SUPPLEMENTARY INFORMATION

MOLECULAR DYNAMICS OF TRICLINIC LYSOZYME IN A CRYSTAL LATTICE

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RMSD convergence in crystal simulations is relatively slow as compared to what is generally seen in solution simulations. All simulations in Figure 2 of the main text appear to level out only after about 400ns of production simulation, but even after that large fluctuations are observed. This is most evident in the lattice backbone RMSDs. To further test the impact of equilibration schemes on the slow convergence rates, we ran additional simulations using Amber ff12SB force field using both the standard equilibration protocol used for all simulations reported in the paper and a more conservative equilibration scheme, slowly relaxing the atomic coordinate restraints over a period of 500ns. Supplementary Data Figure 1shows that structural deviations are essentially the same as for similar ff12SB simulations using our standard 23ns equilibration, indicating that the slow crystal simulation convergence times are independent of solvent equilibration. To further test convergence, we extended the ff99SB and ff14SB simulations for a further two microseconds and compared the first, second, and third microseconds to each other. Supplementary Data Figure 2shows that for ff14SB results are virtually identical, except for the initial 200-400ns of equilibration in the first microsecond, showing that after that initial period, the system does indeed appear to have converged. On the other hand, ff99SB requires about one microsecond to converge to the values observed in the latter two microseconds. To test reproducibility of the simulated results, we ran a second 1 μs simulation using ff12SB (Figure 1). Structural deviations and fluctuations indicate that simulation results using a given force field are reproducible: RMSD and RMSF plots are more similar among the three ff12SB simulations than compared to the other three force fields.

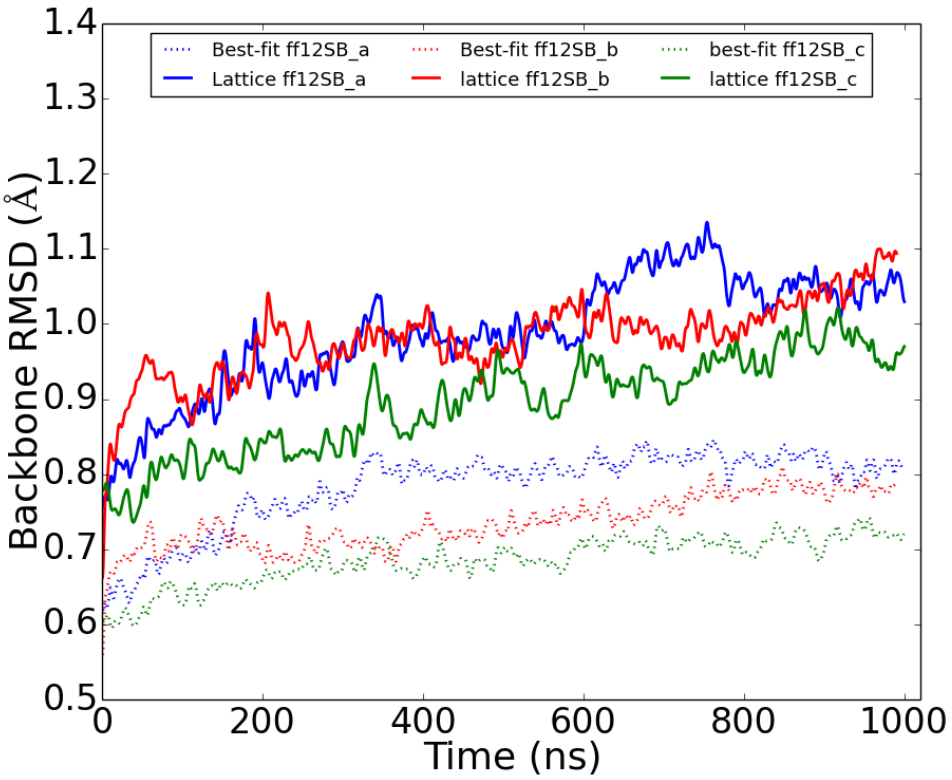

Figure 1: Backbone RMSDComparison of three simulations. ff12SB_a and ff12SB_b are independent simulations using the same protocol as for all the other simulations reported in the paper (23 ns of equilibration) but with ff12SB force field. ff12SB_c used a more conservative 500ns-long solvent equilibration protocol.

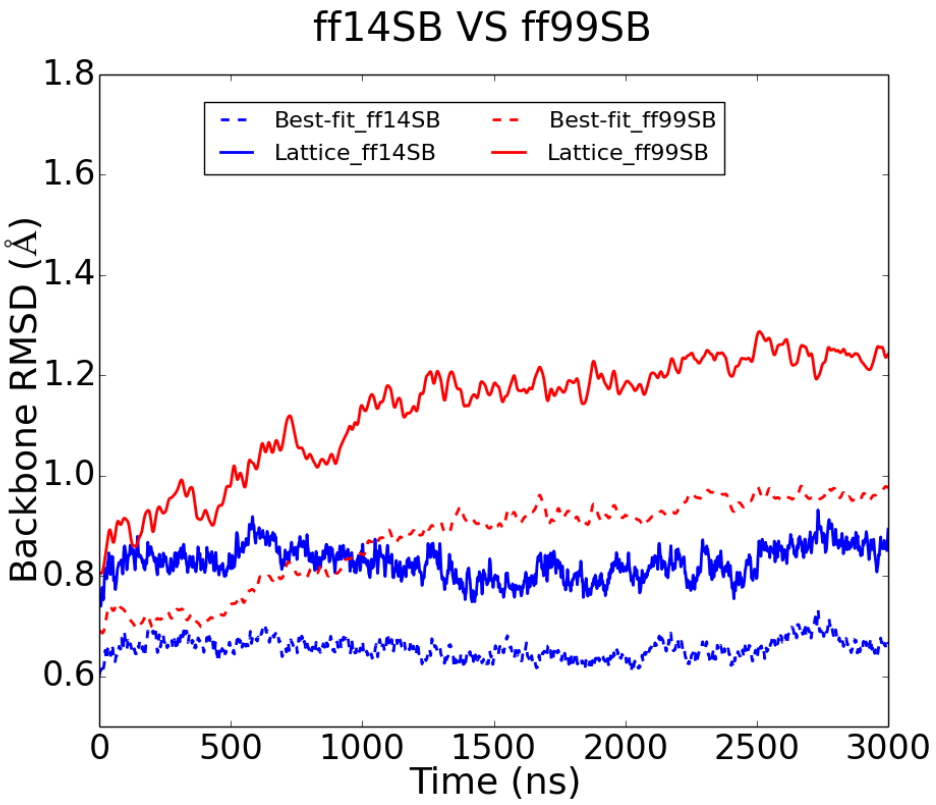

Figure 2: Comparison of 1st, 2nd and 3rd microseconds of the ff14SB and ff99SB simulation backbone RMSD values. Lattice RMSD is shown as a solid line and best-fit RMSD as a dotted line. ff14SB reaches convergence quickly, with all three microseconds showing similar results. ff99Sb requires a significantly longer equilibration period, attaining convergence only after about 1 microsecond of simulation.

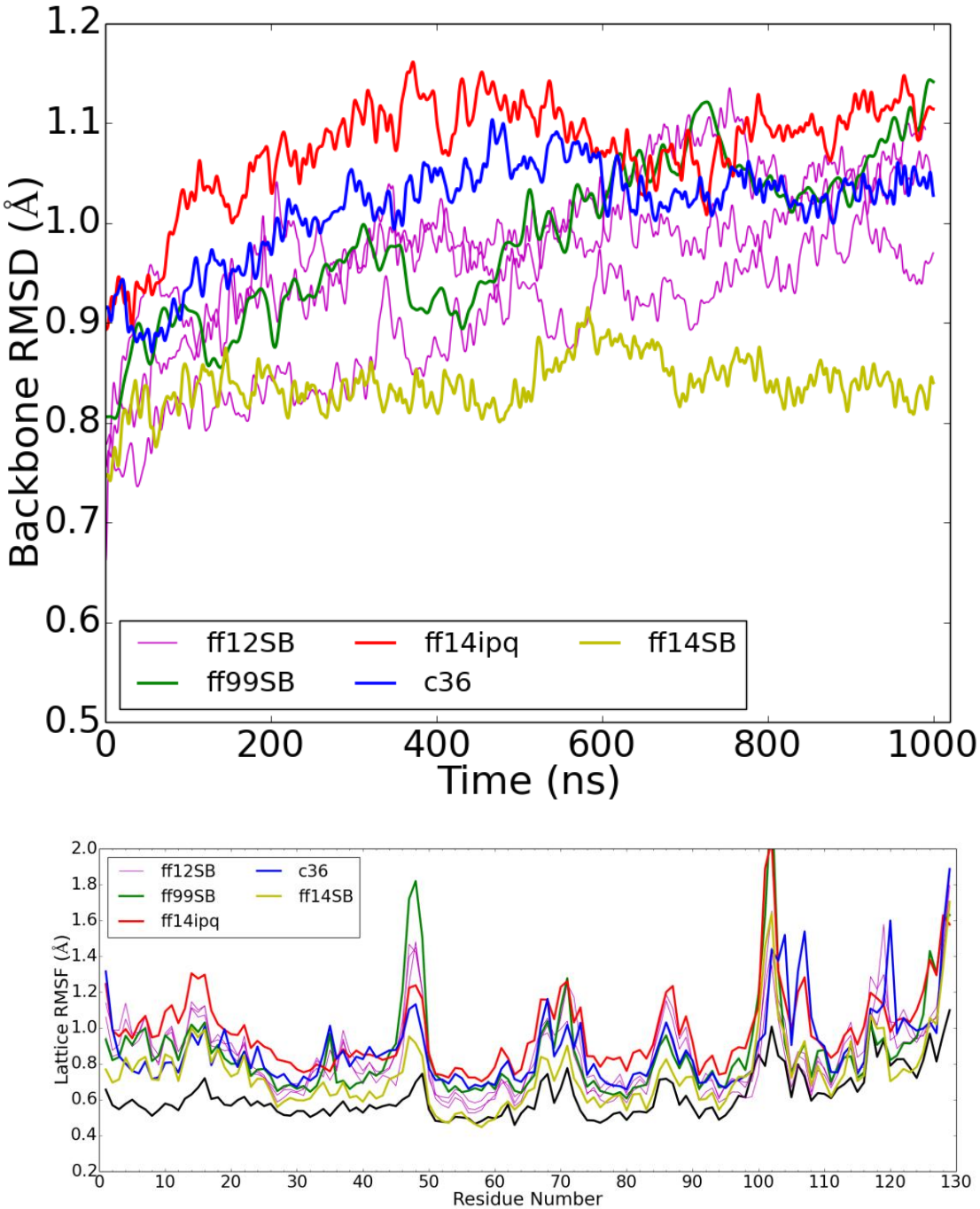

Figure 3: Simulation reproducibility shown by RMSD (top panel) and RMSF (bottom panel). The results of the three ff12SB simulations (ff12SB_a, ff12SB_b, ff12SB_c) all in purple, C36 blue, ff14ipq red, ff14SB yellow.

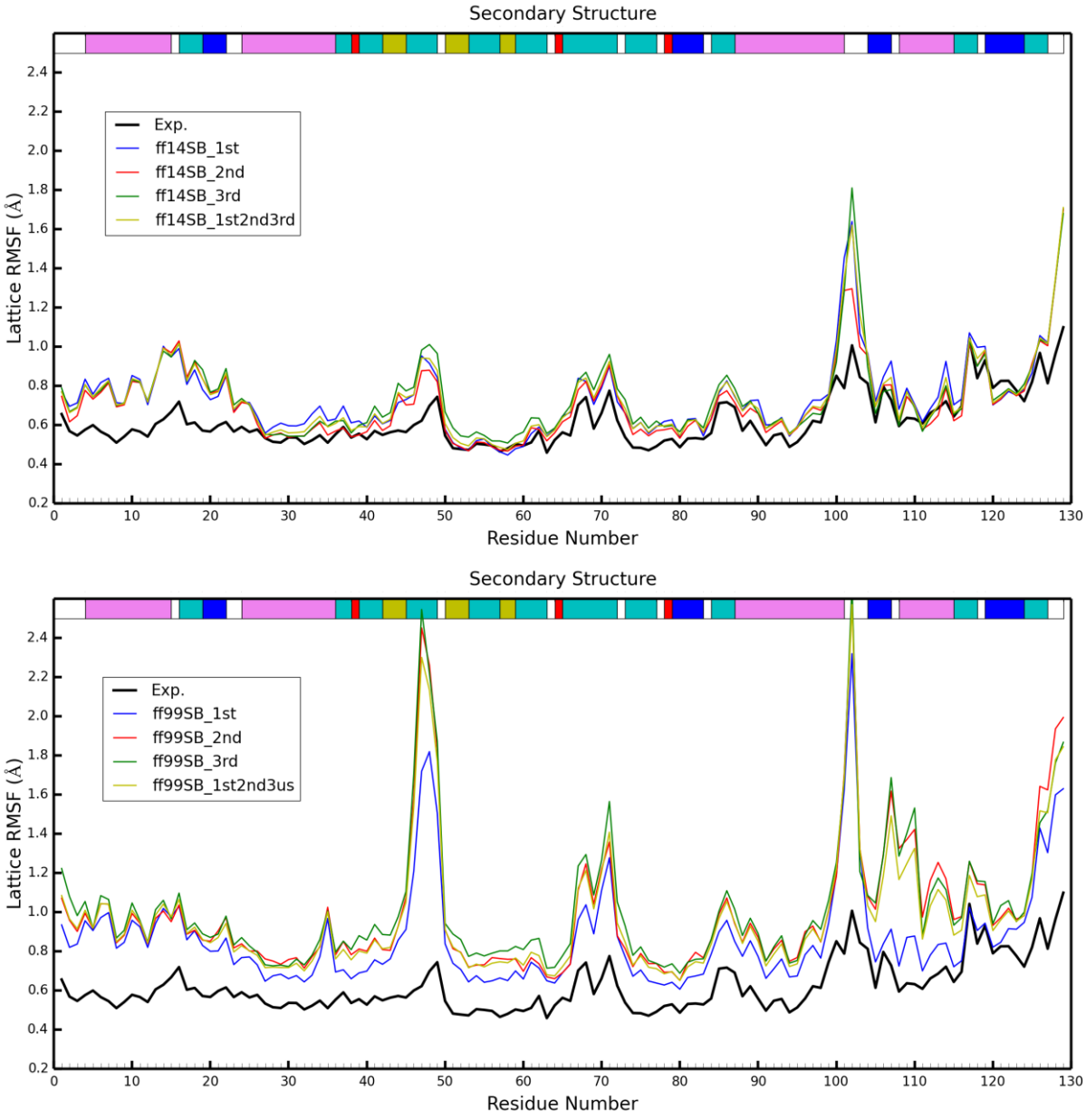

Figure 4: Lattice RMSF comparisons of the 1st, 2ndand 3rd microsecond of the ff14SB and ff99SB simulations

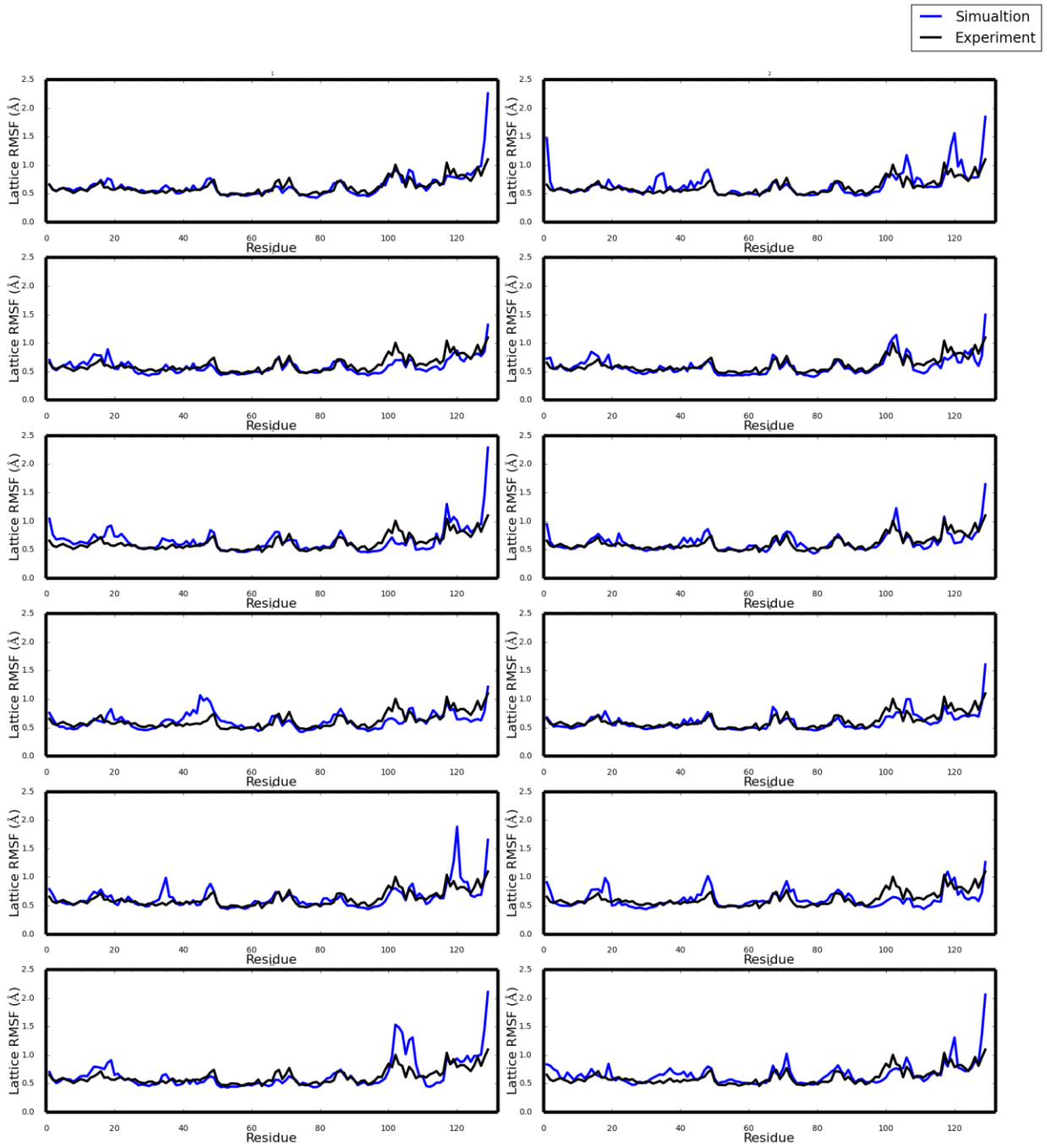

Figure 5: LatticeB-factors of each monomer of the C36 simulation. The overall B-factors show a large peak at residues 120-121. Here we see that this stems from contributions from just four monomers (#2, 9, 10 and 12 in our numbering scheme). This is seen to correlate with secondary structure hydrogen bond breakage shown in Figure 6.

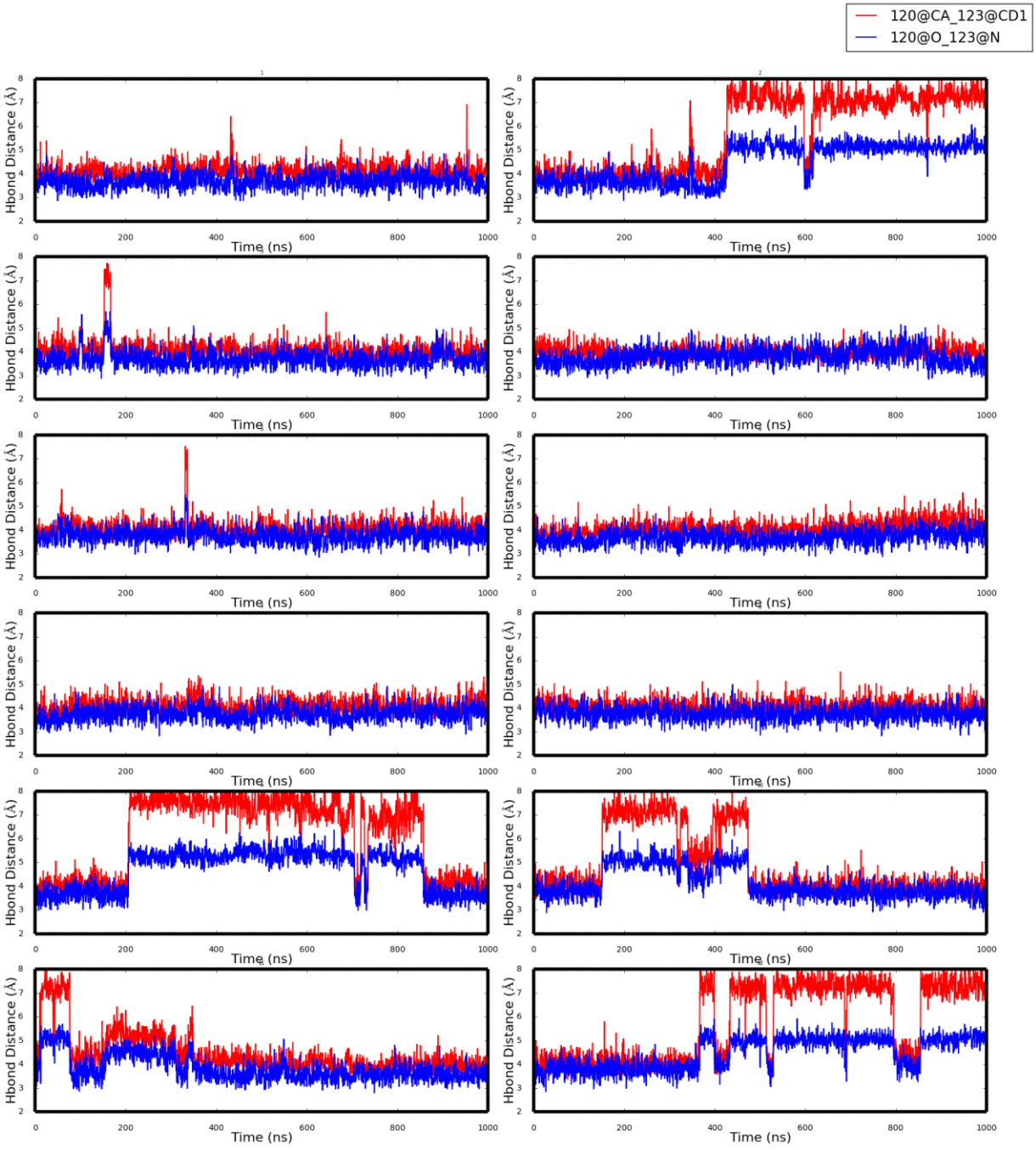

Figure 6: C36 hydrogen bond lengths for residues 120 and 121. Most are well maintained, but hydrogen bonding is disrupted in monomers 2,9,10,12, the same that exhibit high B-factor peaks (Figure 5**).**

	X	Y	Z	XY	XZ	YZ
ff14SB	0.2869	0.2304	0.2339	0.2597	0.2499	0.2098
ff14ipq	0.2578	0.3107	0.3047	0.3864	0.7152	0.4480
C36	0.3738	0.2263	0.2155	0.3023	0.4701	0.2432
ff99SB	0.3173	0.2071	0.2761	0.4561	0.4229	0.2978

Table 1: Standard deviation of interface distances around the experimental value for the 12 independent interfaces in each simulation. The value shown is the mean standard deviation over the entire trajectory of each simulation.

		Cα atom	Backbone atom	Heavy atom	Per-residue (heavy atom)
ff14SB	**Best-fit**	0.82±0.05	0.84±0.02	0.78±0.02	0.77±0.06
	Lattice	0.84±0.05	0.85±0.02	0.79±0.02	0.79±0.05
	Avg. lattice	0.86±0.05	0.80±0.03	0.79±0.02	0.78±0.06
	refined	0.80±0.05	0.80±0.03	0.83±0.02	0.84±0.05
ff14ipq	**Best-fit**	0.79±0.05	0.83±0.02	0.78±0.02	0.78±0.06
	Lattice	0.80±0.05	0.84±0.02	0.77±0.02	0.78±0.06
	Avg. lattice	0.82±0.05	0.81±0.03	0.80±0.02	0.79±0.05
	refined	0.77±0.06	0.76±0.03	0.73±0.02	0.76±0.06
C36	**Best-fit**	0.81±0.05	0.83±0.02	0.72±0.02	0.73±0.06
	Lattice	0.78±0.06	0.80±0.03	0.71±0.02	0.71±0.06
	Avg. lattice	0.85±0.05	0.83±0.02	0.75±0.02	0.75±0.06
	refined	0.76±0.06	0.75±0.03	0.76±0.02	0.78±0.06
ff99SB	**Best-fit**	0.69±0.06	0.77±0.03	0.74±0.02	0.68±0.07
	Lattice	0.71±0.06	0.78±0.03	0.75±0.02	0.70±0.06
	Avg. lattice	0.78±0.06	0.85±0.02	0.80±0.02	0.78±0.06
	refined	0.74±0.06	0.76±0.03	0.71±0.02	0.73±0.06
Exp.	**refined**	0.97±0.02	0.97±0.01	0.97±0.01	0.99±0.01

Table 2: Pearson correlation coefficients between Best-fit, Lattice, Avg. Lattice and Refinement-derivedRMSFs calculated from the simulations and those obtained from the experimental refinement.Standard deviations are calculated using the formula $\frac{\sqrt{1-r^2}}{\sqrt{n-2}}$ where r is the correlation coefficient and n is the number of samples used to calculate the coefficient. The last row reports correlations between fluctuations from the deposited model and our own re-refinement of the model against the experimental data.

				ff99SB	ff14SB	C36	ff14ipq	ff14SB_solv
Res.		exp	Conf.	Distri.	Distri.	Distri.	Distri.	Distri.
1	K	173	g+	4	6	15	5	8
			T	96	93	79	94	88
			g-	1	2	6	1	4
2	V	183	g+	2	9	4	6	11
			T	90	90	95	88	85
			g-	7	1	2	6	4
3	F	275	g+	0	0	0	0	0
			T	1	0	0	2	9
			g-	99	100	100	98	91
4	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
5	R	167	g+	73	98	74	87	53
			T	27	2	25	13	47
			g-	0	0	1	0	0
6	C	294	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
7	E	290	g+	1	0	1	4	4
			T	26	8	17	21	52
			g-	73	92	82	75	44
8	L	184	g+	0	0	0	0	0
			T	100	100	100	100	100
			g-	0	0	0	0	0
9	A	ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
10	A	ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
11	A	ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
12	M	287	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
13	K	184	g+	0	0	1	1	0
			T	98	98	93	97	99
			g-	2	2	6	2	1
14	R	286	g+	3	3	13	5	3
			T	17	10	14	30	53
			g-	80	86	73	65	44
15	H	288	g+	0	0	0	0	0
			T	2	0	1	3	3
			g-	98	100	99	97	97
16	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--

17	L	287	g+	0	0	0	0	0
			T	73	38	15	61	26
			g-	27	62	85	39	74
18	D	191	g+	2	23	61	21	3
			T	98	77	39	79	97
			g-	0	1	0	0	0
19	N	201	g+	2	0	0	0	0
			T	85	17	53	17	37
			g-	13	83	47	83	63
20	Y	182	g+	0	0	0	0	0
			T	100	100	100	100	100
			g-	0	0	0	0	0
21	R	298	g+	0	0	0	0	0
			T	25	5	1	5	3
			g-	75	95	99	95	97
22	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
23	Y	292	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
24	S	63	g+	45	65	51	71	79
			T	1	6	23	7	10
			g-	55	30	27	22	11
25	L	189	g+	0	0	0	0	0
			T	96	83	97	100	77
			g-	4	17	2	0	23
26	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
27	N	284	g+	0	0	0	0	0
			T	5	0	2	0	0
			g-	95	100	98	100	100
28	W	299	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
29	V	177	g+	0	0	0	0	0
			T	97	100	100	99	100
			g-	3	0	0	1	0
30	C	185	g+	0	0	0	0	0
			T	100	100	100	100	100
			g-	0	0	0	0	0
31		ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
32		ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
33	K	171	g+	0	0	0	0	0
			T	100	100	94	100	100
			g-	0	0	6	0	0
34	F	292	g+	0	0	0	0	0
			T	0	0	0	0	0

			g-	100	100	100	100	100
35	E	287	g+	0	0	0	0	0
			T	9	1	1	0	10
			g-	91	99	99	100	90
36	S	66	g+	99	100	100	100	100
			T	0	0	0	0	0
			g-	1	0	0	0	0
37	N	213	g+	0	0	0	0	0
			T	100	86	71	90	74
			g-	0	13	29	10	26
38	F	303	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
39	N	186	g+	0	0	0	0	0
			T	100	100	100	99	99
			g-	0	0	0	1	1
40	T	65	g+	100	100	100	99	100
			T	0	0	0	0	0
			g-	0	0	0	1	0
41	Q	288	g+	2	4	2	1	1
			T	43	58	15	18	34
			g-	54	38	83	81	65
42	A	ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
43	T	59	g+	54	4	22	17	1
			T	14	71	11	7	97
			g-	32	24	67	76	1
44	N	180	g+	0	1	0	1	1
			T	98	83	60	89	61
			g-	1	16	40	10	37
45	R	299	g+	5	0	0	2	2
			T	17	31	0	8	60
			g-	78	69	99	90	38
46	N	302	g+	11	0	0	0	0
			T	38	6	1	5	24
			g-	51	94	99	95	76
47	T	66	g+	64	16	53	56	48
			T	3	71	38	14	6
			g-	34	14	10	30	46
48	D	70	g+	68	100	99	100	100
			T	32	0	1	0	0
			g-	0	0	0	0	0
49	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
50	S	74	g+	95	100	99	100	100
			T	1	0	0	0	0
			g-	4	0	0	0	0
51	T	299	g+	1	0	0	0	0
			T	0	0	0	0	0
			g-	99	100	100	100	100
52	D	305	g+	0	0	0	0	0

			T	0	0	0	0	0
			g-	100	100	100	100	100
53	Y	293	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
54	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
55	I	200	g+	0	1	8	0	0
			T	100	99	92	100	100
			g-	0	0	0	0	0
56	L	285	g+	0	0	0	0	0
			T	6	0	0	3	0
			g-	94	100	100	97	100
57	Q	292	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
58	I	289	g+	1	0	0	0	0
			T	0	0	0	0	0
			g-	99	100	100	100	100
59	N	184	g+	0	0	0	0	0
			T	100	100	100	100	100
			g-	0	0	0	0	0
60	S	65	g+	100	100	100	100	100
			T	0	0	0	0	0
			g-	0	0	0	0	0
61	R	189	g+	0	0	0	0	0
			T	90	96	99	97	100
			g-	9	4	1	2	0
62	W	286	g+	0	0	2	0	0
			T	1	1	1	1	0
			g-	99	99	97	99	100
63	W	303	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
64	C	61	g+	100	100	100	100	100
			T	0	0	0	0	0
			g-	0	0	0	0	0
65	N	183	g+	1	0	0	4	2
			T	99	99	100	96	98
			g-	0	0	0	0	0
66	D	69	g+	98	100	100	100	100
			T	2	0	0	0	0
			g-	0	0	0	0	0
67	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
68	R	300	g+	35	24	48	58	47
			T	22	9	6	25	25
			g-	43	67	46	16	28
69	T	302	g+	0	0	0	0	0
			T	0	0	0	0	1
			g-	100	100	100	100	99

70	P	342	g+	32	31	10	48	63
			T	0	0	0	0	0
			g-	68	70	90	52	37
71	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
72	S	174	g+	7	1	3	20	4
			T	80	98	95	68	93
			g-	13	1	2	12	2
73	R	304	g+	3	1	31	25	3
			T	24	8	2	3	17
			g-	73	92	67	72	80
74	N	193	g+	0	0	0	0	0
			T	100	100	100	100	100
			g-	0	0	0	0	0
75	L	299	g+	0	0	0	0	0
			T	24	1	3	1	4
			g-	76	99	97	99	96
76	C	290	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
77	N	198	g+	0	0	0	1	0
			T	100	95	89	91	36
			g-	0	5	11	9	64
78	I	52	g+	92	74	94	85	42
			T	8	25	6	13	55
			g-	0	1	0	2	2
79	P	25	g+	90	89	92	97	70
			T	0	0	0	0	0
			g-	10	11	8	3	30
80	C	298	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
81	S	62	g+	51	73	27	68	85
			T	1	6	27	3	7
			g-	48	21	47	29	8
82	A	ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
83	L	300	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
84	L	300	g+	0	0	0	0	0
			T	36	12	9	16	48
			g-	64	88	91	84	52
85	S	59	g+	12	6	9	42	4
			T	18	63	75	24	88
			g-	70	31	17	34	8
86	S	290	g+	7	7	31	31	6
			T	2	13	27	3	9
			g-	91	79	43	66	84
87	D	167	g+	5	1	24	51	0
			T	95	95	65	49	100

			g-	0	4	11	0	0
88	I	68	g+	100	96	97	96	98
			T	0	3	3	3	1
			g-	0	1	0	1	1
89	T	293	g+	9	1	11	1	0
			T	0	0	8	0	0
			g-	91	99	81	99	100
90	A	ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
91	S	289	g+	0	0	0	0	0
			T	2	2	1	0	2
			g-	98	98	99	100	98
92	V	168	g+	1	1	0	9	1
			T	51	80	99	56	99
			g-	48	20	0	35	0
93	N	289	g+	0	0	0	0	0
			T	90	17	12	37	15
			g-	1	83	88	63	85
94	C	184	g+	0	0	0	0	0
			T	100	100	100	100	100
			g-	0	0	0	0	0
95	A	ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
96	K	286	g+	0	0	0	2	0
			T	0	1	0	8	3
			g-	100	99	99	90	97
97	K	174	g+	0	0	0	0	0
			T	51	96	100	96	86
			g-	49	4	0	4	14
98	I	292	g+	0	0	2	0	0
			T	0	0	0	0	0
			g-	100	100	98	100	100
99	V	174	g+	3	1	3	1	12
			T	20	46	82	69	88
			g-	77	52	16	30	0
100	S	290	g+	13	20	21	27	13
			T	1	37	43	22	34
			g-	86	42	36	51	53
101	D	271	g+	0	0	0	8	2
			T	91	7	0	8	6
			g-	9	92	100	84	92
102	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
103	N	301	g+	12	3	0	8	0
			T	84	9	3	28	65
			g-	4	88	97	63	35
104	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
105	M	286	g+	0	3	0	0	0

			T	68	38	3	13	15
			g-	32	61	97	87	85
106	N	289	g+	49	51	11	63	8
			T	49	36	30	31	59
			g-	2	13	58	6	33
107	A	ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
108	W	286	g+	0	0	0	0	0
			T	2	3	11	9	0
			g-	98	97	89	91	100
109	V	294	g+	9	17	6	12	12
			T	71	80	78	78	85
			g-	20	4	15	10	2
110	A	ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
111	W	179	g+	0	0	0	0	0
			T	100	100	100	100	100
			g-	0	0	0	0	0
112	R	189	g+	25	20	22	59	27
			T	64	70	10	31	55
			g-	11	10	68	10	18
113	N	289	g+	3	0	0	0	0
			T	50	22	24	2	10
			g-	47	78	75	98	90
114	R	307	g+	0	1	0	0	1
			T	7	14	14	21	6
			g-	93	85	86	79	93
115	C	302	g+	0	0	0	0	0
			T	0	0	0	0	0
			g-	100	100	100	100	100
116	K	185	g+	1	1	2	2	4
			T	94	95	14	89	94
			g-	5	4	85	9	2
117	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
118	T	75	g+	97	92	33	54	74
			T	1	5	58	22	19
			g-	2	3	8	24	7
119	D	169	g+	0	0	0	6	0
			T	100	98	87	92	98
			g-	0	2	13	2	2
120	V	293	g+	4	1	11	2	6
			T	0	0	15	3	0
			g-	96	99	75	95	93
121	Q	201	g+	0	1	0	2	0
			T	67	83	8	75	65
			g-	33	16	92	23	35
122	A	ALA	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--

123	W	288	g+	0	0	1	0	0
			T	0	0	0	0	0
			g-	100	100	99	100	100
124	I	67	g+	96	48	74	77	43
			T	0	0	0	0	0
			g-	3	52	26	23	56
125	R	192	g+	4	4	8	5	13
			T	55	59	56	81	26
			g-	41	37	36	14	60
126	G	GLY	g+	--	--	--	--	--
			T	--	--	--	--	--
			g-	--	--	--	--	--
127	C	300	g+	4	0	3	1	0
			T	0	0	0	0	0
			g-	96	100	97	99	100
128	R	344	g+	15	39	38	42	5
			T	44	33	8	27	33
			g-	41	28	54	31	62
129	L	269	g+	2	1	0	1	0
			T	37	9	3	9	9
			g-	61	90	97	90	91

Table 3: χ1 rotamer distribution for each residue. First two columns provide residue sequence number and one letter amino acid code. Third column gives the value of the χ1 rotamer in the deposited model. Following columns provide the percent of the χ1 angle found in each of the three major conformations (g+: gauche plus, g-: gauche minus, T: trans) for five different simulations.

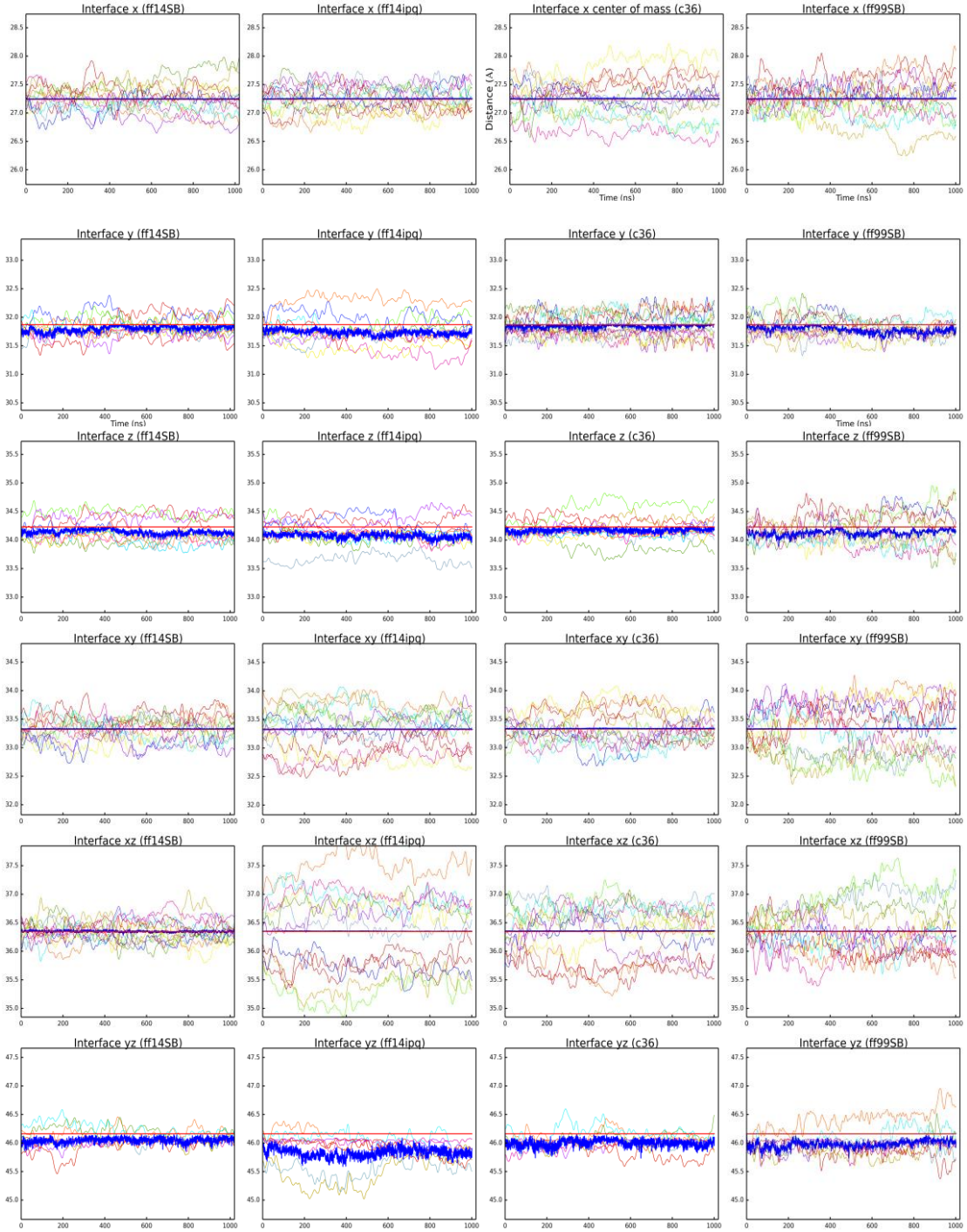

Figure 7: Distance between lysozyme monomer pairs across each of the crystal interfaces. Each line represents a pair of monomers (12 independent pairs in each simulation). The heavy blue line is the mean distance. The red line is the distance in the experimental model.

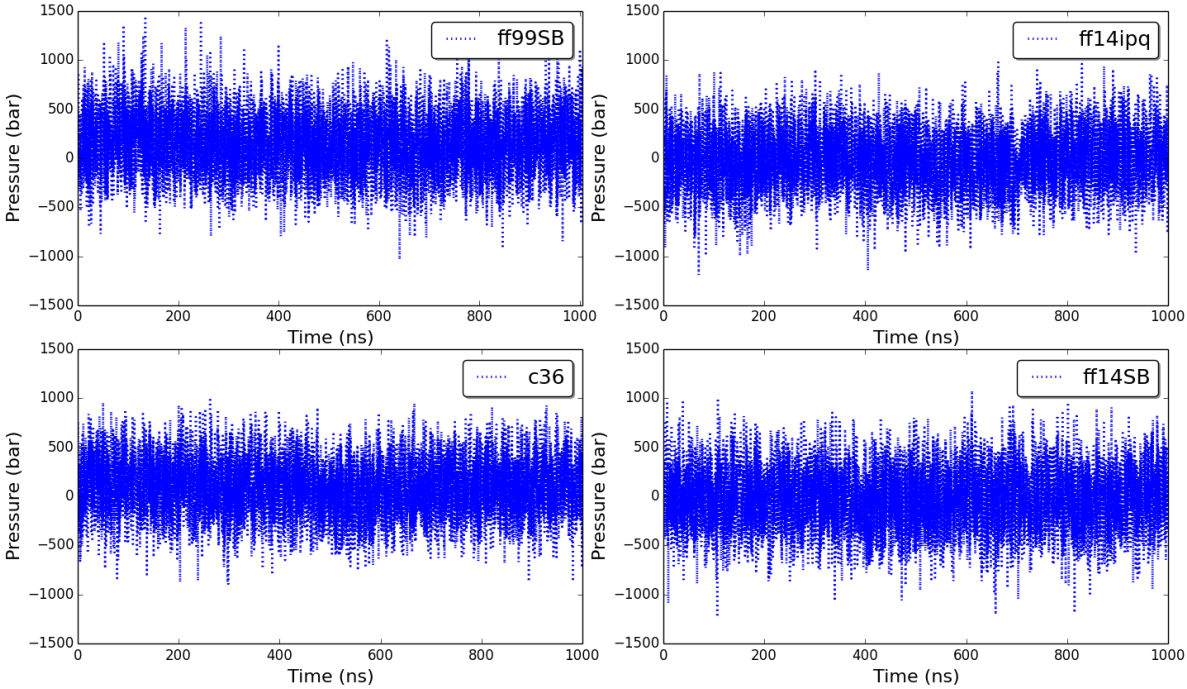

Figure 8:The instantaneous pressures (in bar) in the 1000ns crystal simulations.

Iface	Bondname(c36)	cryst	total	1	2	3	4	5	6	7	8	9	10	11	12
Y	:19@ND2–:81@O	100.0	32	12	5	43	5	30	60	63	47	6	42	10	62
	:21@NH2–:66@O	100.0	31	49	5	28	0	15	56	0	62	68	24	20	48
	:19@O–:81@OG	0	20	18	40	17	23	9	10	46	15	4	18	10	25
	:68@NH1–:21@O	0	25	4	1	57	2	0	21	0	16	84	82	27	0
	:68@NH1–:102@O	0	27	24	71	13	0	90	23	93	5	0	0	0	3
	:81@OG–:22@N	0	41	45	35	45	54	67	26	37	15	33	68	23	47
	:84@O–:19@ND2	0	22	21	34	29	43	9	19	13	8	41	6	27	16
	:41@NE2–:19@OD1	0	21	20	50	47	28	5	8	3	1	44	0	36	12
Z	:3@O–:73@NH1	100.0	7	12	7	11	1	7	2	10	0	8	6	17	4
	:100@OG–:128@NH1	100.0	4	24	15	0	0	0	0	9	0	1	0	2	0
	:5@NH2–:101@O	100	59	82	86	50	12	30	58	90	49	80	75	59	37
	:7@OE1–:97@NZ	0	52	47	67	0	0	59	76	70	80	27	73	47	75
	:7@OE2–:97@NZ	0	53	32	65	0	0	55	68	60	81	72	67	63	72
	:101@O–:5@NH2	0	59	86	82	12	50	58	30	49	90	75	80	39	59
	:5@NH2–:103@OD1	0	35	42	46	28	1	11	51	78	45	29	74	9	2
X	:37@ND2–:14@O	100.0	32	47	16	47	31	31	57	56	24	23	14	30	4
	:45@O–:77@ND2	100.0	56	37	51	58	65	50	54	48	47	73	50	61	74
	:114@NH2–:18@O	100.0	29	3	71	10	51	46	8	39	0	36	54	12	18
	:114@NH1–:16@O	100.0	38	7	92	10	79	40	6	5	3	77	74	8	51
	:46@O–:77@ND2	100.0	22	28	21	30	25	22	23	20	13	30	15	23	11
XZ	:47@O–:1@NZ	100.0	36	15	26	2	4	12	61	50	66	52	46	74	22
	:47@OG1–:7@OE2	0	16	7	4	0	2	17	1	29	10	0	33	46	39
XY	:116@NZ–:77@OD1	100.0	77	91	97	92	70	55	47	53	48	85	94	96	96
	:113@O–:81@OG	100.0	7	3	7	1	6	35	20	2	2	5	3	3	1

Table 4: Crystal interface hydrogen bonds in the 4lzt experimental model and simulation in six interfaces with c36. Hydrogen bonds are listed if they are present in the X-ray crystal structure or if they are present for more than 10% simulation time averaged over the 12 monomers in the crystal simulation. A hydrogen bond is counted if the distance between the donor atom and the acceptor atom is maximally 3.2 Å.

Iface	Bondname(ff14SB)	cryst	total	1	2	3	4	5	6	7	8	9	10	11	12
Y	:19@ND2–:81@O	100.0	11	9	7	0	13	39	9	12	3	14	1	1	18
	:21@NH2–:66@O	100.0	3	0	3	4	1	4	8	0	19	0	3	1	0
	:68@NH2–:21@O	0	33	88	6	25	0	61	25	17	2	29	32	36	77
	:84@O–:19@ND2	0	14	19	7	12	18	19	23	6	8	17	9	10	23
	:41@NE2–:19@OD1	0	34	43	45	38	36	24	42	29	47	37	20	26	23
	:45@NH2–:22@O	0	10	22	5	25	14	6	23	0	4	4	4	9	8
Z	:73@NH1–:3@O	100.0	37	39	43	47	49	25	42	44	10	17	42	15	69
	:100@OG–:128@NH1	100.0	3	2	2	1	0	11	3	0	7	1	4	1	0
	:101@O–:5@NH2	100.0	34	56	5	13	67	7	50	62	14	56	11	9	64
	:7@OE1–:97@NZ	0	38	14	5	1	76	65	63	50	56	52	28	36	15
	:7@OE2–:97@NZ	0	38	83	7	21	23	27	31	41	37	35	30	38	83
	:101@O–:5@NH2	0	34	56	5	13	67	7	50	62	14	56	11	9	64
	:37@OD1–:73@NH2	0	33	37	25	37	49	39	17	10	57	32	22	57	14
	:37@O–:73@NH2	0	12	9	21	20	12	11	5	3	15	8	11	26	4
	:126@O–:102@N	0	10	19	3	1	20	8	21	0	3	16	3	4	23
X	:45@O–:77@ND2	100.0	66	83	62	81	85	53	80	42	80	60	62	55	53
	:114@NH2–:18@O	100.0	68	91	51	49	72	89	75	62	89	59	57	35	90
	:114@NH1–:16@O	100.0	50	79	23	44	74	43	34	14	48	67	41	40	88
	:37@ND2–:14@O	100.0	30	40	7	6	48	38	45	25	11	23	49	33	31
	:46@O–:77@ND2	100.0	7	7	15	9	4	8	5	3	9	2	17	4	2
	:114@NH2–:16@O	(0)	42	9	40	41	58	52	51	69	32	68	46	20	13
	:114@NH1–:18@O	0	32	3	47	18	14	36	55	66	34	4	54	48	3
XZ	:47@O–:1@NZ	100.0	61	50	39	54	60	74	51	50	73	70	65	68	78
XY	:116@NZ–:77@OD1	100.0	78	85	79	78	88	81	83	46	76	89	67	87	76
	:113@O–:81@OG	100.0	25	3	21	20	16	31	38	77	21	9	30	17	19

Table 5: Same as Table 4, but for ff14SB

Iface	Bondname(ff14ipq)	cryst	total	1	2	3	4	5	6	7	8	9	10	11	12
Y	:19@ND2–:81@O	100.0	15	83	0	5	0	25	9	0	3	3	56	0	0
	:21@NH2–:66@O	100.0	14	7	11	4	17	46	2	9	31	6	9	0	23
	:68@NH2–:21@O	0	36	0	3	84	0	76	35	0	92	21	67	60	0
	:84@O–:19@ND2	0	32	59	8	11	59	41	20	37	34	27	15	51	20
	:45@NH1–:22@O	0	30	28	42	36	32	13	27	36	18	9	52	63	0
	:41@NE2–:19@OD1	0	29	19	75	2	7	4	72	9	27	43	58	31	1
	:45@NH2–:22@O	0	22	2	12	53	2	63	10	12	35	16	22	38	0
	:68@NE–:103@O	0	14	0	0	35	6	7	28	0	82	0	1	11	0
	:68@NE–:102@O	0	12	26	0	0	0	5	0	45	0	0	0	0	70
	:68@NH1–:103@O	0	10	2	0	4	20	0	0	0	17	76	6	0	0
Z	:73@NH1–:3@O	100.0	4	0	7	0	0	0	14	5	0	4	2	0	13
	:100@OG–:128@NH1	100.0	1	0	5	0	2	0	0	2	0	0	0	0	0
	:101@O–:5@NH2	100.0	29	3	38	3	34	62	39	36	26	20	25	53	3
	:7@OE1–:97@NZ	0	37	33	54	7	12	47	42	26	28	50	70	0	78
	:7@OE2–:97@NZ	0	37	66	49	8	6	53	48	66	53	39	29	1	21
	:101@O–:5@NH2	0	29	3	38	3	34	62	39	36	26	20	25	53	3
	:128@NE–:101@OD2	0	21	0	0	17	0	19	0	10	82	79	0	44	0
	:5@NH1–:101@O	0	29	57	6	57	17	29	32	27	30	23	34	7	36
	:128@NH1–:101@OD1	0	22	65	0	1	0	31	0	28	60	24	0	52	0
	:128@NH1–:101@OD2	0	20	38	0	1	0	23	0	34	66	14	0	60	0
	:128@NH2–:101@OD1	0	19	61	0	35	0	60	0	28	0	53	0	1	0
	:128@NH2–:101@OD2	0	16	38	0	78	0	26	0	18	0	37	0	0	0
	:128@NE–:101@OD1	0	15	0	0	84	0	0	0	4	18	25	0	56	0
	:126@O–:102@N	0	12	0	0	4	24	13	15	17	27	3	0	37	5
	:128@N–:101@OD1	0	11	0	0	80	0	0	38	0	0	19	0	3	0
X															
	:45@O–:77@ND2	100.0	70	76	71	71	91	67	81	84	85	20	57	90	45
	:114@NH2–:18@O	100.0	56	61	78	36	79	78	45	92	34	2	75	3	84
	:114@NH1–:16@O	100.0	47	67	61	25	27	47	27	92	24	29	82	36	47
	:37@ND2–:14@O	100.0	45	26	65	42	24	53	74	28	47	74	30	21	51
	:114@NH2–:16@O	(0)	40	26	27	56	63	51	66	4	45	6	12	88	37
	:46@O–:77@ND2	100.0	16	21	23	24	14	35	11	13	8	11	27	2	3
	:114@NH1–:18@O	0	66	37	61	82	78	75	82	77	79	0	94	97	28
	:46@O–:77@ND2	0	16	21	23	24	14	35	11	13	8	11	27	2	3
	:44@OD1–:93@ND2	0	25	59	37	10	9	40	7	5	1	55	43	5	35
	:113@OD1–:21@NH1	0	13	3	16	12	10	5	32	40	5	2	1	0	27
	:47@OG1–:75@O	0	11	22	32	10	11	29	1	2	0	11	15	0	3
XZ	:47@O–:1@NZ	100.0	14	56	0	28	0	1	15	0	0	15	0	53	1
	:47@OG1–:7@OE1	0	25	6	19	16	11	6	0	70	58	33	6	46	26
XY	:116@NZ–:77@OD1	100.0	70	89	86	76	93	80	37	89	71	85	22	30	84
	:113@O–:81@OG	100.0	32	20	35	39	13	40	10	53	31	17	60	29	38

Table 6: Same as Table 4, but for ff14ipq.

Iface	Bondname(ff99SB)	cryst	ave.	1	2	3	4	5	6	7	8	9	10	11	12
Y	:19@ND2–:81@O	100.0	69	88	53	44	52	34	91	81	80	73	83	67	78
	:21@NH2–:66@O	100.0	9	2	0	0	12	0	2	58	8	3	17	0	7
	:68@NH2–:21@O	0	27	56	11	5	7	50	0	2	79	29	0	13	76
	:84@O–:19@ND2	0	10	19	13	4	9	8	4	28	3	8	7	7	5
	:41@NE2–:19@OD1	0	5	12	8	0	2	2	0	22	0	5	1	3	1
	:45@NH2–:22@O	0	5	9	5	1	10	0	0	0	0	9	9	9	4
	:68@NH1–:103@O	0	11	0	26	1	18	1	31	25	0	31	3	3	0
	:68@NH1–:23@OH	0	11	1	13	4	8	8	20	13	3	17	30	8	9
Z	:73@NH1–:3@O	100.0	35	48	48	17	21	56	33	29	76	1	73	16	4
	:100@OG–:128@NH1	100.0	1	0	0	5	0	2	0	1	0	0	0	0	0
	:101@O–:5@NH2	100.0	37	42	56	45	16	2	6	42	83	0	22	77	53
	:7@OE1–:97@NZ	0	14	1	1	14	28	41	7	8	23	9	0	33	6
	:7@OE2–:97@NZ	0	12	1	1	19	15	42	17	11	12	10	2	5	4
	:37@OD1–:73@NH2	0	39	57	42	34	37	49	59	35	46	62	5	8	32
	:37@O–:73@NH2	0	16	19	15	3	12	16	21	39	29	19	0	3	10
	:126@O–:102@N	0	12	3	11	26	3	5	47	0	7	34	5	0	1
X	:45@O–:77@ND2	100.0	56	59	49	38	77	28	47	46	62	70	89	75	27
	:114@NH2–:18@O	100.0	73	64	50	39	85	80	88	84	65	89	68	76	87
	:114@NH1–:16@O	100.0	57	0	10	14	64	90	95	90	33	93	42	81	70
	:37@ND2–:14@O	100.0	44	64	48	59	39	30	57	22	54	44	34	56	22
	:46@O–:77@ND2	100.0	10	15	16	7	8	9	7	7	13	4	16	5	8
	:114@NH2–:16@O	0	29	62	42	7	31	18	44	27	38	13	18	23	22
	:114@NH1–:18@O	0	26	84	67	31	28	1	0	2	58	2	20	10	14
	:44@OD1–:93@ND2	0	23	48	48	74	22	4	17	6	33	3	2	5	10
	:46@O–:77@ND2	0	10	15	16	7	8	9	7	7	13	4	16	5	8
XZ	:47@O–:1@NZ	100.0	47	37	0	30	10	38	78	27	68	84	45	68	73
	:47@OG1–:7@OE1		15	22	0	10	22	26	11	19	9	13	17	11	16
XY	:116@NZ–:77@OD1	100.0	86	89	84	82	77	92	81	88	90	86	83	86	93
	:113@O–:81@OG	100.0	22	21	44	45	50	6	14	10	18	26	9	13	8

Table 7: Same as Table 4, but for ff99SB.

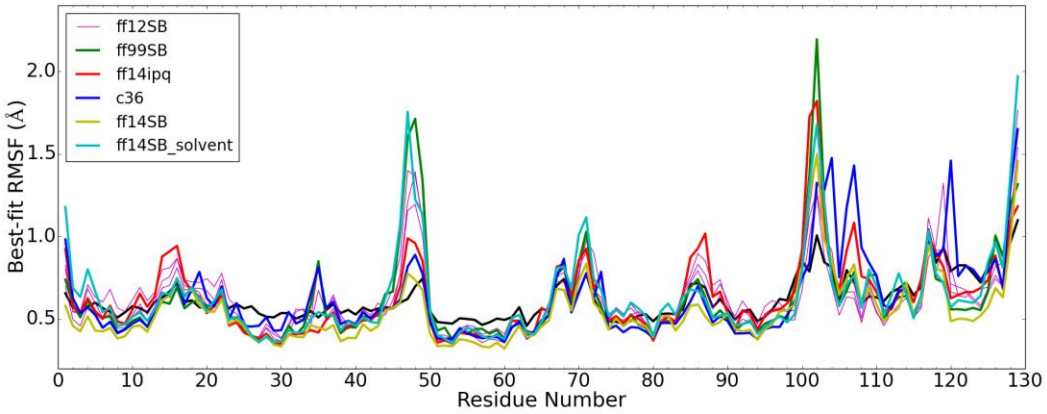

Figure 9: Simulation reproducibility shown by best-fit RMSF. The results of the three ff12SB simulations (ff12SB_a, ff12SB_b, ff12SB_c) all in purple, c36 blue, ff14ipq red, ff14SB yellow, ff14SB_sol cyan.

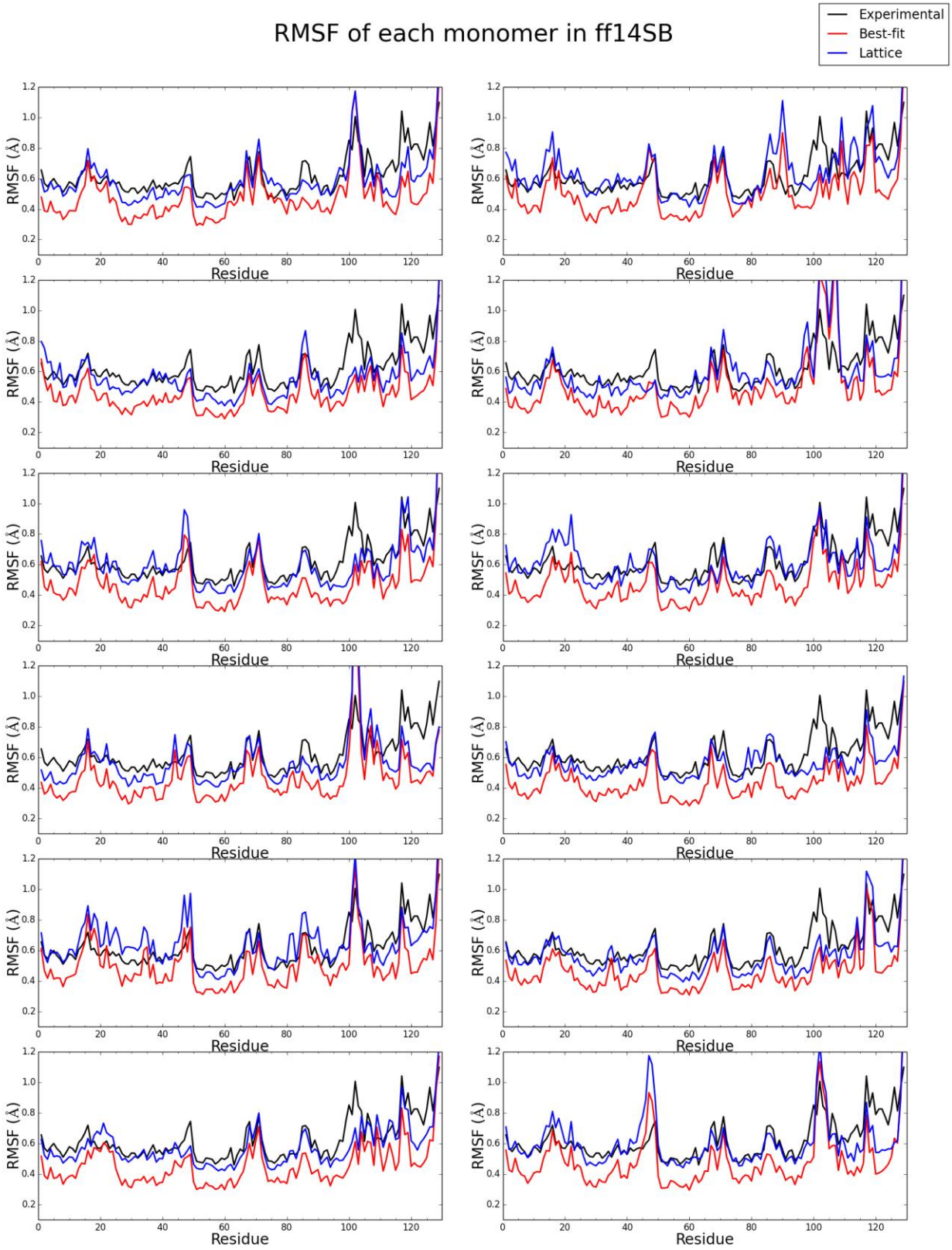

Figure 10: RMSF fluctuations for each individual monomer in the ff14SB simulation.

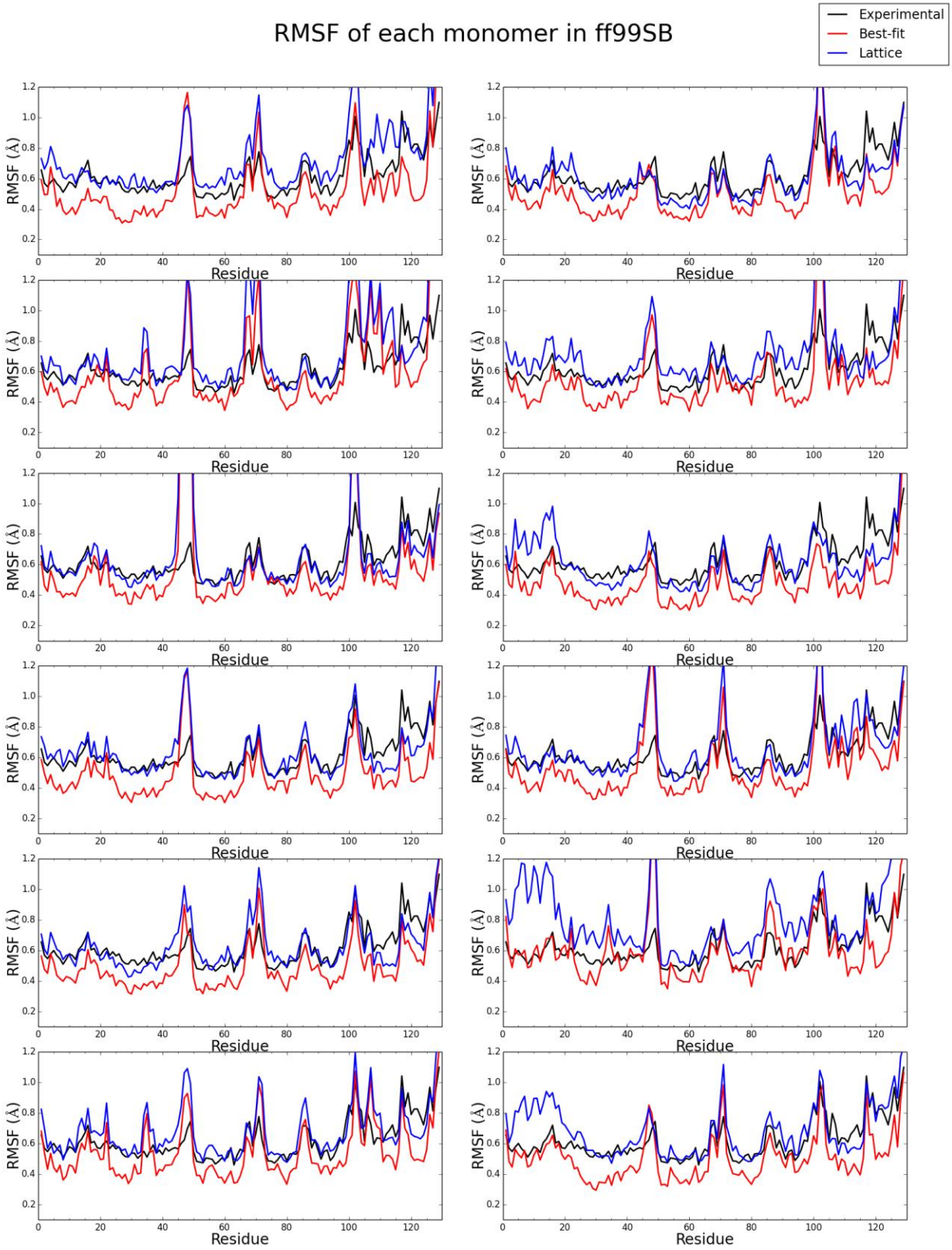

Figure 11: RMSF fluctuations for each individual monomer in the ff99SB simulation.

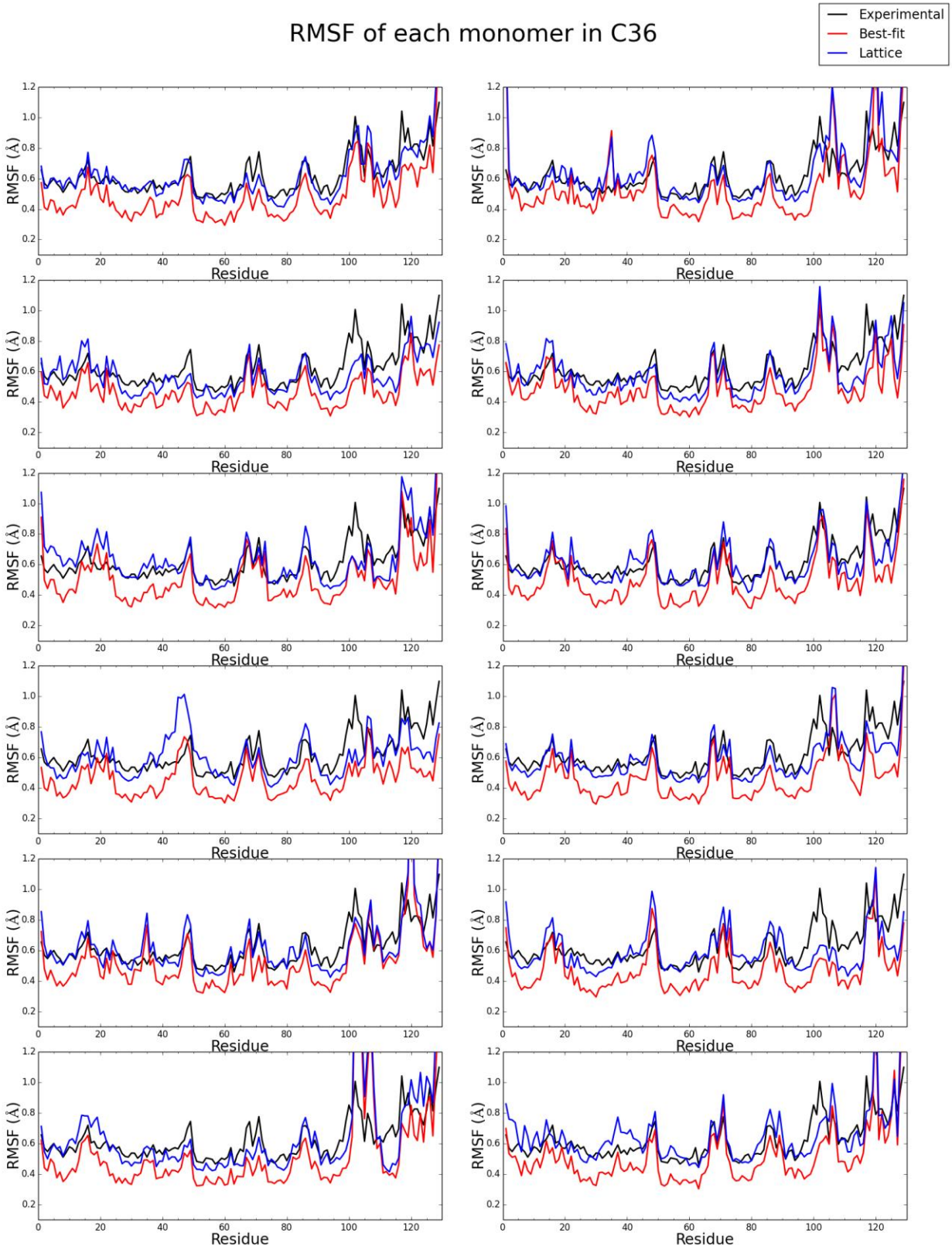

Figure 12: RMSF fluctuations for each individual monomer in the c36 simulation.

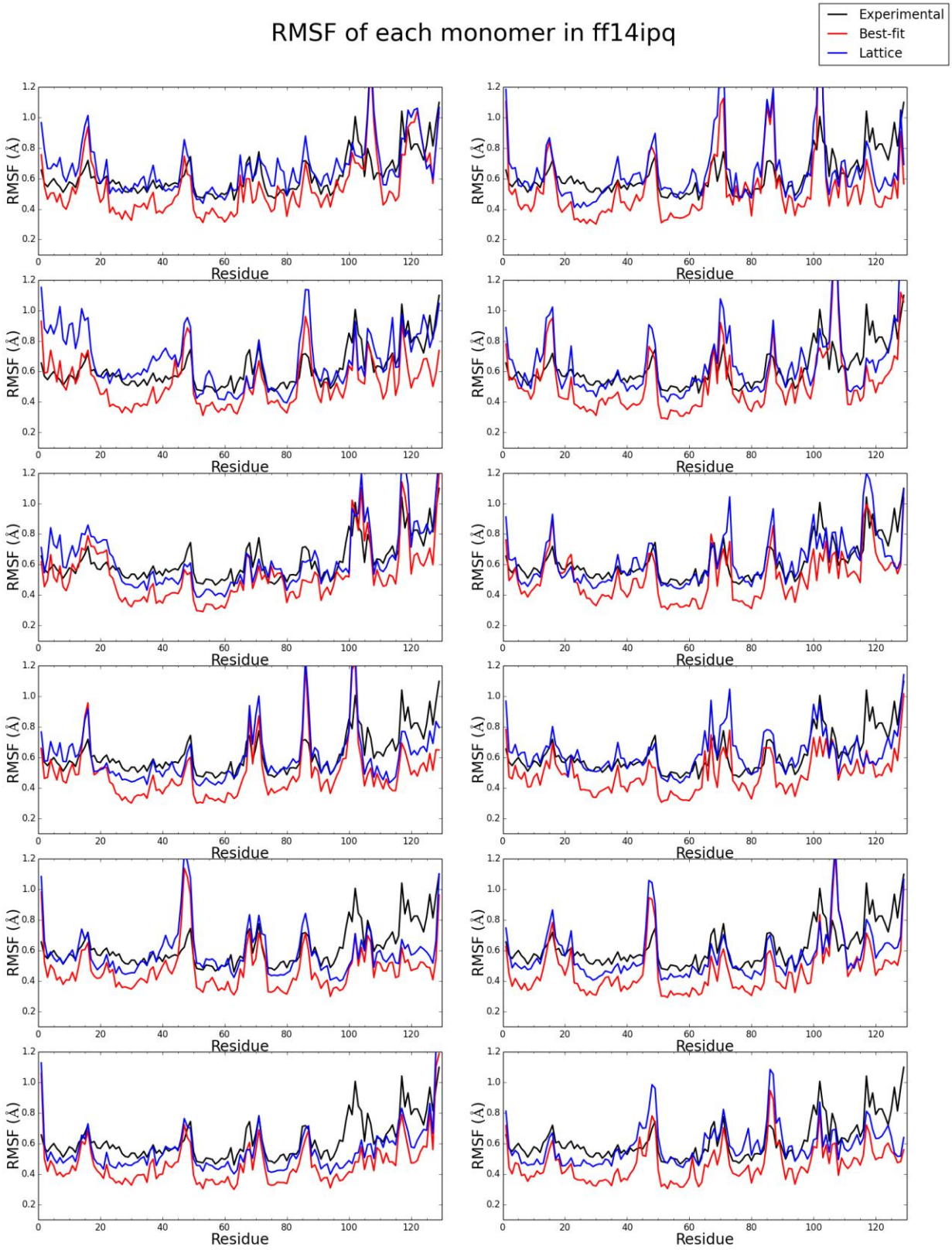

Figure 13: RMSF fluctuations for each individual monomer in the ff14ipq simulation.

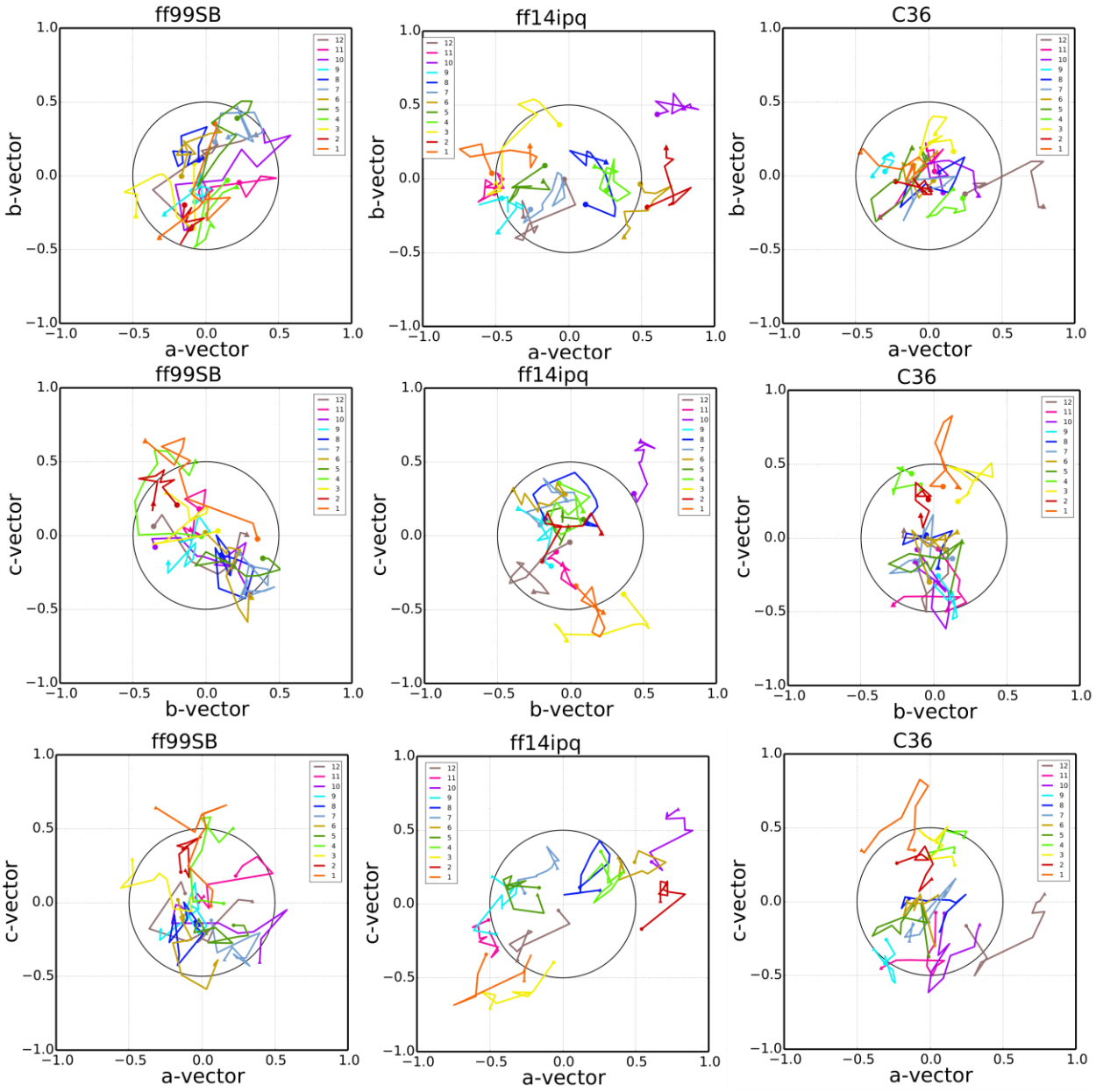

Figure 14:Mean position of each ASU's center of mass plotted over intervals of 100ns over the course of simulation in ff99SB, ff14ipq and C36. Start position (<t=0-100ns>) indicated by a circle an ending position (<t=900-1000ns>) indicated by a triangle.

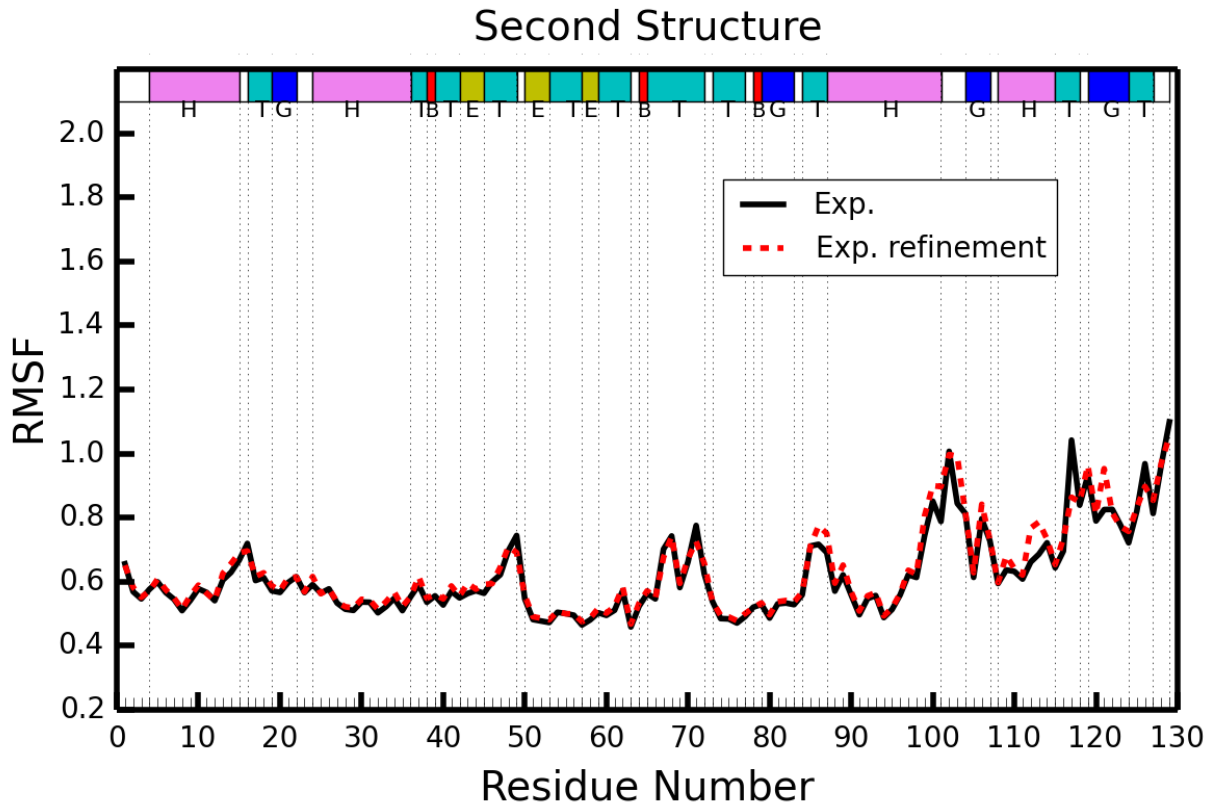

Figure 15: C_αB-factors resulting from a re-refinement of the model against the experimental data compared to the deposited B-factors. Pearson correlation is 0.97. The re-refined model backbone RMSD against the deposited model was 0.04Å. R-free was 14.4 vs. a reported R-free of 14.7.