Supporting Information

Insights into the specific feature of electrostatic recognition binding mechanism between BM2 and BM1: A molecular dynamics simulations study

Guixuan Xing[b], Qingchuan Zheng[a,b*]

[a]School of Pharmaceutical Sciences, Jilin University, Changchun, 130023, China

[b]Institute of Theoretical Chemistry, College of Chemistry, Jilin University, Changchun, 130023, China

***Corresponding authors**

E-mail addresses: zhengqc@jlu.edu.cn (Qingchuan Zheng).

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Figure S17 Distance between negatively charged O atoms and positively charged N atoms in the R2 and R3 region of the 98-100A system.

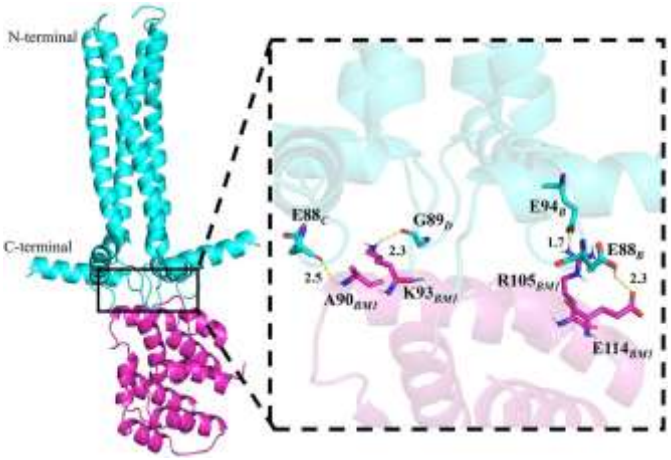
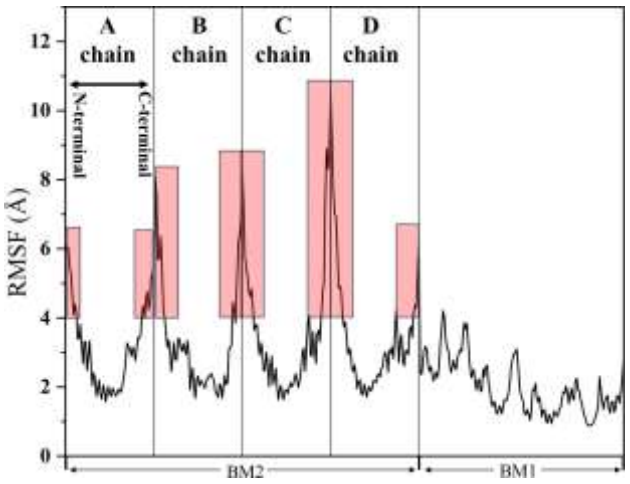


Figure S1 Initial model and distance monitoring of the BM2-BM1 complex.



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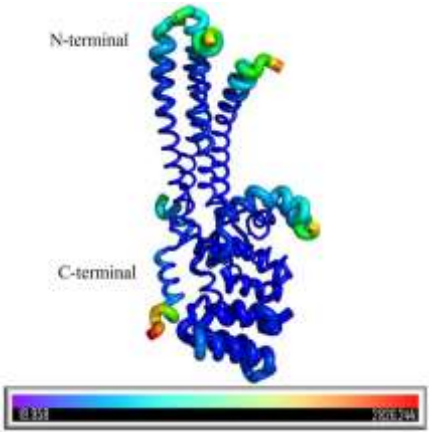

Figure S3 B-factor analysis of complex system. Close to red indicates that the residue is more flexible, and close to blue indicates that the residue is more stable.

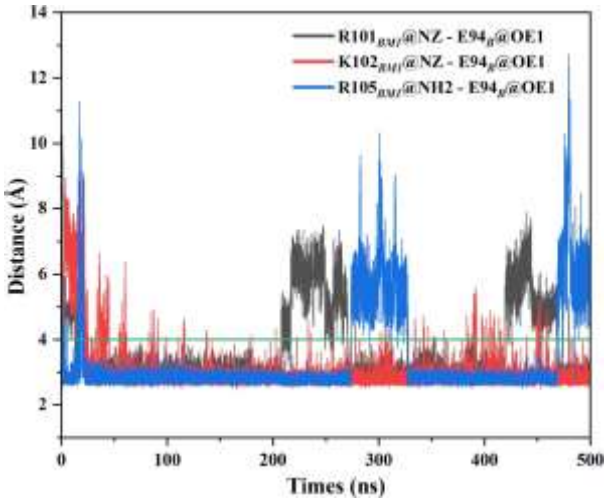

Figure S4 Distance between negatively charged O atoms and positively charged N atoms in the R1 region of the Wild-Type system.

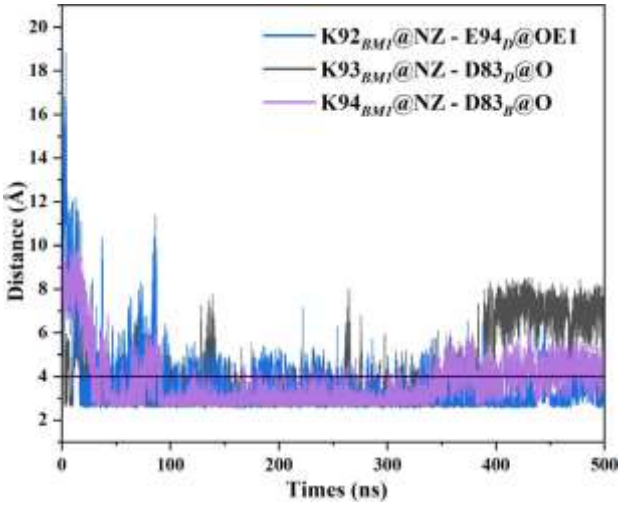

Figure S5 Distance between negatively charged O atoms and positively charged N atoms in the R2 region of the Wild-Type system.

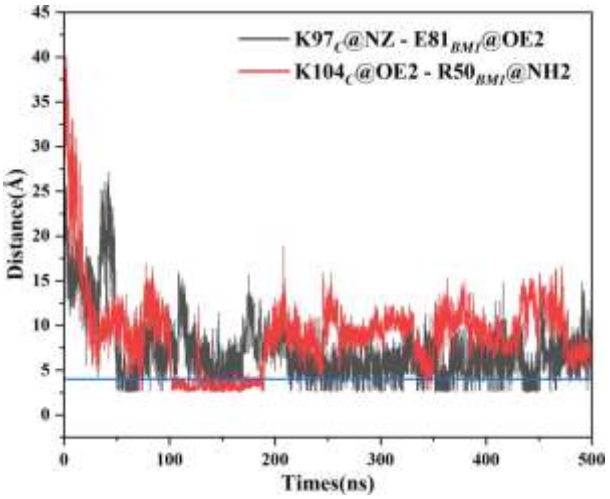

Figure S6 Distance between negatively charged O atoms and positively charged N atoms in the R3 region of the Wild-Type system.

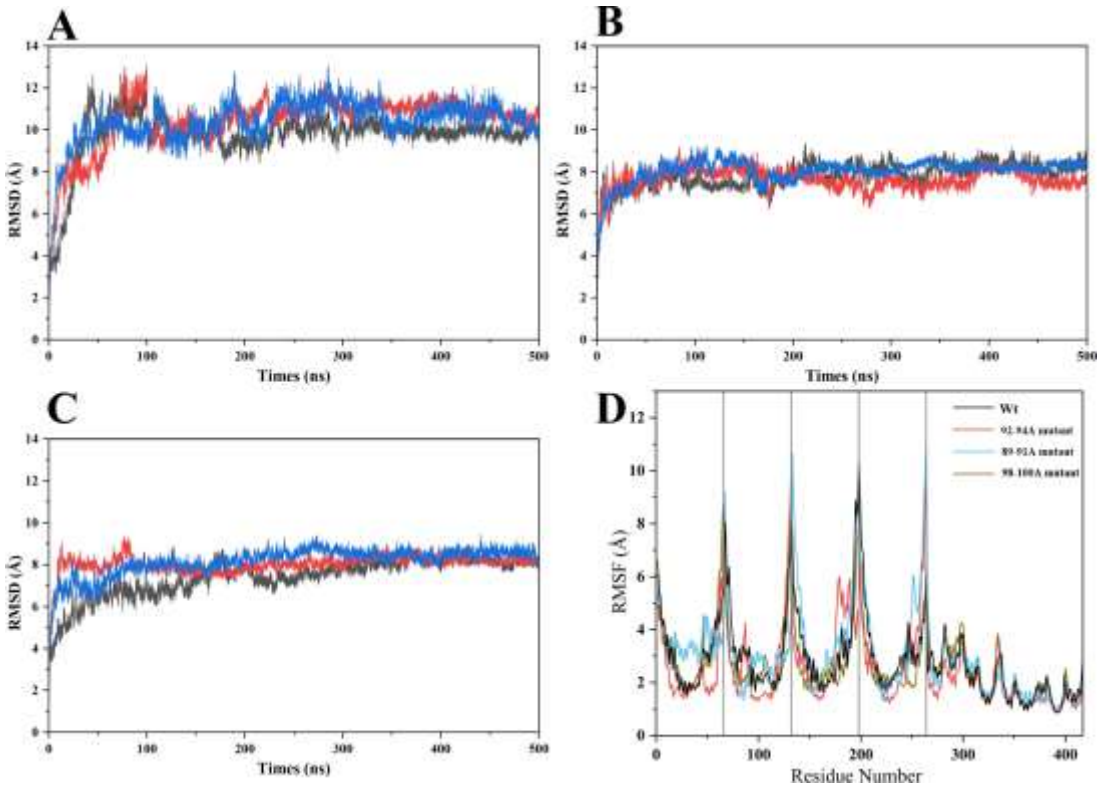

Figure S7 RMSD as a function of time for three groups of mutant systems and RMSF values of four systems.

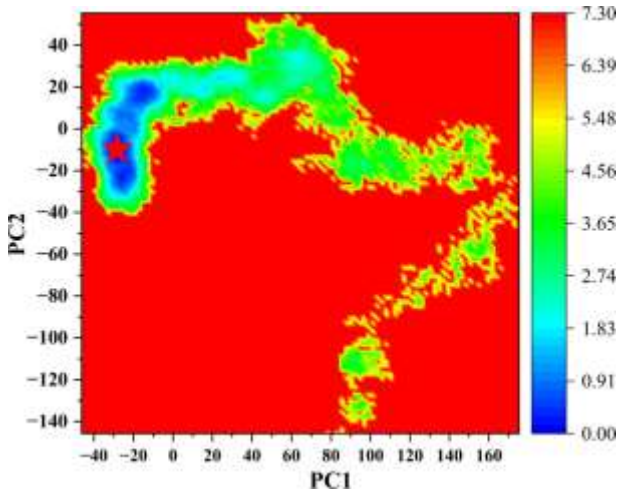

Figure S8 Free energy landscape of the 92-94A system. The star marks the lowest energy conformation of the system.

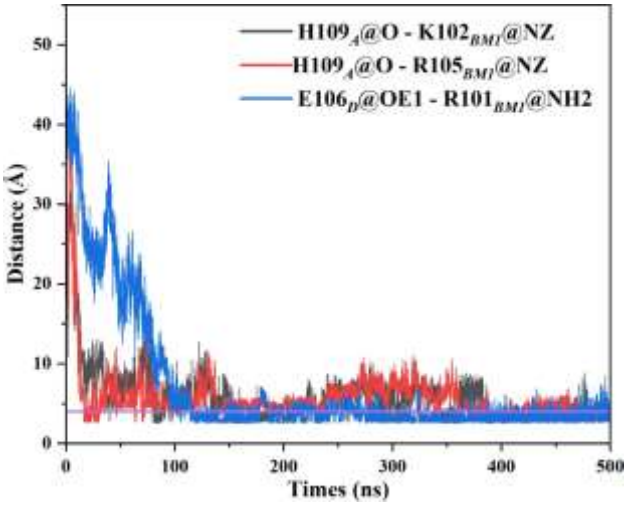

Figure S9 The distance between the C terminal residue of the chain A and the chain D of BM1 protein and the charged residues in the R1 region.

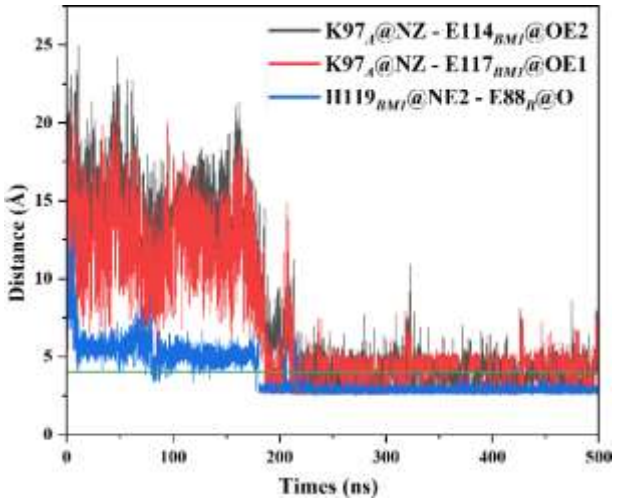

Figure S10 The distance between the charged residue atoms in the R1′ region of the 92-94A system.

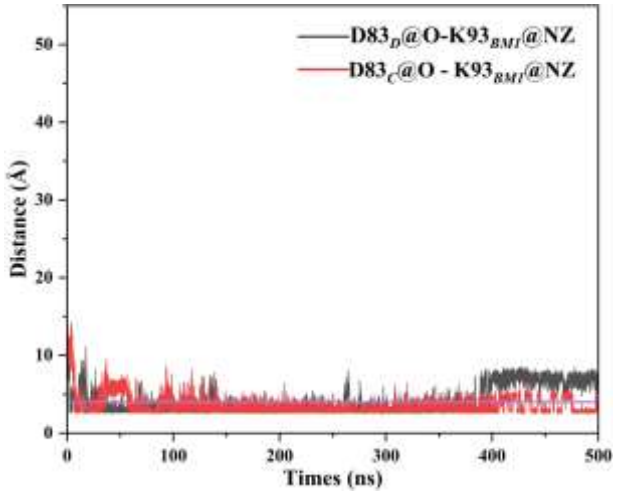

Figure S11 The distance between the charged residue atomsin the R2 region of the 92-94A system.

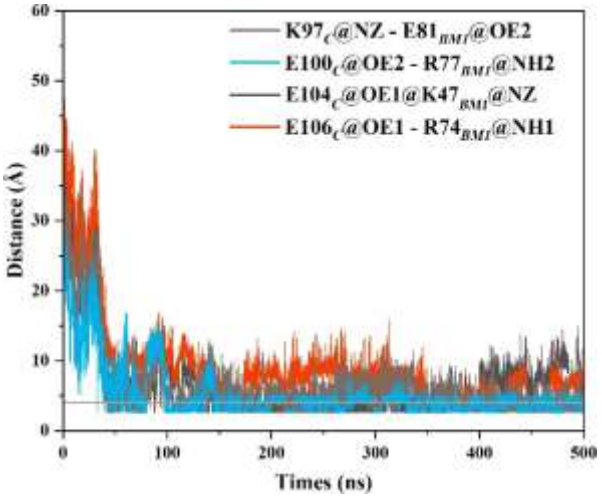

Figure S12 The distance between the charged residue atoms in the R3 region of the 92-94A system.

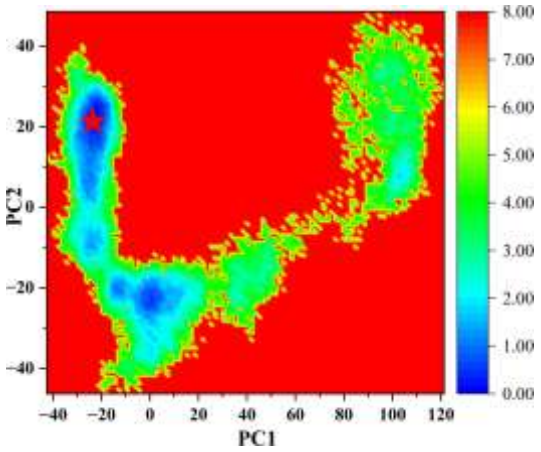

Figure S13 Free energy landscape of the 89-91A system. The star marks the lowest energy conformation of the system.

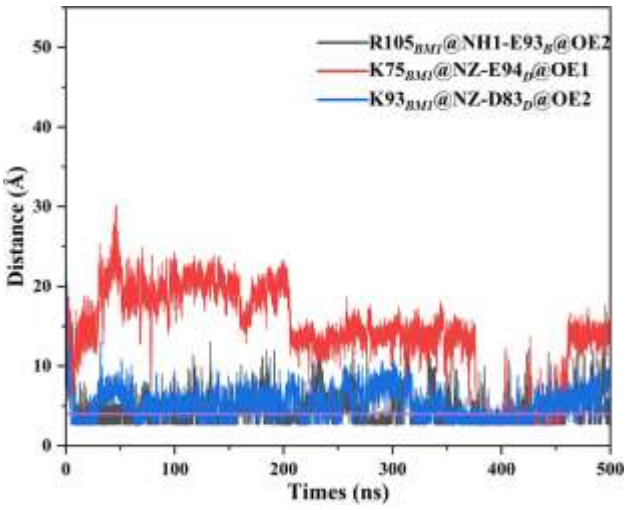

Figure S14 The distance between the charged residue atoms in the 89-91A system.

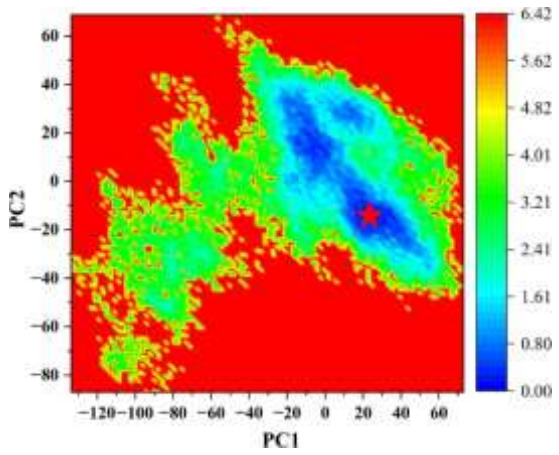

Figure S15 Free energy landscape of the 98-100A system. The star marks the lowest energy conformation of the system.

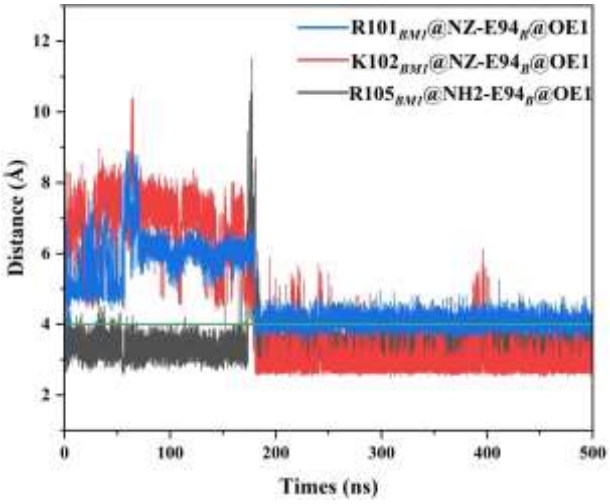

Figure S16 Distance between negatively charged O atoms and positively charged N atoms in the R1 region of the 98-100A system.

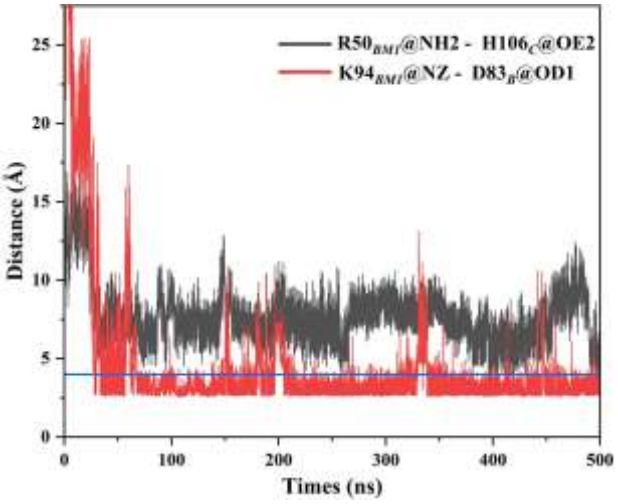

Figure S17 Distance between negatively charged O atoms and positively charged N atoms in the R2 and R3 region of the 98-100A system.

TABLE LISTS

Table S1 The binding free energies (kcal·mol^{-1}) contributed by key residues ($\Delta G_{bind} \leq$ -2.0 kcal·mol^{-1}) in the Wild-Type system.

	Residue	ΔE_{vdW}	ΔE_{ele}	ΔE_{polar}	ΔE_{nonpol}	ΔE_{total}
BM2	$E94_B$	-1.73	-113.96	98.11	-0.59	-18.17
	$E104_B$	0.61	-92.15	85.77	-0.26	-6.03
	$E93_B$	0.25	-65.45	60.45	-0.01	-4.77
	$I87_A$	-3.73	-3.34	3.76	-0.34	-3.65
	$L90_D$	-3.54	1.85	-1.07	-0.58	-3.34
	$L85_D$	-1.22	-7.97	6.43	-0.36	-3.12
	$T101_C$	-3.12	-5.06	5.74	-0.66	-3.10
	$I85_A$	-3.27	1.15	0.11	-0.62	-2.64
	$L60_B$	-2.72	-7.09	7.54	-0.29	-2.55
	$E94_C$	-1.28	-73.09	72.51	-0.46	-2.32
BM1	$R105_{BM1}$	-0.83	-312.86	303.95	-0.58	-10.32
	$R101_{BM1}$	-3.45	-292.52	288.57	-0.70	-8.11
	$M86_{BM1}$	-3.98	-3.38	3.99	-0.81	-4.17
	$R50_{BM1}$	-1.78	-181.06	179.22	-0.45	-4.08
	$I97_{BM1}$	-3.64	-0.03	0.50	-0.66	-3.82
	$K102_{BM1}$	-2.07	-323.01	322.60	-0.68	-3.16
	$R77_{BM1}$	-0.10	-206.77	203.99	-0.17	-3.06
	$T53_{BM1}$	-1.90	-5.87	5.08	-0.32	-3.00
	$H119_{BM1}$	-3.58	-5.59	6.64	-0.37	-2.90
	$E120_{BM1}$	-4.33	-252.49	254.86	-0.50	-2.46
	$K47_{BM1}$	-0.84	-190.47	189.32	-0.19	-2.18
	$L96_{BM1}$	-2.14	-1.72	2.22	-0.43	-2.08

Table S2 Occupancy of hydrogen bond interactions in the three regions of BM2 and BM1 binding interface in the Wild-Type system.

	Acceptor	Donor	AvgDist	Occupied (%)
R1 Region	E94$_{B}$@OE1	R105$_{BM1}$@NH2	2.77	67.75
	E94$_{B}$@OE1	R101$_{BM1}$@NH2	2.78	65.61
	E94$_{B}$@OE2	K102$_{BM1}$@NZ	2.78	27.11
	E88$_{B}$@O	K102$_{BM1}$@NZ	2.78	8.63
	G89$_{B}$@O	H119$_{BM1}$@NE2	2.85	46.47
	E104$_{B}$@OE2	R101$_{BM1}$@NH2	2.78	34.88
R2 Region	S91$_{B}$@O	K94$_{BM1}$@NZ	2.88	1.09
	I85$_{D}$@O	K93$_{BM1}$@NZ	2.80	15.74
R3 Region	E94$_{C}$@OE1	M86$_{BM1}$@N	2.84	31.22
	T101$_{C}$@O	D54$_{BM1}$@N	2.86	48.18
	E104$_{C}$@OE2	C51$_{BM1}$@N	2.84	7.36

Table S3 The binding free energy and its components (kcal·mol^{-1}) of the Wild-Type system and three mutation complex systems (92-94A, 89-91A, 98-100A).

System	BM2-BM1 complex system	92-94A System	89-91A System	98-100A System
ΔE_{ele}	-1885.00	-2083.35	-1372.76	-1293.03
ΔE_{vdW}	-146.36	-133.70	-89.89	-109.65
ΔG_{SA}	-23.24	-22.30	-13.75	-16.81
ΔG_{GB}	1958.80	2124.74	1431.43	1353.07
ΔG_{pol} [a]	73.80	41.39	58.68	60.05
ΔG_{nonpol} [b]	-169.61	-156.01	-103.64	-126.47
$\Delta G_{MM\text{-}GBSA}$ [c]	-95.80	-114.63	-44.96	-66.42
$T\Delta S$	-91.89	-81.95	-53.15	-58.01
$\Delta G_{binding}$ [d]	-3.92	-32.68	8.18	-8.42

[a] $\Delta G_{pol} = \Delta E_{ele}+\Delta G_{GB}$ [b] $\Delta G_{nonpol} = \Delta E_{vdW}+\Delta G_{SA}$

[c] $\Delta G_{MM\text{-}GBSA} = \Delta E_{ele}+\Delta E_{vdW}+\Delta G_{GB}+\Delta G_{SASA}$ [d] $\Delta G_{binding} = \Delta G_{MM\text{-}GBSA}-T\Delta S$

Table S4 The binding free energies (kcal·mol^{-1}) contributed by key residues ($\Delta G_{bind} \leq$ -2.0 kcal·mol^{-1}) in the 92-94A system.

	Residue	ΔE_{vdW}	ΔE_{ele}	ΔE_{polar}	ΔE_{nonpol}	ΔE_{total}
	$K97_{A}$	-1.086	-92.578	82.672	-0.77124	-11.7632
	$L90_{C}$	-5.641	-4.7407	4.4405	-0.92022	-6.86142
	$H109_{A}$	-0.7095	-63.312	59.9268	-0.28658	-4.38128
	$E100_{B}$	-0.9579	-50.6247	48.0381	-0.26547	-3.80997
	$L90_{D}$	-1.8789	-7.7803	6.3729	-0.44666	-3.73296
BM2	$E106_{C}$	0.7936	-65.2047	60.9972	-0.28609	-3.69999
	$L108_{A}$	-1.381	-10.7907	9.2267	-0.33961	-3.28461
	$I85_{A}$	-2.8074	1.391	-1.0981	-0.56293	-3.07743
	$D83_{C}$	0.2872	-88.3939	85.4739	-0.14406	-2.77686
	$L60_{B}$	-2.8577	-4.1112	4.6166	-0.3622	-2.7145
	$E106_{D}$	-0.6344	-79.3482	78.3392	-0.36713	-2.01053
	$R74_{BM1}$	0.4234	-201.2	189.8906	-0.73443	-11.6202
	$R105_{BM1}$	-0.8845	-263.455	253.5649	-0.69236	-11.4665
	$R77_{BM1}$	-4.6987	-196.791	193.8819	-0.85752	-8.46562
	$R101_{BM1}$	-3.3305	-234.46	233.0921	-0.99148	-5.68958
	$H119_{BM1}$	-3.0676	-10.824	11.0654	-0.43986	-3.26606
BM1	$E81_{BM1}$	-3.8425	-140.8904	-139.423	-0.50025	-2.87575
	$K93_{BM1}$	-2.6392	-261.173	261.9647	-0.8685	-2.7162
	$I97_{BM1}$	-3.1571	-0.5191	1.5432	-0.46824	-2.60124
	$K97_{BM1}$	-3.6486	8.4641	-6.7214	-0.53969	-2.44559
	$K47_{BM1}$	-0.2886	-170.051	168.4381	-0.35909	-2.26099
	$L98_{BM1}$	-2.1612	1.8997	-1.6133	-0.14572	-2.02052

Table S5 Occupancy of hydrogen bond interactions in the four regions of BM2 and BM1 binding interface in the 92-94A system.

	Acceptor	Donor	AvgDist	Occupied (%)
R1 Region	H109$_{A}$@OXT	R105$_{BM1}$@NH2	2.76	43.80
	H109$_{A}$@OXT	K102$_{BM1}$@NZ	2.77	9.97
	E106$_{D}$@OXT	R101$_{BM1}$@NH1	2.81	38.60
R1′ Region	S91$_{A}$@N	E120$_{BM1}$@OE2	2.94	1.03
	K97$_{A}$@NZ	E117$_{BM1}$@OE2	2.91	2.07
	K97$_{A}$@NZ	E114$_{BM1}$@OE1	2.84	0.04
R2 Region	L90$_{C}$@O	T89$_{BM1}$@N	2.77	15.07
	L90$_{C}$@O	K92$_{BM}$@NZ	2.82	4.16
R3 Region	K97$_{C}$@HD2	E81$_{BM1}$@OE1	2.95	0.55
	E104$_{C}$@OE1	R76$_{BM1}$@NH1	2.78	1.83
	E104$_{C}$@OE1	R4 $_{BM1}$@NH1	2.77	10.9
	E106$_{C}$@O	R74$_{BM1}$@NH2	2.78	27.55
	E100$_{C}$@O	R77$_{BM1}$@NH1	2.84	41.97

Table S6 The binding free energies (kcal·mol^{-1}) contributed by key residues ($\Delta G_{bind} \leq$ -2.0 kcal·mol^{-1}) in the 89-91A system.

	Residue	ΔE_{vdW}	ΔE_{ele}	ΔE_{polar}	ΔE_{nonpol}	ΔE_{total}
BM2	$A91_{B}$	-1.19145	-6.8308	4.05429	-0.37613	-4.3441
	$G88_{B}$	-1.95628	-19.5339	18.18634	-0.60464	-3.90844
	$M98_{D}$	-3.55294	-1.41872	2.49405	-0.76113	-3.23874
	$I95_{D}$	-2.78152	-0.93961	1.26042	-0.42306	-2.88376
	$I87_{D}$	-2.38734	0.3183	0.09765	-0.52793	-2.49932
	$A90_{B}$	-1.85181	-0.70662	0.68129	-0.206	-2.08313
BM1	$K105_{BM1}$	-0.81712	-196.219	193.3244	-0.43916	-4.15077
	$T87_{BM1}$	-2.44024	-2.54994	3.16956	-0.47521	-2.29582
	$K101_{BM1}$	-4.38663	-232.862	236.0125	-1.01897	-2.25526

Table S7 Occupancy of hydrogen bond interactions in the four regions of BM2 and BM1 binding interface in the 89-91A system.

	Acceptor	Donor	AvgDist	Occupied (%)
R1 Region	E88$_{B}$@OE2	E114$_{BM1}$@OE2	2.86	0.02
	A89$_{B}$@O	R105$_{BM1}$@NH1	2.83	5.16
	A90$_{B}$@O	R101$_{BM1}$@NH2	2.83	7.54
	A91$_{B}$@O	R101$_{BM1}$@NH2	2.81	69.09
	A93$_{B}$@OE2	R105$_{BM1}$@NH2	2.79	28.61
R2 Region	S82$_{B}$@O	K94$_{BM1}$@NZ	2.83	4.73
	D83$_{D}$@OD2	K93$_{BM1}$@NZ	2.79	6.18
R3 Region	E94$_{D}$@O	Y126$_{BM1}$@OH	2.80	5.37
	E94$_{D}$@OE1	T80$_{BM1}$@OG1	2.69	6.57
	E94$_{D}$@OE1	K75$_{BM1}$@NZ	2.78	6.45

Table S8 The binding free energies (kcal·mol^{-1}) contributed by key residues ($\Delta G_{bind} \leq$ -2.0 kcal·mol^{-1}) in the 98-100A system.

	Residue	ΔE_{vdW}	ΔE_{ele}	ΔE_{polar}	ΔE_{nonpol}	ΔE_{total}
BM2	E94$_{B}$	-0.91	-102.93	95.72	-0.52	-8.63
	E88$_{D}$	-1.02	-69.52	64.18	-0.25	-6.61
	D83$_{A}$	-2.11	-76.55	74.26	-0.55	-4.96
	M98$_{D}$	-4.35	0.06	0.77	-0.68	-4.22
	I85$_{A}$	-3.67	-0.87	1.52	-0.80	-3.83
	V102$_{D}$	-4.58	2.05	-0.55	-0.68	-3.76
	L60$_{B}$	-3.54	-1.01	1.47	-0.57	-3.65
	M98$_{B}$	-2.86	0.82	-0.35	-0.53	-2.92
	I95$_{D}$	-2.68	-0.32	0.59	-0.39	-2.79
	T89$_{BM1}$	-4.21	-13.31	10.68	-0.79	-7.62
BM1	R101$_{BM1}$	-4.22	-189.42	188.69	-0.81	-5.76
	R105$_{BM1}$	0.42	-181.55	175.93	-0.15	-5.36
	T87$_{BM1}$	-2.37	-9.06	8.23	-0.39	-3.59
	I97$_{BM1}$	-2.77	-2.14	2.77	-0.51	-2.65
	K75$_{BM1}$	-0.84	-149.06	147.89	-0.38	-2.39
	A90$_{BM1}$	-2.53	-2.38	3.27	-0.49	-2.13

Table S9 Occupancy of hydrogen bond interactions in the four regions of BM2 and BM1 binding interface in the 98-100A system.

	Acceptor	**Donor**	**AvgDist**	**Occupied (%)**
R1 Region	E94$_{B}$@OE2	R105$_{BM1}$@NH1	2.80	92.16
	E94$_{B}$@OE1	R101$_{BM1}$@NH1	2.76	92.12
	E94$_{B}$@OE2	K102$_{BM1}$@NZ	2.78	24.84
	E93$_{B}$@OE2	K102$_{BM1}$@NZ	2.78	20.33
	E88$_{B}$@OE1	K102$_{BM1}$@NZ	2.84	8.36
	E106$_{B}$@OE1	R101$_{BM1}$@NH2	2.77	55.23
	H109$_{B}$@OXT	R104$_{BM1}$@NH1	2.80	40.92
R2 Region	G89$_{D}$@O	K93$_{BM1}$@NZ	2.81	14.71
	D83$_{B}$@OD2	K94$_{BM1}$@NZ	2.80	0.64
	I95$_{D}$@O	T89$_{BM1}$@OG1	2.77	66.39
	E88$_{C}$@O	T88$_{BM1}$@OG1	2.77	67.20
R3 Region	H109$_{C}$@NE2	G81$_{BM1}$@OE1	2.81	0.18
	T101$_{C}$@OG1	D54$_{BM1}$@N	2.90	40.06
	E106$_{C}$@OE2	R50$_{BM1}$@NH2	2.82	42.52