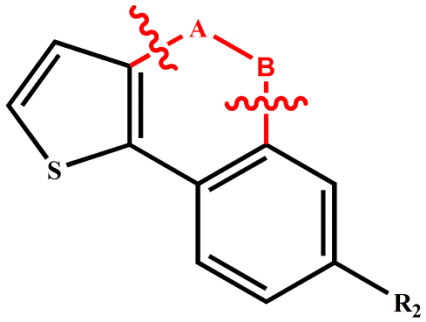
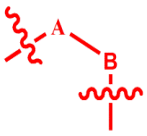
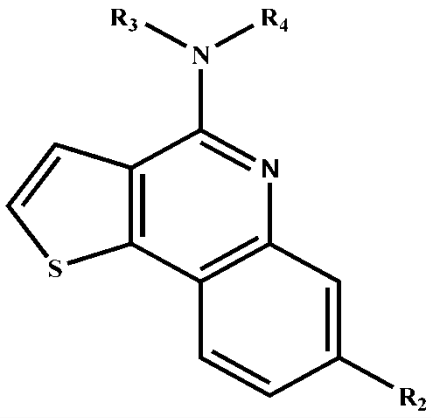
Supporting Materials

Table S1 The structures and biological activities of the 48 inhibitors of CK2

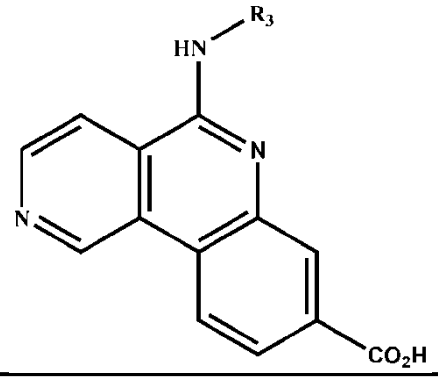


No.		R_2	IC_{50}(μM)	pIC_{50}
1	-CO-NH-	CO_2H	2.1	5.678
2	-CO-N($(CH_2)_3OH$)-	CO_2H	1.5	5.824
3	-(C-O$(CH_2)_3OH$)=N-	CO_2H	0.99	6.004
4	-(C-NH$(CH_2)_3OH$)=N-	CO_2H	0.75	6.125

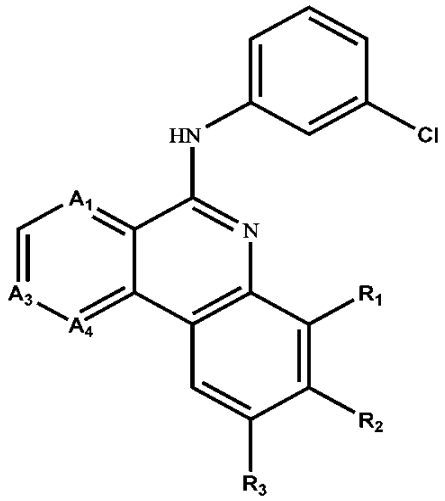


NO.	$-NR_3R_4$	R_2	IC_{50}(μM)	pIC_{50}
5	-NH-$(CH_2)_2OH$	CO_2H	1.26	5.900
6	-NH-$(CH_2)_2NMe_2$	CO_2H	0.102	6.991
7	-Pyrrolidino	CO_2H	1.78	5.750
8	-NH-phenyl	CO_2H	0.092	7.036
9	-NMe-phenyl	CO_2H	1.07	5.971
10	-NH-(2-Me-phenyl)	CO_2H	0.97	6.013
11	-NH-phenyl	*C*-(1*H*-tetrazol-5-yl)	0.096	7.018
12	-NH-$(CH_2)_2Ph$	CO_2H	0.516	6.287
13	-NH-(4-F-phenyl)	CO_2H	0.219	6.660

14	-NH-(3-F-phenyl)	CO_2H	0.068	7.167
15	-NH-(4-Cl-phenyl)	CO_2H	0.178	6.750
16	-NH-(3-Cl-phenyl)	CO_2H	0.032	7.495
17	-NH-(3-MeO-phenyl)	CO_2H	0.077	7.114
18	-NH-(3-acetylenyl-phenyl)	CO_2H	0.028	7.553
19	-NH-(3-(PhO)-phenyl)	CO_2H	0.395	6.403
20	-NH-(3-(CONHMe)-phenyl)	CO_2H	0.129	6.889
21	-NH-(3-Cl-phenyl)	*C*-(1*H*-tetrazol-5-yl)	0.129	6.889
22	-NH-(3-F-phenyl)	*C*-(1*H*-tetrazol-5-yl)	0.075	7.125



NO.	R_3	IC_{50}(μM)	pIC_{50}
23	-phenyl	0.006	8.222
24	$-(CH_2)_2NMe_2$	0.025	7.602
25	-cyclopentyl	0.027	7.569
26	-OMe	0.008	8.097
27	-cyclopropyl	0.016	7.796
28	$-(CH_2)_2O$-*i*-Pr	0.011	7.959
29	$-(CH_2)$phenyl	0.009	8.046
30	$-(CH_2)_2$phenyl	0.003	8.523
31	$-(CH_2)_3$phenyl	0.016	7.796
32	-(3-MeO-phenyl)	0.004	8.398
33	-(3-Cl, 4-F-phenyl)	0.004	8.398
34	-(3-F-phenyl)	0.005	8.301
35	-(2-Cl-phenyl)	0.008	8.097
36	-(3-Cl-phenyl)	0.001	9.000
37	-(4-Cl-phenyl)	0.007	8.155
38	-(3-acetylenyl-phenyl)	0.003	8.523
39	-(3-CN-phenyl)	0.004	8.398
40	-(4-(PhO)-phenyl)	0.069	7.161
41	-(3-(PhO)-phenyl)	0.019	7.721
42	$-(3-(SO_2NH_2)$-phenyl)	0.043	7.367



NO.	A_1	A_3	A_4	R_1	R_2	R_3	IC_{50}(μM)	pIC_{50}
43	CH	N	CH	H	*C*-(1*H*-tetrazol-5-yl)	H	0.045	7.347
44	CH	N	CH	H	$CONH_2$	H	0.417	6.380
45	CH	N	CH	Me	CO_2H	H	0.006	8.222
46	CH	N	CH	H	H	CO_2H	0.35	6.456
47	N	CH	N	H	CO_2H	H	0.22	6.658
48	N	N	CH	H	CO_2H	H	0.007	8.155

Table S2. Docking scores of 48 inhibitors predicted by different docking protocols

No.	pIC50	HTVS score	SP score	XP score	IFD score
1	5.678	-8.654	-8.799	-7.960	-7.901
2	5.824	-8.020	-9.050	-8.862	-8.954
3	6.004	-8.943	-9.173	-9.382	-9.437
4	6.125	-8.611	-8.726	-8.715	-9.088
5	5.900	-8.137	-8.554	-8.689	-8.951
6	6.991	-8.201	-8.360	-7.810	-8.502
7	5.750	-8.804	-9.024	-8.026	-8.633
8	7.036	-8.861	-9.001	-8.607	-6.162
9	5.971	-8.522	-8.429	-5.787	-8.790
10	6.013	-8.850	-9.035	-2.823	-7.120
11	7.018	-7.926	-8.022	-6.788	-5.299
12	6.287	-8.181	-8.720	-8.167	-9.104
13	6.660	-8.912	-9.045	-8.932	-9.192
14	7.167	-9.046	-9.414	-8.996	-8.842
15	6.750	-8.849	-9.005	-8.908	-9.376
16	7.495	-8.958	-9.401	-9.271	-9.603
17	7.114	-8.958	-9.321	-9.190	-7.815
18	7.553	-9.064	-9.265	-9.280	-8.934
19	6.403	-6.803	-8.429	-9.633	-10.369
20	6.889	-8.767	-9.304	-4.878	-9.537
21	6.889	-8.229	-8.302	-7.819	-8.139
22	7.125	-7.886	-8.089	-7.791	-7.003
23	8.222	-10.493	-10.620	-11.224	-12.120
24	7.602	-10.318	-10.481	-11.468	-11.299
25	7.569	-10.535	-10.664	-11.792	-12.360
26	8.097	-10.391	-10.528	-11.231	-10.857
27	7.796	-10.332	-10.518	-11.266	-11.360
28	7.959	-9.714	-10.475	-11.767	-11.571
29	8.046	-10.068	-10.468	-11.158	-12.179
30	8.523	-10.448	-10.550	-12.387	-12.969
31	7.796	-10.635	-10.836	-12.258	-11.621
32	8.398	-10.823	-10.949	-10.472	-12.555
33	8.398	-10.745	-11.030	-12.108	-12.508
34	8.301	-10.899	-11.081	-11.247	-12.101
35	8.097	-10.462	-10.703	-10.347	-11.791
36	9.000	-10.826	-10.986	-11.480	-12.492
37	8.155	-10.409	-10.580	-11.720	-12.231
38	8.523	-10.701	-10.846	-12.071	-12.526
39	8.398	-11.047	-11.157	-11.826	-12.150
40	7.161	-9.885	-10.313	-11.474	-12.062
41	7.721	-10.850	-11.126	-12.485	-13.267
42	7.367	-11.055	-11.396	-12.572	-13.287

43	7.347	-8.569	-9.574	-8.439	-11.799
44	6.380	-7.883	-10.149	-10.624	-10.824
45	8.222	-11.009	-11.092	-12.178	-12.912
46	6.456	-7.783	-7.956	-9.194	-9.343
47	6.658	-8.711	-8.931	-9.350	-9.416
48	8.155	-10.700	-11.032	-12.044	-12.332

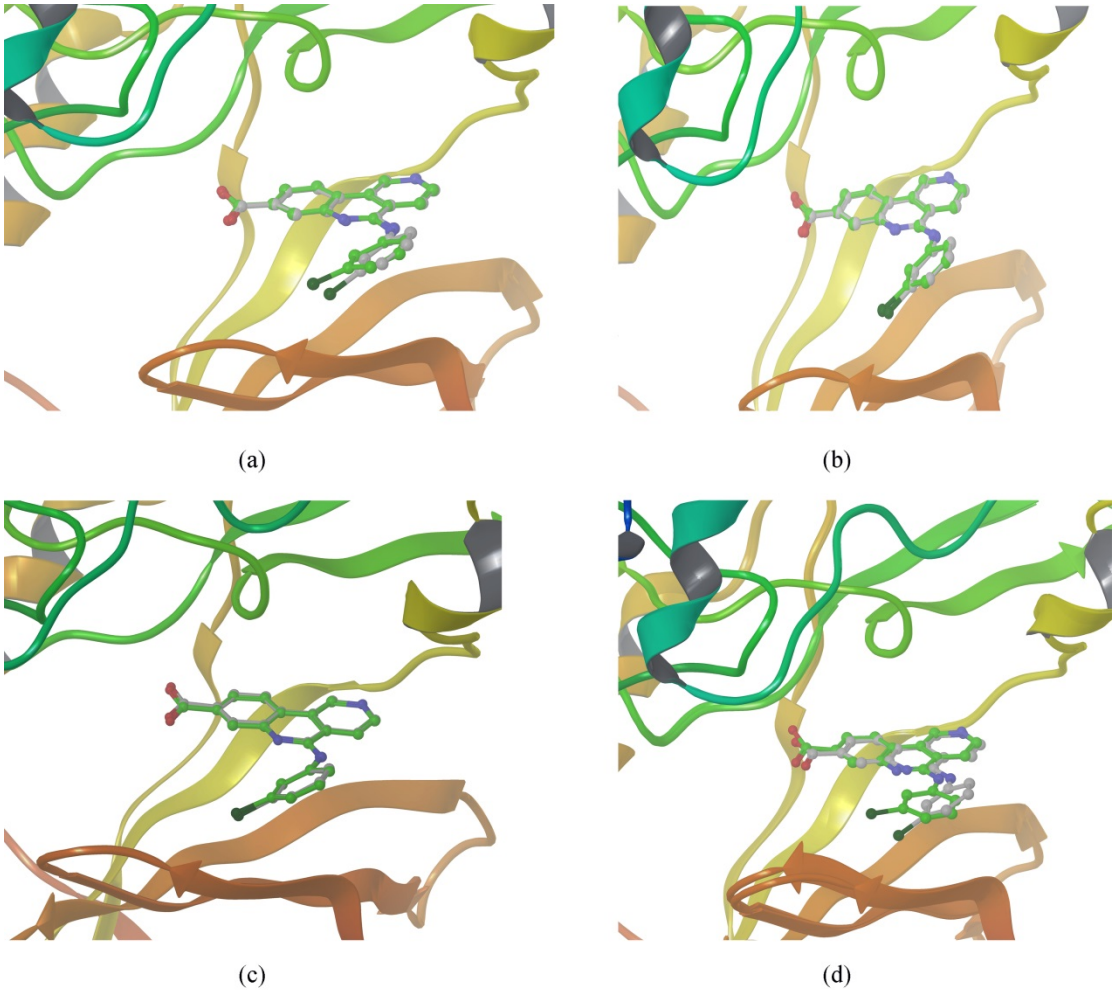


Figure S1. The superposition of the docked structures of CX-4945 predicted with (a) *Glide* HTVS docking, (b) *Glide* SP docking, (c) *Glide* XP docking and (d) induced fit docking with its original structure in the crystallographic complex. (carbon atoms in the crystal structure are colored in gray, and those in the redocked structures in green)

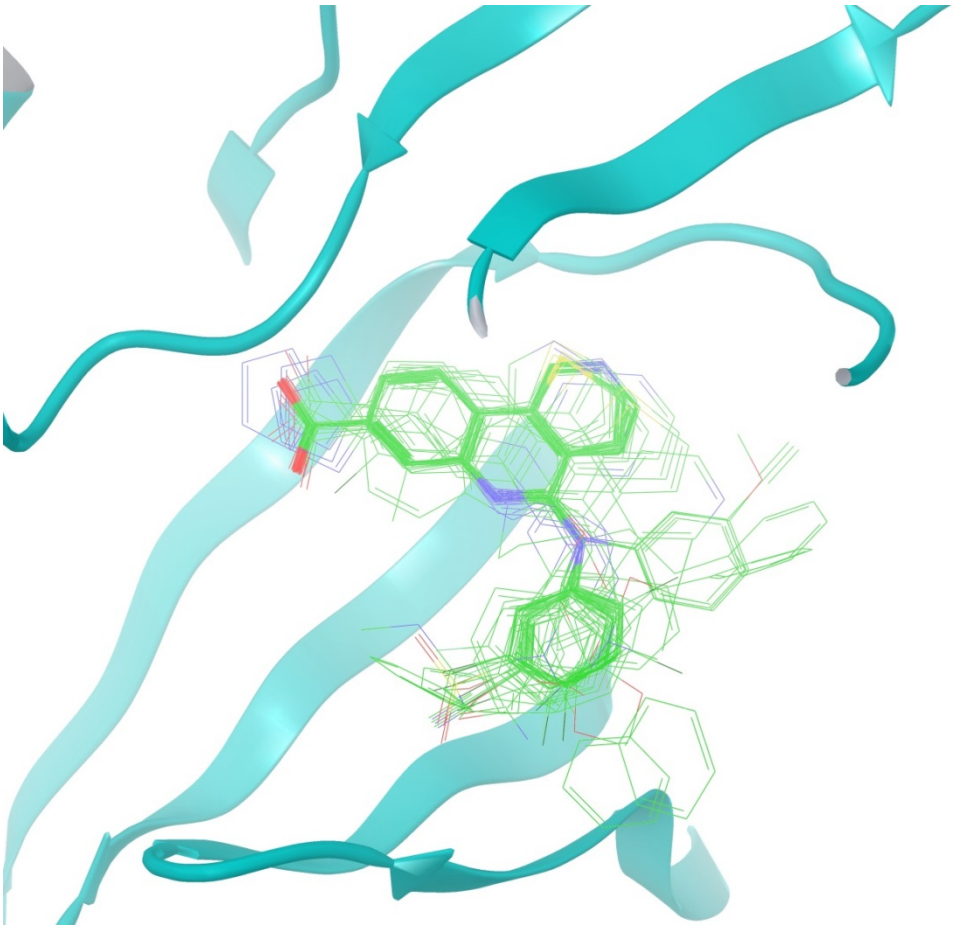


Figure S2. The superposition of the docked structures of the 48 inhibitors (carbon atoms are colored in green)

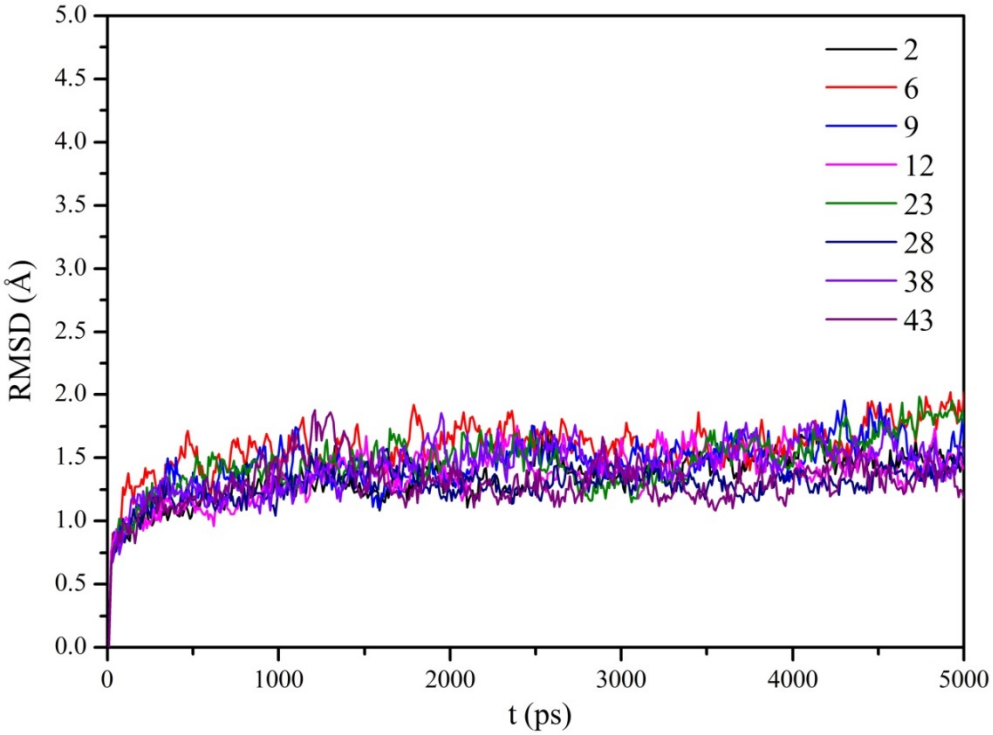


Figure S3. Root-mean-square displacement (RMSD) of the backbone Cα atoms of the CK2/inhibitor complexes (2, 6, 9, 12, 23, 28, 38 and 43) with respect to the first snapshot as a function of time.