange), Mg^{2+}_{PS} (red).

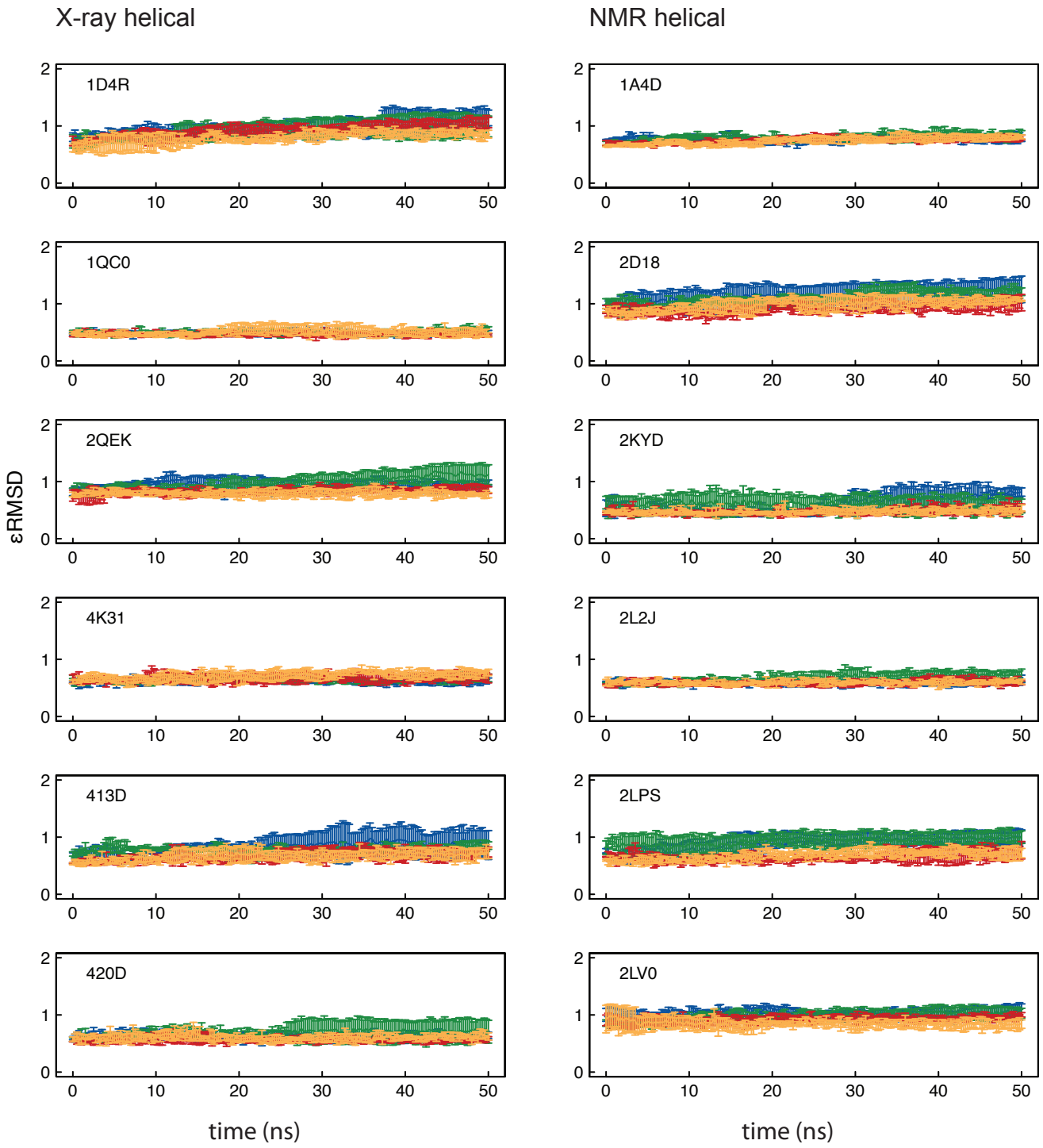

Figure S6. ϵRMSD values are calculated to the original PDB structure over 50 ns production runs for three replicas in each system. The average ϵRMSD and its error are shown for each helical RNA obtained by X-ray or NMR. The four systems are shown in different colors (as in Fig. 1): Na^{+}_{CI} (green), Na^{+}_{PS} (blue), Mg^{2+}_{CI} (orange), Mg^{2+}_{PS} (red).

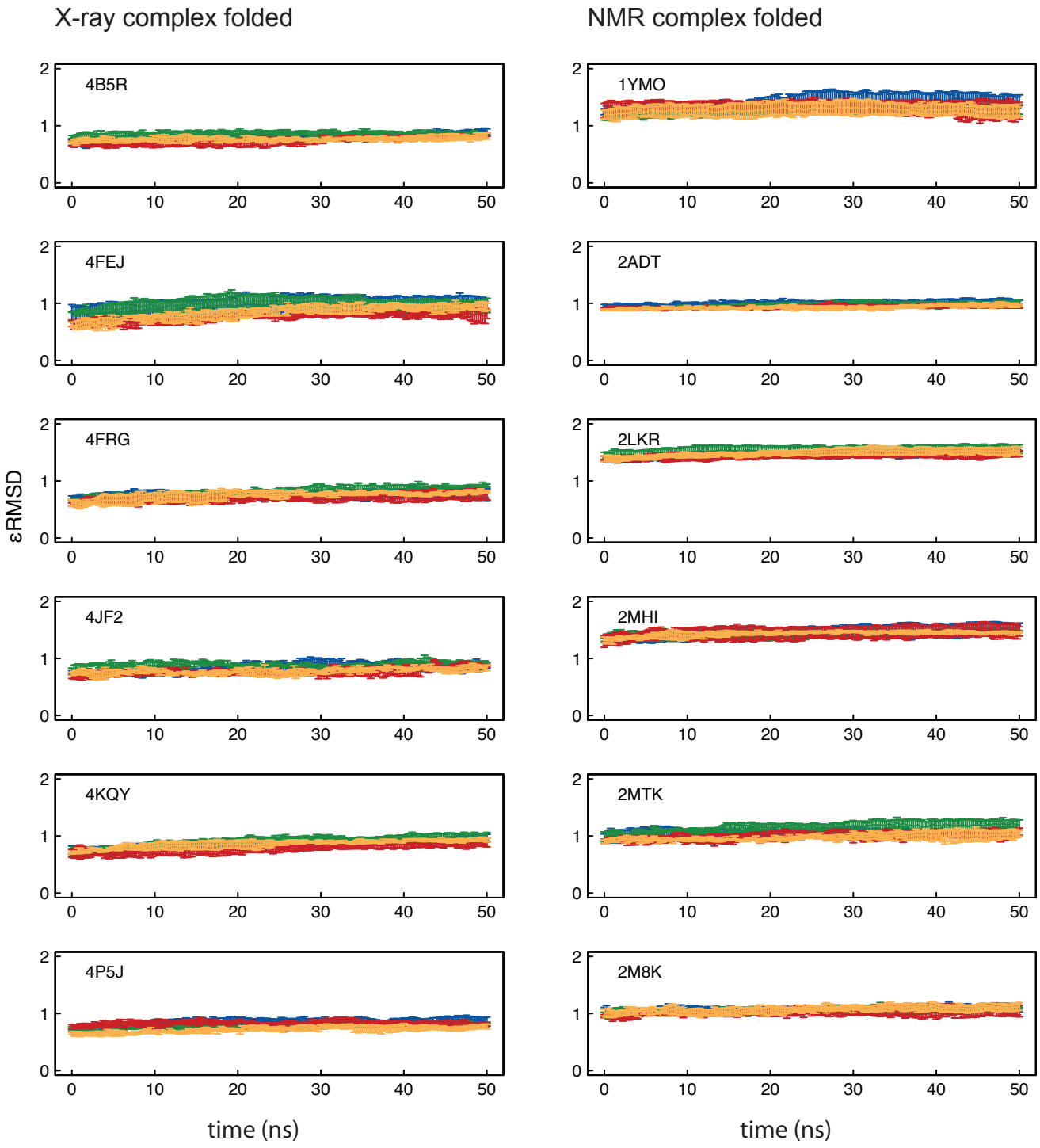

Figure S7. ϵRMSD values are calculated to the original PDB structure over 50 ns production runs for three replicas in each system. The average ϵRMSD and its error are shown for each complex folded RNA obtained by X-ray or NMR. The four systems are shown in different colors (as in Fig. 1): Na^{+}_{CI} (green), Na^{+}_{PS} (blue), Mg^{2+}_{CI} (orange), Mg^{2+}_{PS} (red).

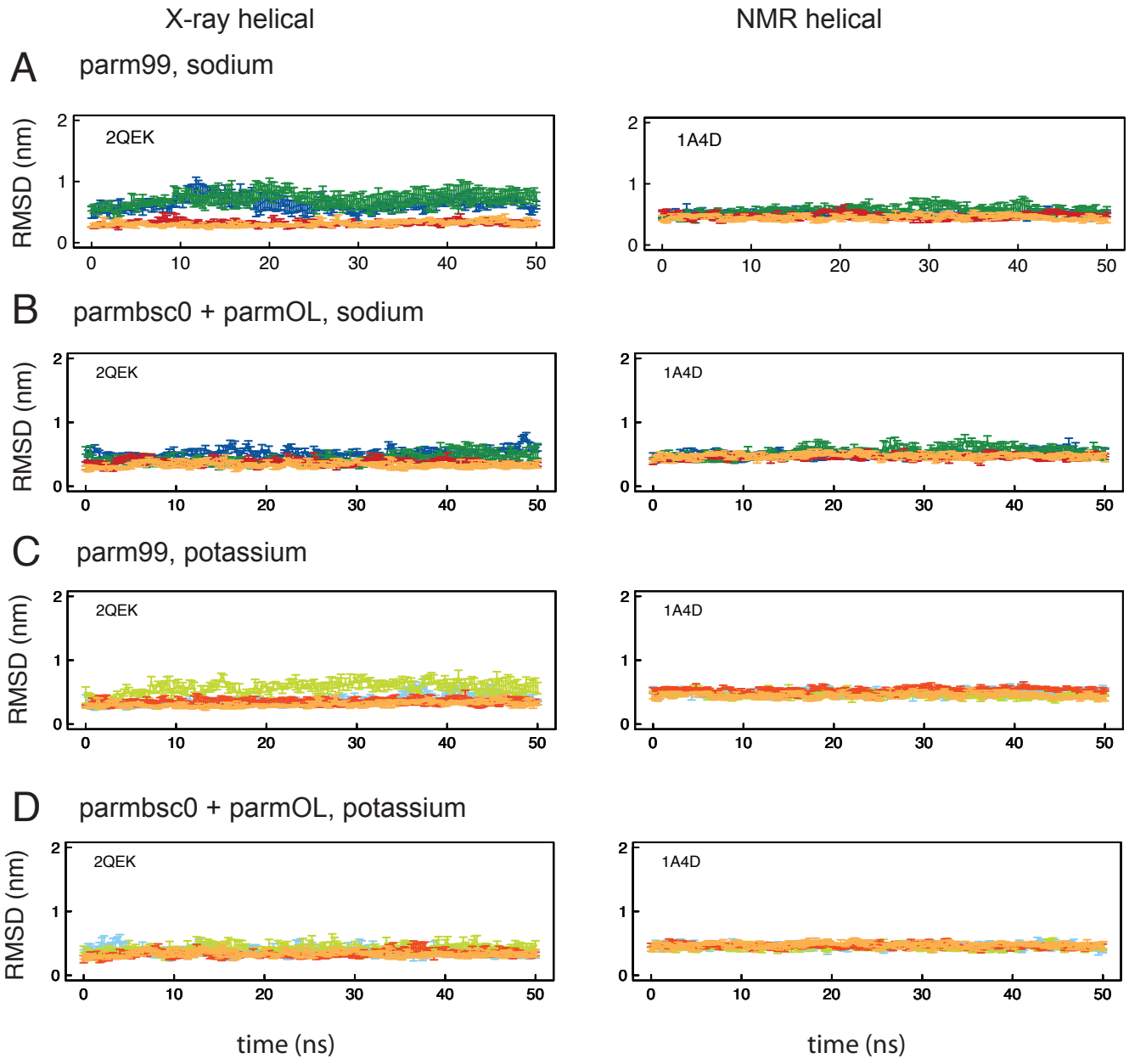

Figure S8. RMSD values are calculated to the original PDB structure over 50 ns production runs for three replicas in each system. The average RMSD and its error are shown for two selected helical structures obtained by X-ray (PDB id: 2QEK) or NMR (PDB id: 1A4D). (A) is the same plot as in Fig. S2 using parm99, (B) with parmbsc0 and parmOL. For A and B the four systems are shown in different colors (as in Fig. 1): Na^+_{CI} (green), Na^+_{PS} (blue), Mg^{2+}_{CI} (orange), Mg^{2+}_{PS} (red). (C) is using parm99 and (D) using parmbsc0 and parmOL. For C and D the four systems are shown in lighter colors: (1) K^+ (light green), (2) K^+ and KCl (light blue), (3) Mg^{2+} (orange), (4) Mg^{2+} and KCl (light red).

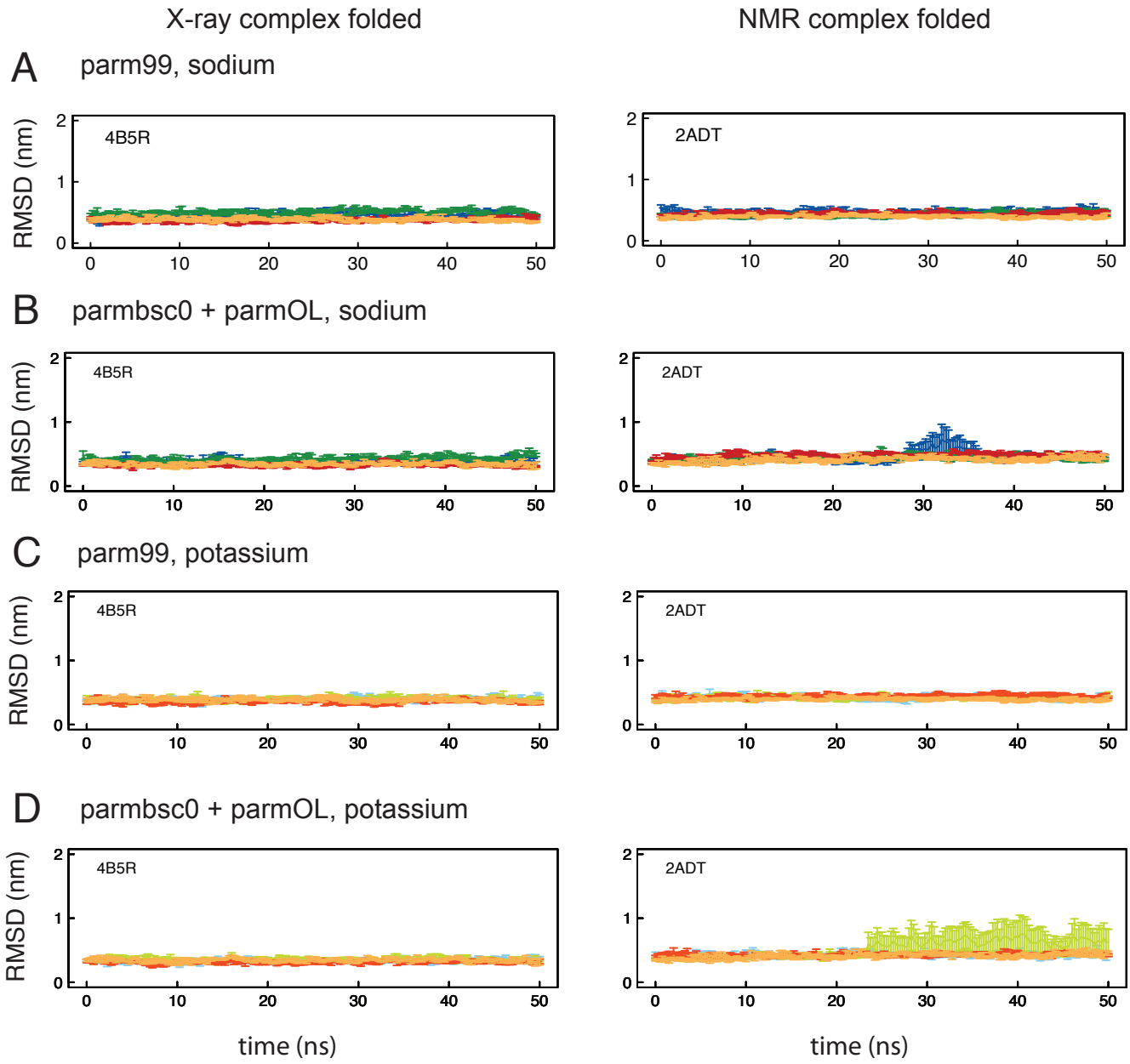

Figure S9. RMSD values are calculated to the original PDB structure over 50 ns production runs for three replicas in each system. The average RMSD and its error are shown for two selected complex folded structures obtained by X-ray (PDB id: 4B5R) or NMR (PDB id: 2ADT). (A) is the same plot as in Fig. S2 using parm99, (B) with parmbsc0 and parmOL. For A and B the four systems are shown in different colors (as in Fig. 1): Na^{+}_{CI} (green), Na^{+}_{PS} (blue), Mg^{2+}_{CI} (orange), Mg^{2+}_{PS} (red). (C) is using parm99 and (D) using parmbsc0 and parmOL. For C and D the four systems are shown in lighter colors: (1) K^{+} (light green), (2) K^{+} and KCl (light blue), (3) Mg^{2+} (orange), (4) Mg^{2+} and KCl (light red).

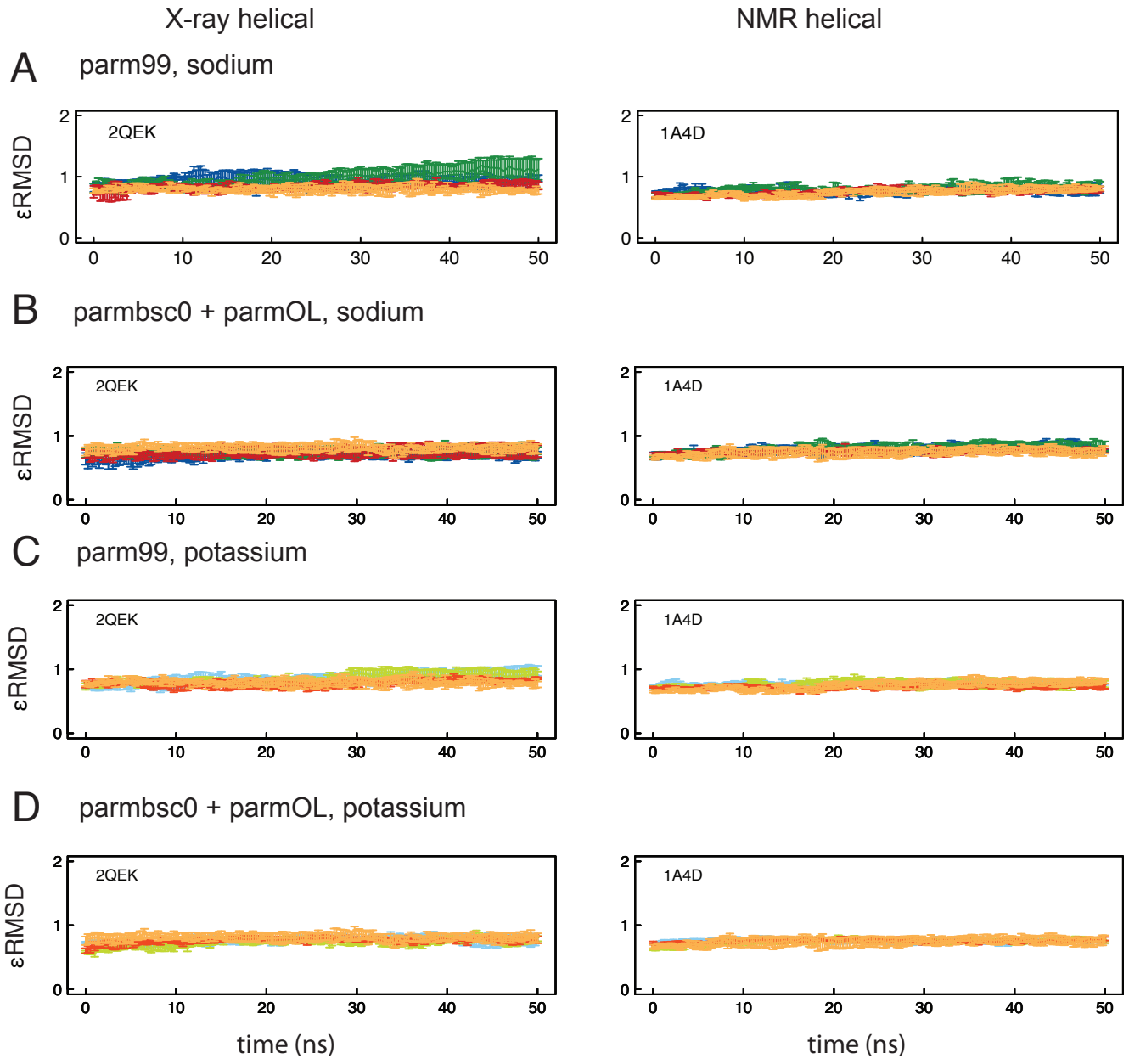

Figure S10. ϵRMSD values are calculated to the original PDB structure over 50 ns production runs for three replicas in each system. The average ϵRMSD and its error are shown for two selected helical structures obtained by X-ray (PDB id: 2QEK) or NMR (PDB id: 1A4D). (A) is the same plot as in Fig. S2 using parm99, (B) with parmbsc0 and parmOL. For A and B the four systems are shown in different colors (as in Fig. 1): Na^{+}_{CI} (green), Na^{+}_{PS} (blue), Mg^{2+}_{CI} (orange), Mg^{2+}_{PS} (red). (C) is using parm99 and (D) using parmbsc0 and parmOL. For C and D the four systems are shown in lighter colors: (1) K^{+} (light green), (2) K^{+} and KCl (light blue), (3) Mg^{2+} (orange), (4) Mg^{2+} and KCl (light red).

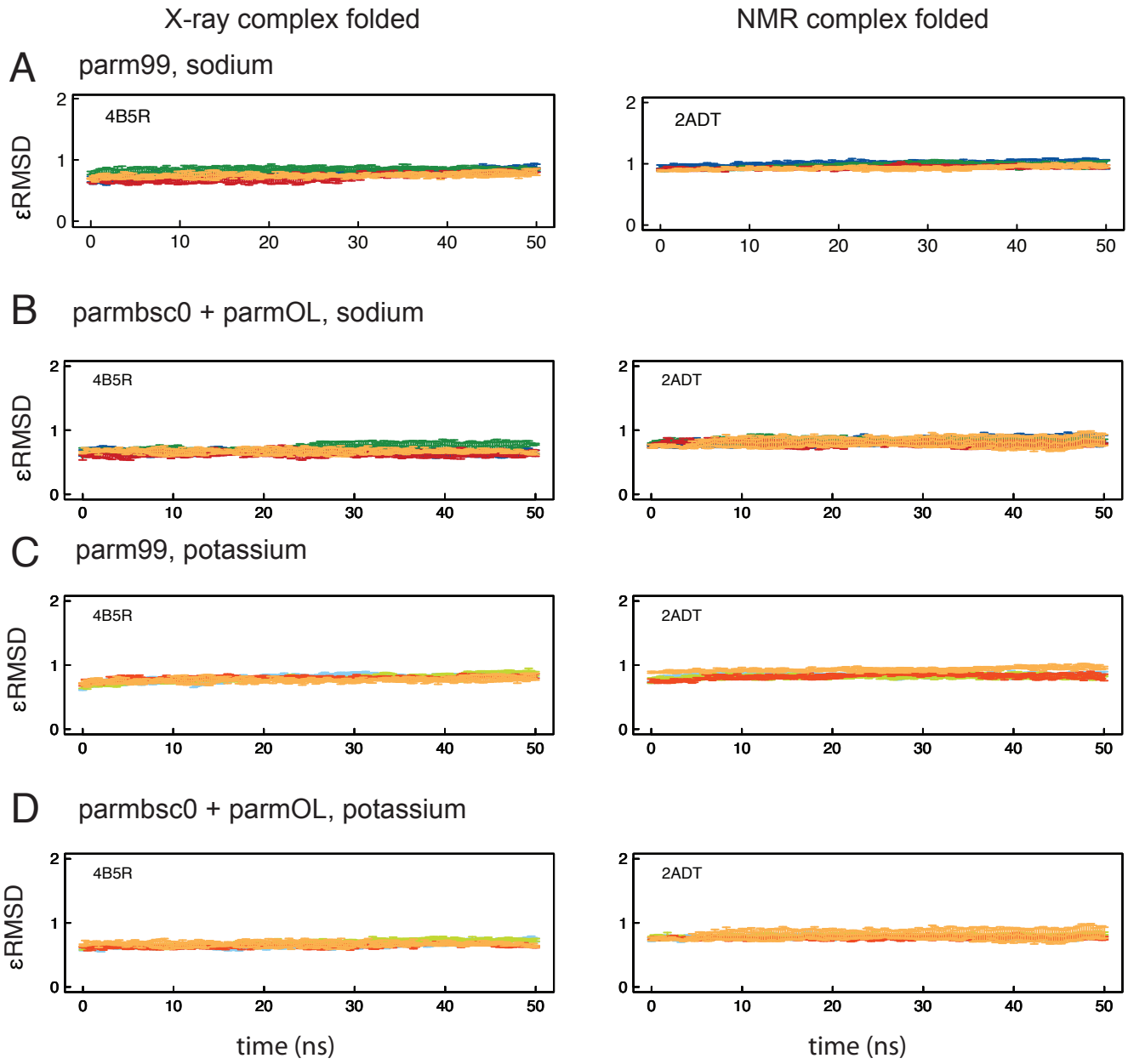

Figure S11. ϵRMSD values are calculated to the original PDB structure over 50 ns production runs for three replicas in each system. The average ϵRMSD and its error are shown for two selected complex folded structures obtained by X-ray (PDB id: 4B5R) or NMR (PDB id: 2ADT). (A) is the same plot as in Fig. S2 using parm99, (B) with parmbsc0 and parmOL. For A and B the four systems are shown in different colors (as in Fig. 1): Na^{+}_{CI} (green), Na^{+}_{PS} (blue), Mg^{2+}_{CI} (orange), Mg^{2+}_{PS} (red). (C) is using parm99 and (D) using parmbsc0 and parmOL. For C and D the four systems are shown in lighter colors: (1) K^{+} (light green), (2) K^{+} and KCl (light blue), (3) Mg^{2+} (orange), (4) Mg^{2+} and KCl (light red).

Table S3. Average RMSD values (Å) between experimental and predicted binding sites during the equilibration phase. The position of ions are predicted with MobyWat. The resulting top 50 ion positions are considered for each replica.

System	Na^+_{CI}	Na^+_{PS}	Mg^{2+}_{CI}	Mg^{2+}_{PS}	
Ion	Na^+	Na^+	Mg^{2+}	Na^+	Mg^{2+}
1D4R					
MG-90	1.14±0.12	1.14±0.41	1.60±0.12	1.69±1.09	1.77±0.07
MG-91	0.74±0.13	3.33±3.07	2.03±0.14	1.83±1.12	3.73±1.30
2MTK					
MG-48	6.03±1.26	7.70±0.75	5.17±1.52	6.13±1.57	3.72±1.12
MG-49	2.59±0.87	3.39±0.61	4.25±1.34	6.69±3.74	4.09±0.65
MG-50	2.94±1.77	3.12±1.32	4.27±2.36	4.93±0.73	5.12±1.47
MG-51	2.55±0.60	2.60±0.90	3.87±2.14	3.81±1.85	3.17±0.70
MG-52	3.36±1.36	2.37±1.15	3.87±2.40	3.36±1.56	3.50±0.54
MG-53	1.50±0.25	2.49±1.58	2.26±1.19	4.67±1.79	2.37±0.68
2QEK					
K-47	0.60±0.08	1.26±1.05	3.44±1.19	0.51±0.11	6.16±3.47
K-48	1.65±1.67	1.20±1.14	4.24±3.31	1.01±0.73	3.71±2.26
MG-49	2.86±0.51	2.22±0.48	1.32±0.30	3.22±0.19	1.07±0.29
K-50	0.56±0.06	1.73±1.02	2.53±0.06	1.41±0.85	3.03±1.92
4FRG					
MG-179	0.99±0.66	0.98±0.19	1.35±0.17	0.82±0.35	5.08±1.80
MG-180	1.69±0.11	1.32±0.20	3.52±0.31	1.41±0.26	6.21±0.74
MG-181	1.18±0.38	2.10±0.56	1.57±0.19	1.82±0.21	1.87±0.35
MG-182	3.41±0.25	3.93±0.66	2.44±1.00	3.09±0.98	3.38±1.84
MG-183	1.80±0.68	2.25±2.16	2.17±0.82	2.04±0.68	3.91±1.88
MG-184	1.35±0.18	1.41±0.26	0.55±0.12	1.46±0.13	6.05±0.42
MG-185	1.34±0.15	1.69±0.84	3.20±0.08	1.26±0.28	6.04±0.10
4JF2					
MG-94	0.46±0.10	1.43±0.96	2.30±0.52	0.56±0.48	3.39±1.17
MG-95	5.51±0.95	4.76±1.03	3.58±0.95	5.43±0.54	5.20±2.35
MG-96	1.19±0.29	1.47±0.38	2.81±0.65	1.14±0.54	4.62±2.24
MG-97	8.46±0.09	6.78±2.41	8.25±0.48	8.26±0.46	8.56±1.14
4KQY					
MG-121	2.00±0.20	2.16±0.14	4.46±1.39	1.19±0.60	8.98±1.62
MG-122	4.98±0.47	2.66±1.91	2.25±0.20	4.46±0.71	2.16±1.14
4P5J					
MG-85	0.88±0.26	2.34±0.55	0.32±0.06	1.57±0.55	5.78±0.92
MG-86	1.77±0.05	2.58±1.07	2.46±0.97	2.05±0.06	7.60±1.51