

Supplemental Material

Interactions of Amino Acid Side Chain Analogs within Membrane Environments

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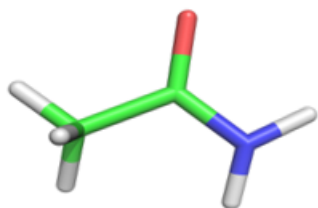
Table S2: Improved HDGB parameters, dielectric profile (ϵ) and non-polar profile (γ)

z	$\epsilon(z)$ - old	$\epsilon(z)$ - new	z	$\gamma(z)$
0.0	1.80	1.15	0.0	0.0000
0.5	1.80	1.15	0.6	0.0001
1.0	1.81	1.16	1.2	0.0002
1.5	1.82	1.17	1.8	0.0010
2.0	1.83	1.18	2.4	0.0050
2.5	1.84	1.19	3.0	0.0075
3.0	1.85	1.20	3.6	0.0100
3.5	1.86	1.21	4.2	0.0150
4.0	1.87	1.22	4.8	0.0200
4.5	1.89	1.24	5.4	0.0250
5.0	1.91	1.26	6.0	0.0300
5.5	1.93	1.28	6.6	0.0350
6.0	1.97	1.32	7.2	0.0410
6.5	2.00	1.35	7.8	0.0470
7.0	2.04	1.49	8.4	0.0520
7.5	2.09	1.64	9.0	0.0610
8.0	2.15	1.80	9.6	0.0720
8.5	2.22	1.87	10.2	0.0850
9.0	2.31	1.96	10.8	0.1000
9.5	2.41	2.06	11.4	0.1200
10.0	2.53	2.18	12.0	0.1500
10.5	3.23	2.28	12.6	0.1900
11.0	3.63	2.38	13.2	0.2500
11.5	4.13	2.58	13.8	0.3200
12.0	4.73	2.89	14.4	0.4000
12.5	5.43	3.42	15.0	0.5000
13.0	6.13	4.00	15.6	0.6200
13.5	6.98	5.08	16.2	0.7500
14.0	7.84	6.04	16.8	0.8753
14.5	8.80	7.50	17.4	0.9500
15.0	10.96	10.06	18.0	1.0308
15.5	14.05	13.75	18.6	1.0680
16.0	19.04	19.04	19.2	1.0921
16.5	25.85	25.85	19.8	1.1000
17.0	35.38	35.38	20.4	1.1000
17.5	45.88	45.88	21.0	1.0927
18.0	54.11	54.11	21.6	1.0690
18.5	60.79	60.79	22.2	1.0468
19.0	65.52	65.52	22.8	1.0328
19.5	69.42	69.42	23.4	1.0197
20.0	72.31	72.31	24.0	1.0130
20.5	74.07	74.07	24.6	1.0052
21.0	75.53	75.53	25.2	1.0005
21.5	76.63	76.63	25.8	1
22.0	77.14	77.14	26.4	1
22.5	77.83	77.83	27.0	1
23.0	78.22	78.22	27.6	1
23.5	78.92	78.92	28.2	1
24.0	79.35	79.35	28.8	1
24.5	79.66	79.66	29.4	1
25.0	80.00	80.00	30.0	1

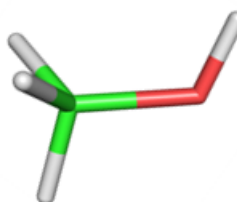
Figures

Figure S1: Amino acid analogs used in this study: acetamide (Asn), methanol (Ser), toluene (Phe) and propane (Val)

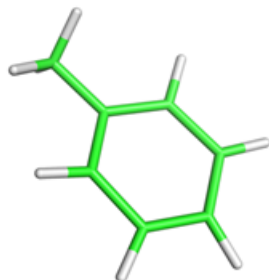
Acetamide (Asn)



Methanol (Ser)



Toluene (Phe)



Propane (Val)

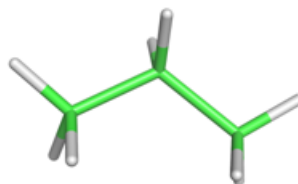


Figure S2: Root mean square deviation between the PMF profiles for each umbrella in forward and backward directions.

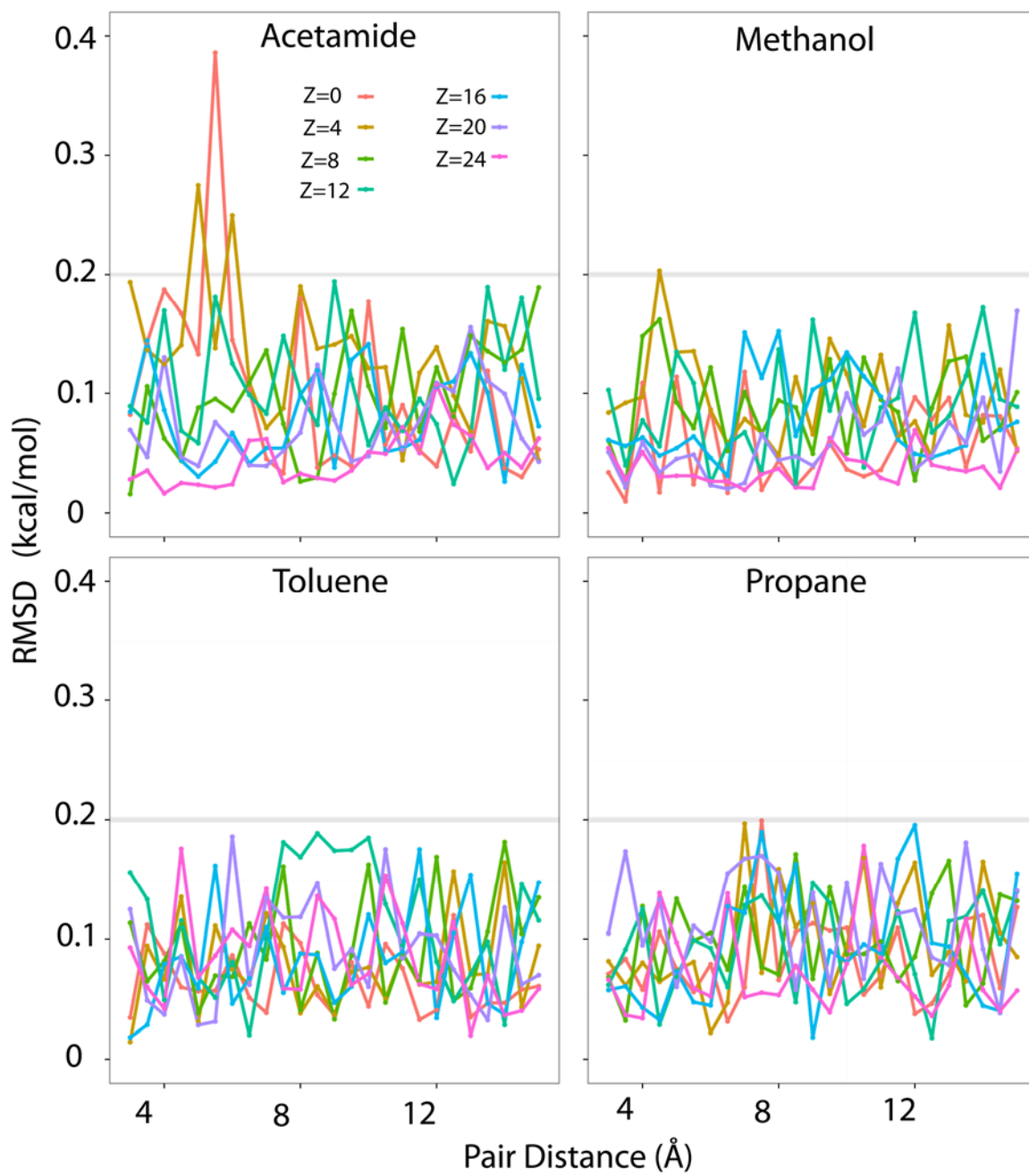


Figure S3. A: 2D PMF of acetamide pair association at $z=0$ and water density in biasing cylinder; B: Corrected 1D PMF as a function of pair distance after Boltzmann averaging along the water density reaction coordinate.

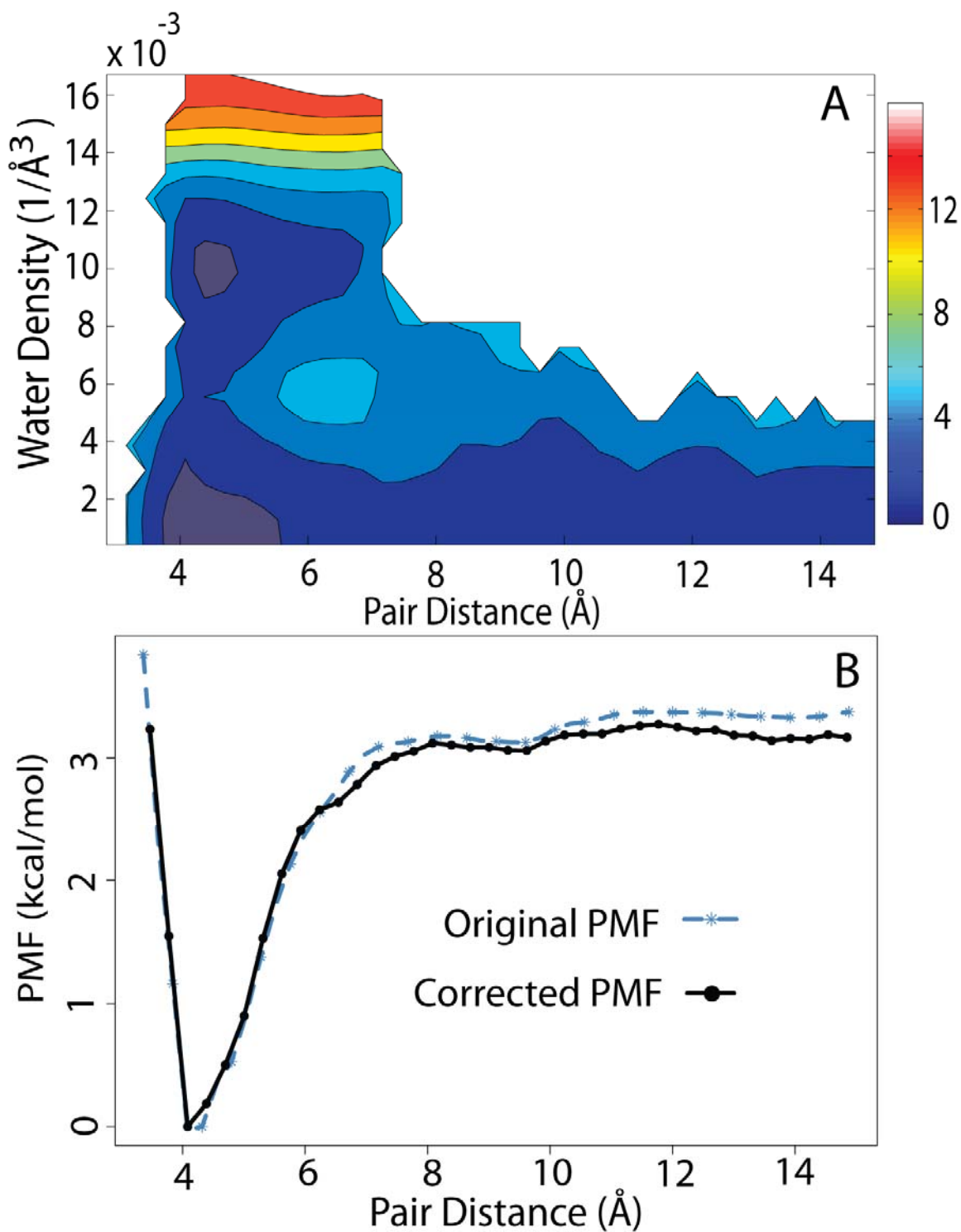


Figure S4. A: 2D PMF of methanol pair association at $z=4$ Å and water density in biasing cylinder; B: Corrected 1D PMF as a function of pair distance after Boltzmann averaging along the water density reaction coordinate.

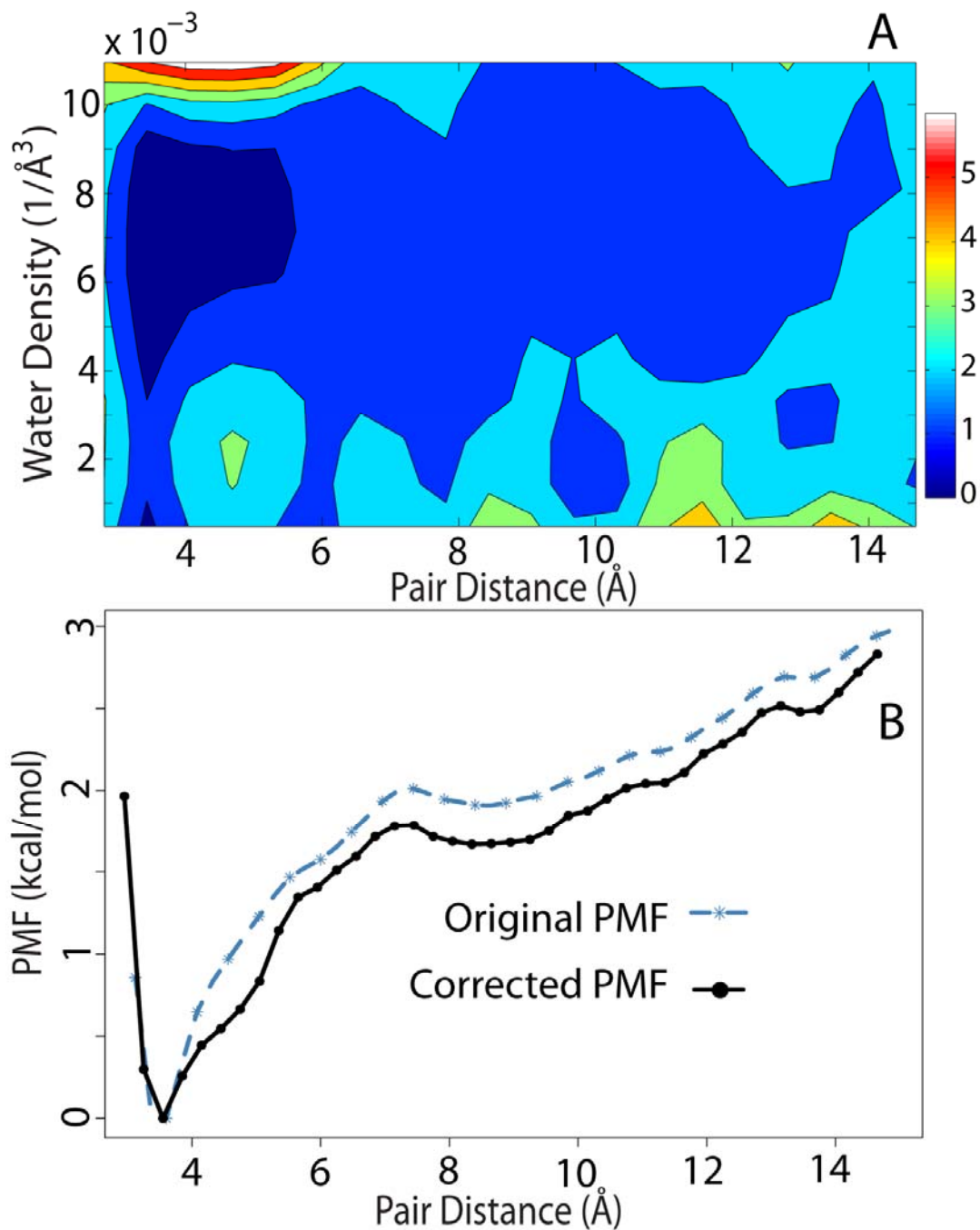
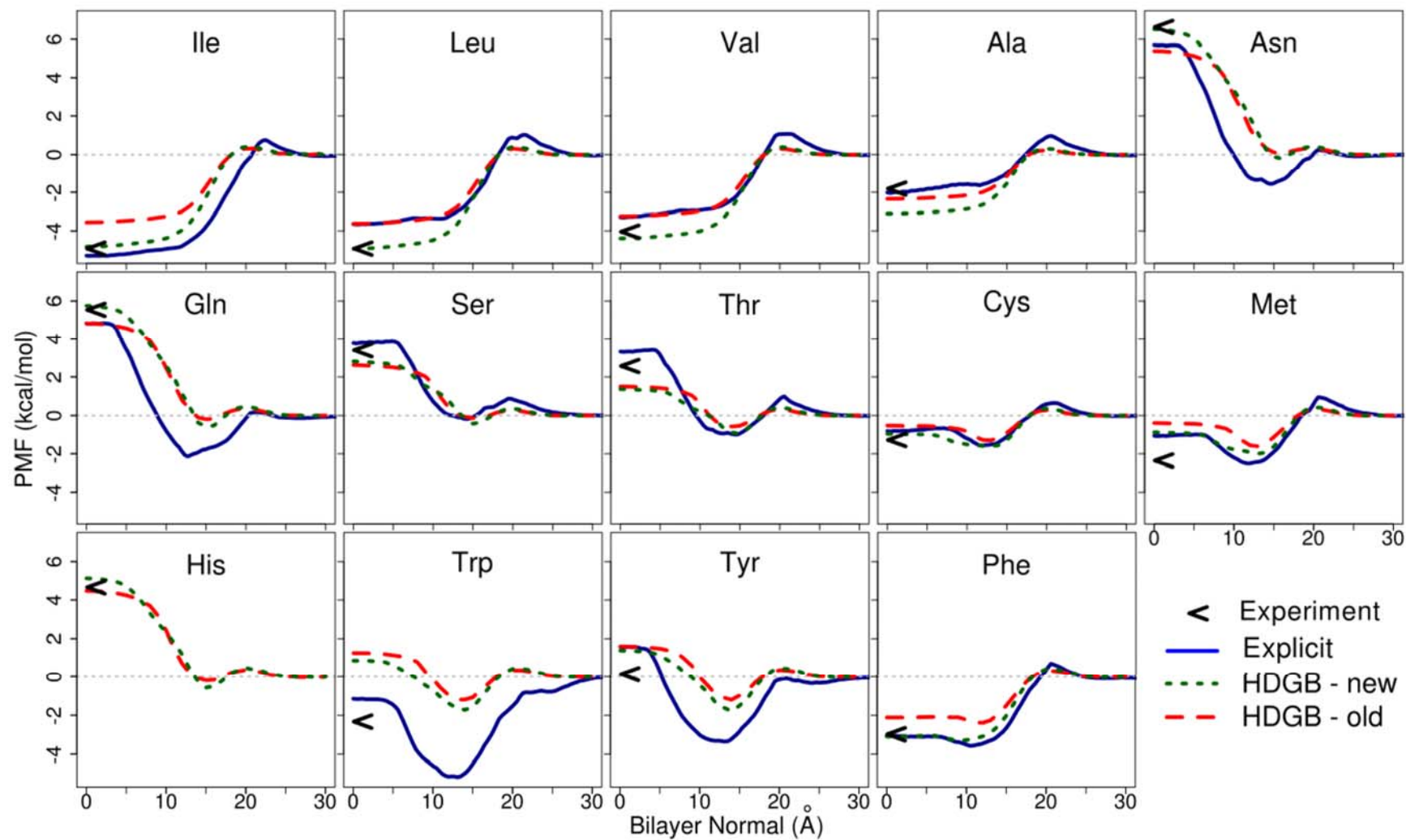


Figure S5: Free energy profiles of insertion of single amino acid side-chain analogs using HDGB simulations with old and improved parameters compared with results of explicit simulation¹ and experimental measurements²



1. MacCallum JL, Bennett WFD, Tieleman DP. Distribution of Amino Acids in a Lipid Bilayer from Computer Simulations. *Biophys J* 2008;94:3393-3404.
2. Radzicka A, Wolfenden R. Comparing the polarities of the amino acids: side-chain distribution coefficients between the vapor phase, cyclohexane, 1-octanol, and neutral aqueous solution. *Biochemistry* 1988;27:1664-1670.