Supplementary Materials

Table S1. Summary of the datasets.

Name	No. of complexes	Peptide length	`Application
dataset I	19	5 - 12	Prediction capability for binding free energies
dataset II	34	20 - 25	Prediction capability for binding free energies
dataset III	25	5 - 12	Rescoring capability in global docking
dataset IV	17	20 - 25	Rescoring capability in global docking
dataset V	50	5 - 15	Rescoring capability in local docking
dataset VI	20	20 - 25	Rescoring capability in local docking

Table S2. The experimentally determined dissociation constants and binding free energies for the dataset I.

PDB code	Chain id	Peptide length	K_d (M)	ΔG_{bind} (kJ/mol)
1w9e	B:S	5	1.00E-03	-17.38
2hpl	A:B	5	3.60E-06	-31.02
1tw6	B:D	6	3.00E-08	-42.87
3d1e	A:P	6	1.42E-06	-33.32
1se0	A:B	7	7.60E-08	-39.89
2foj	A:B	7	2.10E-05	-26.66
1pz5	AB:C	8	4.00E-06	-30.76
2ak5	AB:D	8	1.40E-05	-27.01
1cka	A:B	9	1.90E-06	-31.84
1mfg	A:B	9	5.00E-05	-24.51
1t4f	M:P	9	8.00E-08	-40.44
1x2r	A:B	9	1.81E-07	-38.42
1t7r	A:B	10	1.10E-06	-33.96
2ho2	A:B	10	1.16E-04	-22.28
2o9v	A:B	10	2.88E-04	-20.18
2r7g	A:B	10	9.00E-07	-33.3
1d4t	A:B	11	6.50E-07	-35.26
2b9h	A:C	12	8.00E-08	-40.44
2cch	AB:E	12	2.03E-08	-43.84

Table S3. The experimentally determined dissociation constants for dataset II.

PDB code	Chain id	Peptide length	K_d (M)
1fmo	E:I	20	2.30E-09
1pjm	A:B	20	1.80E-07
2djy	A:B	20	4.00E-05
2f31	A:B	20	1.02E-07
2ihs	B:D	20	4.00E-08
2kqs	A:B	20	5.53E-05
2lp0	A:B	20	2.22E-05
2w84	A:B	20	7.00E-08
1yk1	AB:E	21	4.57E-08
2i32	A:E	21	1.30E-06
3r85	B:F	21	4.13E-05
4cu4	A:B	21	1.20E-06
5glh	A:B	21	2.07E-11
5m72	A:B	21	3.30E-08
1g9i	E:I	22	1.20E-07
1jgn	A:B	22	1.60E-07
1xr0	A:B	22	1.00E-05
1zsg	A:B	22	7.50E-06
2a7u	A:B	22	1.20E-07
2gww	A:B	22	1.10E-10
4bxl	AB:C	22	2.40E-07
4niq	A:C	22	5.00E-06
4zrk	C:G	22	1.00E-06
2n01	A:B	23	1.00E-06
3kz0	B:D	23	2.73E-07
5fzt	A:B	23	4.80E-05
1pd7	A:B	24	3.00E-07
1q0w	A:B	24	2.77E-04
3dvu	B:D	24	1.10E-06
4q5u	A:C	24	1.00E-12
1sb0	A:B	25	1.50E-05
1vyt	A:E	25	2.00E-08
2mv7	A:B	25	1.56E-09
2mzd	A:B	25	8.77E-07

Table S4. The ranks given by pepATTRACT and MM/PBSA for the dataset III.

PDB	peptide	pepATTRACT	ff99 implicit (ε_{in})				ff99 explicit (ε_{in})				ff14SB implicit (ε_{in})			
code	length		1	2	4	6	1	2	4	6	1	2	4	6
1jwg	5	14	10	8	2	1	5	3	1	1	13	6	1	1
1nvr	5	5	20	20	8	5	18	26	27	18	21	18	8	6
2h9m	5	49	1	1	1	1	1	1	1	1	1	1	1	1
2hpl	5	12	1	1	1	2	1	2	4	5	1	1	1	1
1awr	6	26	1	1	1	1	1	1	4	3	1	1	1	1
1tp5	6	23	9	11	9	11	20	25	27	27	12	11	13	14
1vzq	6	48	4	2	3	4	2	3	4	7	3	2	3	4
1czy	7	1	4	3	3	5	7	10	6	7	2	4	4	6
1se0	7	43	49	42	27	23	48	44	33	24	45	39	23	16
2foj	7	42	28	24	20	17	11	18	18	8	29	24	20	18
1er8	8	11	23	19	14	17	32	32	32	27	22	20	19	17
1n7f	8	1	24	6	2	1	22	5	3	3	23	7	1	1
1ou8	8	10	3	13	9	5	6	4	1	1	3	10	5	2
2c3i	8	2	7	10	8	6	13	12	7	2	7	12	8	5
2j6f	8	30	8	10	10	9	21	18	15	16	15	13	12	12
1cka	9	49	12	12	14	16	5	7	11	22	17	15	15	18
1mfg	9	47	5	9	14	21	28	34	35	31	3	6	11	15
1x2r	9	15	36	32	17	12	19	20	14	9	38	28	13	9
1z9o	9	44	1	1	1	3	13	10	12	17	1	1	3	3
1ywo	10	30	1	1	5	9	1	1	1	1	1	1	5	8
2ho2	10	39	3	3	3	3	4	5	4	3	3	4	4	5
2o9v	10	20	1	2	2	3	3	10	18	22	1	2	5	16
1nx1	11	45	4	3	2	1	13	12	13	13	3	3	2	1
1ssh	11	36	1	1	1	1	1	1	1	3	1	1	1	1
2cch	12	50	43	37	25	10	12	9	8	7	41	35	13	7

Table S5. The 73 complexes extracted from PepBDB and the ranks given by HPEPDOCK and MM/GBSA in global docking.

PDB	Peptide	Free	HPEPDOCK	GB^{OBC1}				GB^{OBC2}			
code	length	protein^{a}		1	2	4	6	1	2	4	6
1vpp	20	1mkk:A									
1wkw	20	5gw6:A									
2cny	20	2co3:A	51	22	9	10	10	10	9	8	7
2k7w	20	5w60:A									
2kqs	20	2mw5:A:1									
2nnu	20	1dto:A	7	17	15	13	12	12	15	13	12
2xpn	20	2xpl:A									
3owt	20	3cz6:A	1	1	1	2	2	1	1	2	2
3x2v	20	1re8:A	32	1	3	12	18	1	2	11	14
4bd6	20	4bd8:A									
4ika	20	3n6m:A									
4v0v	20	1jk7:A									
5mk0	20	5mjz:A	1	1	1	1	1	1	1	1	1
1m2z	21	1nhz:A									
1rpq	21	1f2q:A									
2bn5	21	2bn6:A:1									
2yle	21	2ylf:A									
2z34	21	2cu9:A									
3aa1	21	3aa7:A	41	37	42	47	47	58	49	45	43
3plv	21	1m94:A									
4cu4	21	1qfg:A	60	94	67	46	44	94	65	47	41
4cyd	21	3r6s:C									
4gnt	21	5wfx:A	27	20	21	26	30	16	19	27	35
4ig9	21	4i5i:A									
4w8p	21	2x0c:A	17	4	10	17	23	4	9	15	23
5glh	21	5gli:A									
5wy2	21	3hpc:X									
1dt7	22	4pe0:X									
1wa7	22	1w1f:A:1									
1zsg	22	2esw:A									
2a7u	22	1abv:A	43	7	8	12	13	6	7	12	13
2wh6	22	1q59:A									
3h0t	22	5jw5:A									
4jhk	22	2i2o:A									
4rey	22	4kfv:A									
5lhz	22	2n19:A:14									
5xod	22	1khx:A									
2mak	23	2maj:AC									
2nud	23	2nun:A									

3ul0	23	4u5u:A	13	6	2	1	1	15	2	1	1
4afj	23	4acc:A									
5anr	23	4ct4:D									
5fw5	23	4fcj:A	23	1	2	5	5	2	2	4	4
5gtb	23	5d9r:A									
5hvz	23	3ezw:AB									
5yip	23	2r2q:A	1	16	12	18	21	12	12	16	18
1iq5	24	3if7:A									
1q0w	24	5nvg:A									
2b3g	24	4ipc:A									
2drn	24	1l6e:AB:1	85	3	4	4	6	3	2	5	6
2m8s	24	2lwp:A:1									
2okr	24	2fst:X									
2qme	24	1mh1:A									
3c66	24	1fa0:B									
3ech	24	1lnw:AB									
3wn7	24	1x2j:A									
4b1w	24	2fxu:A									
4ux6	24	2bhj:A									
5gtu	24	1z2w:B									
6dei	24	3n4s:AB									
1l4w	25	1kfh:A									
1qfn	25	1grx:A									
1vyt	25	1vyu:A	2	1	1	1	1	1	1	1	1
2jmx	25	2bo5:A:1									
2m04	25	3spf:A									
2mzd	25	1f81:A									
2qiy	25	1zx2:A									
3lcn	25	2v75:A	3	5	8	8	10	3	7	7	7
3lu9	25	3u69:H									
3sri	25	4r1a:A									
4jo6	25	2bc3:AB	86	34	10	8	7	45	10	7	7
5j3t	25	2qkm:AB									
5jtm	25	1qyn:AC									

[a] Since some structures have multiple conformations, the number represents the serial number of the conformation.

Table S6. The ranks given by HPEPDOCK and MM/PBSA for the dataset V.

PDB	Peptide	HPEPDOCK	ff99 implicit (ε_{in})				ff99 explicit (ε_{in})				ff14SB implicit (ε_{in})			
code	length		1	2	4	6	1	2	4	6	1	2	4	6
1gyb	5	1	1	1	1	1	1	3	2	1	1	1	1	1
1jwg	5	3	1	1	1	1	1	1	3	2	1	1	1	1
1nvr	5	1	5	1	1	1	1	1	2	3	11	4	1	1
1w9e	5	1	1	1	1	1	1	1	1	1	1	1	1	1
2h9m	5	1	1	1	1	1	1	1	1	1	1	1	1	1
2hpl	5	1	1	1	1	1	1	1	1	1	1	1	1	1
1awr	6	1	1	1	1	1	1	1	1	1	1	1	1	1
1ddv	6	1	7	2	2	2	7	2	2	1	9	7	2	2
1tp5	6	1	1	1	1	1	1	1	1	1	1	1	1	1
1tw6	6	1	1	1	1	1	1	1	1	2	1	1	1	1
1vzq	6	1	2	1	1	1	5	4	4	4	3	2	2	2
2ds8	6	1	2	1	1	2	1	1	2	3	1	1	2	2
3d1e	6	7	1	1	2	2	4	4	8	9	1	1	3	2
1czy	7	1	1	1	1	1	1	1	1	1	1	1	1	1
1lvm	7	1	17	1	1	1	4	7	5	2	13	3	1	1
1se0	7	1	1	1	1	1	1	1	1	1	1	1	1	1
2fnt	7	1	22	21	28	14	29	19	4	2	19	23	18	12
2foj	7	1	30	14	4	2	71	67	23	9	32	14	3	2
1er8	8	1	27	31	37	32	26	22	8	5	28	32	35	30
1n7f	8	2	1	1	1	1	1	1	3	3	1	1	2	2
1ou8	8	2	4	2	1	1	5	2	1	1	4	3	1	1
1pz5	8	4	2	1	1	1	4	4	1	1	1	1	1	1
2ak5	8	2	1	3	5	15	10	16	12	13	2	3	13	17
2c3i	8	4	4	3	3	2	10	7	4	3	4	3	1	1
2fgr	8	6	9	8	4	4	3	1	1	1	8	7	4	3
2j6f	8	4	9	8	3	3	3	4	1	1	12	10	3	1
2vj0	8	3	1	1	1	1	1	1	1	1	1	1	1	1
1cka	9	47	7	12	32	45	2	6	16	27	7	13	38	51
1mfg	9	29	61	69	73	73	18	38	34	37	56	68	76	76
1oai	9	55	55	58	56	52	2	2	5	7	89	92	91	90
1x2r	9	8	19	14	7	6	7	5	3	1	23	27	20	17
1nq7	10	1	1	1	1	1	1	1	1	1	1	1	1	1
1t7r	10	8	3	2	1	1	10	7	6	5	2	1	1	1
1ywo	10	2	1	1	1	1	1	1	1	2	1	1	1	1
2fvj	10	12	28	13	7	7	64	35	19	16	36	26	14	12
2ho2	10	4	21	26	16	12	14	7	6	5	25	23	18	13
2o9v	10	2	4	4	6	10	1	1	2	2	3	2	3	2
2puy	10	1	1	1	1	1	1	1	2	3	1	1	1	1
2r7g	10	2	1	1	1	1	5	5	4	4	1	1	1	1
2zjd	10	4	4	2	2	1	1	1	1	1	4	2	2	1
1nx1	11	10	5	5	4	5	2	2	5	7	7	5	5	6

1rxz	11	9	10	1	1	1	4	5	5	8	12	1	2	2
2a3i	12	34	27	27	24	25	3	7	13	12	25	22	19	18
2b9h	12	6	3	2	1	1	3	1	1	1	2	1	1	1
2cch	12	1	5	4	2	1	4	4	5	4	6	5	2	2
2o4j	12	3	1	2	2	3	5	16	21	17	1	1	2	2
2p54	12	6	1	1	1	1	3	2	2	2	1	1	2	1
1eg4	13	3	15	21	20	16	15	11	3	2	12	23	24	26
2o02	14	5	13	8	6	3	4	4	3	2	9	7	5	5
1klu	15	1	5	2	2	2	3	2	2	1	3	2	2	2

Table S7. The detail ranks given by HPEPDOCK and MM/GBSA for dataset VI and the polar buried areas of the predicted protein-peptide binding interfaces.

PDB code	Peptide length	Free protein	Hit number	Polar buried area[a]	HPEPDOCK	GB^{OBC1}					GB^{OBC2}				
						1	2	4	6	Optimal ε_{in}[b]	1	2	4	6	Optimal ε_{in}[b]
3lcn	25	2v75:A	1	551.1	81	25	30	36	40	1,2	32	38	39	41	1
4bd6	20	4bd8:A	1	667.8	27	1	2	11	14	1,2	1	2	9	13	1,2
2nnu	20	1dto:A	11	710.4-1114	10	15	29	33	34	1	21	23	28	28	1,2
5fw5	23	4fcj:A	1	735.2	7	44	18	8	8	4,6	43	18	9	8	4,6
4ika	20	3n6m:A	2	748.6-939.1	57	22	7	5	3	2,4,6	20	6	4	4	2,4,6
4gnt	21	5wfx:A	3	762.6-1021.8	72	75	65	55	54	4,6	63	61	62	62	1,2,4,6
1q0w	24	5nvg:A	2	763.4-806.5	49	4	1	1	1	1,2,4,6	4	1	1	1	1,2,4,6
4b1w	24	2fxu:A	2	795.9-1085.3	13	78	38	27	24	4,6	57	49	29	26	4,6
3x2v	20	1re8:A	3	826-909.3	1	16	15	16	17	1,2,4,6	21	19	17	17	1,2,4,6
5yip	23	2r2q:A	5	827.8-1088.2	1	24	9	5	5	2,4,6	22	10	5	5	2,4,6
4w8p	21	2x0c:A	13	852.1-1047.7	2	1	1	1	1	1,2,4,6	1	1	1	1	1,2,4,6
3owt	20	3cz6:A	10	902.3-1232.6	2	1	1	1	1	1,2,4,6	1	1	1	1	1,2,4,6
3ul0	23	4u5u:A	2	983.2-1249.2	5	6	1	1	1	1,2,4,6	19	1	1	1	2,4,6
4v0v	20	1jk7:A	1	990.5	5	28	7	6	5	2,4,6	27	7	6	4	2,4,6
3lu9	25	3u69:H	1	1089.1	64	23	22	24	25	1,2,4,6	22	26	27	28	1,2,4
3aa1	21	3aa7:A	1	1167.7	77	47	21	14	11	4,6	67	28	19	14	4,6
4jo6	25	2bc3:AB	2	1185.3-1256.3	31	16	4	6	8	2,4,6	26	8	8	8	2,4,6
2cny	20	2co3:A	1	1287.6	98	27	13	11	11	2,4,6	28	13	12	12	2,4,6
1vyt	25	1vyu:A	38	/	1	2	2	2	2	1,2,4,6	2	2	2	2	1,2,4,6
5mk0	20	5mjz:A	96	/	1	1	1	1	1	1,2,4,6	1	1	1	1	1,2,4,6

[a] Since some structures have multiple correct hits, their polar buried areas will be a range rather than a value; [b]Optimal ε_{in} are considered as the ε_{in} with the best rank or a rank ≤ the best rank plus 5.

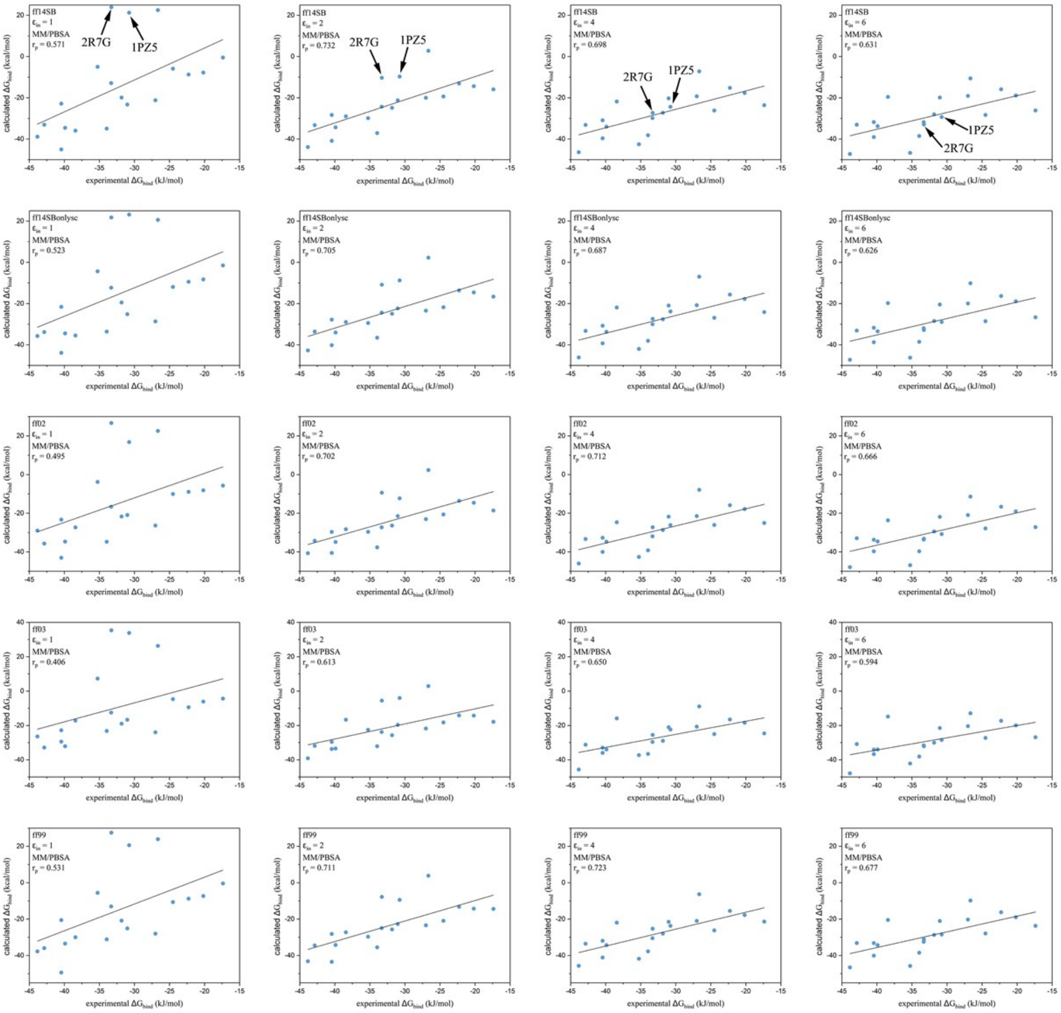

Figure S1. Scatter plots of the experimental ΔG_{bind} (kJ/mol) *versus* calculated ΔG_{bind} (kcal/mol) predicted by MM/PBSA based on the structures minimized in implicit solvent for the 19 complexes in the dataset I.

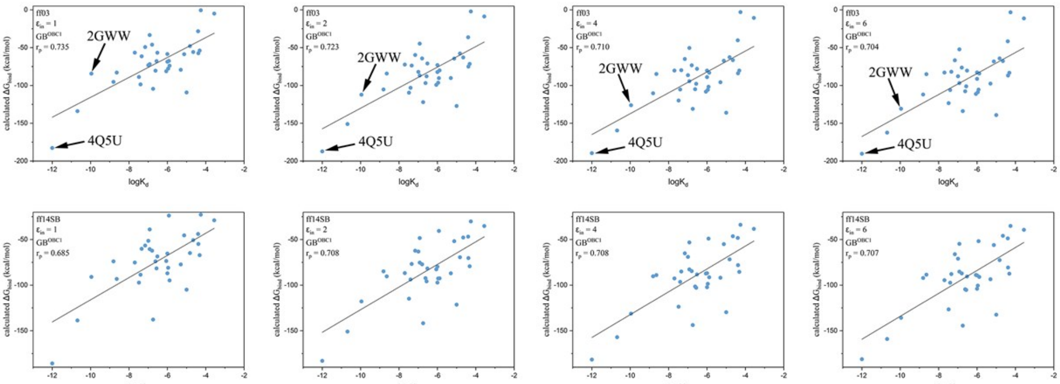

Figure S2. Scatter plots of the experimental binding affinities (logK_d) *versus* calculated ΔG_{bind} (kcal/mol) predicted by MM/GBSA based on the short MD simulations in implicit solvent for the 34 complexes in the dataset II.