

**Table S1.** Gay-Berne parameters for the coarse-grained particles defined in dipeptide models.

<b>Index of Gay-Berne Site</b>	<b><math>L</math> (Å)</b>	<b><math>D</math> (Å)</b>	<b><math>d_w</math></b>	<b><math>\epsilon_0</math> (kcal/mol)</b>	<b><math>\epsilon_E</math> (kcal/mol)</b>	<b><math>\epsilon_S</math> (kcal/mol)</b>
111	2.475	2.475	0.931	0.363	1.000	1.000
122	3.763	2.462	1.202	0.481	1.479	1.437
152	3.763	2.462	0.942	0.381	1.479	1.437
182	2.475	2.475	0.943	0.363	1.000	1.000
192	2.475	2.475	1.243	0.263	1.000	1.000
202	2.275	2.275	1.243	0.263	1.000	1.000
222	4.257	2.484	0.977	0.496	1.446	0.411
232	2.475	2.475	0.931	0.143	1.000	1.000
242	3.763	2.462	0.942	0.481	1.479	0.437
262	3.722	2.662	0.862	0.732	1.441	0.463
272	2.475	2.475	0.931	0.243	1.000	1.000
281	2.434	2.434	0.897	0.455	1.000	1.000
292	2.475	2.475	1.231	0.243	1.000	1.000
302	2.475	2.475	1.231	0.243	1.000	1.000
312	3.763	2.462	0.902	0.481	1.479	1.437
341	2.434	2.434	0.831	0.113	1.000	1.000
352	2.475	2.475	1.231	0.243	1.000	1.000
372	2.475	2.475	1.231	0.124	1.000	1.000
382	2.475	2.475	0.931	0.243	1.000	1.000
392	2.475	2.475	1.231	0.243	1.000	1.000
402	3.722	2.497	1.261	0.432	1.341	0.763
412	2.475	2.475	1.231	0.243	1.000	1.000
422	2.894	2.461	0.957	0.461	0.957	0.918
432	2.475	2.475	0.983	0.243	1.000	1.000
442	2.475	2.475	1.231	0.243	1.000	1.000
452	3.230	3.230	0.831	0.484	1.000	1.000
462	2.475	2.475	0.943	0.243	1.000	1.000
472	2.789	2.416	0.726	0.693	1.475	0.726
482	2.475	2.475	0.931	0.243	1.000	1.000
492	2.743	4.527	0.588	0.246	1.452	0.692
511	2.475	2.475	1.231	0.010	1.000	1.000
522	2.775	2.775	0.931	0.234	1.000	1.000
532	2.475	2.475	1.231	0.243	1.000	1.000
541	2.073	2.073	1.131	0.115	1.000	1.000
552	2.475	2.475	1.251	0.023	1.000	1.000
561	2.275	2.275	1.231	0.343	1.000	1.000
571	2.075	2.075	0.931	0.145	1.000	1.000

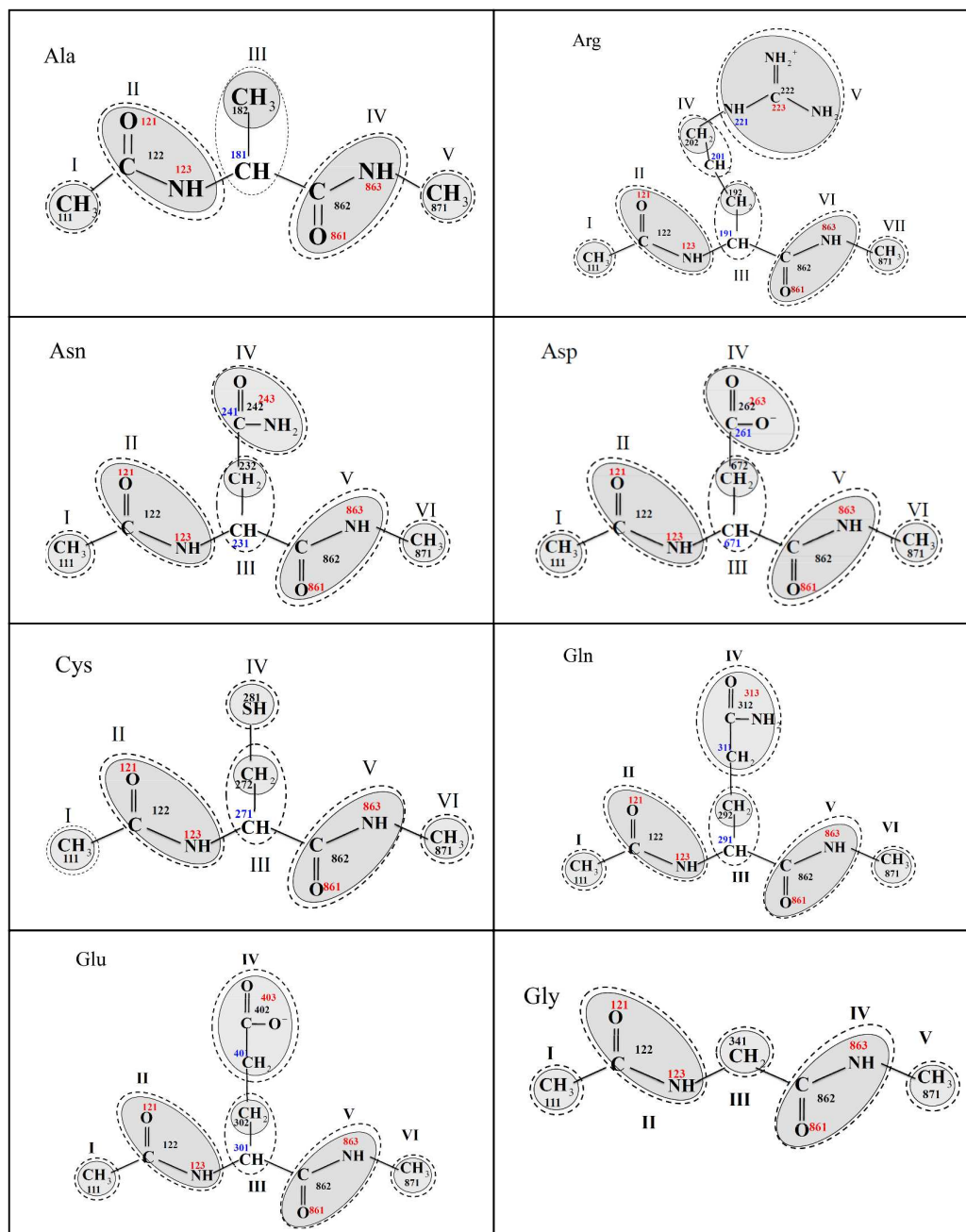
<b>582</b>	2.475	2.475	0.931	0.243	1.000	1.000
<b>592</b>	3.548	6.206	0.668	0.147	1.667	0.322
<b>612</b>	2.475	2.475	0.931	0.243	1.000	1.000
<b>622</b>	2.443	4.645	0.968	0.368	1.000	1.000
<b>632</b>	2.475	2.475	1.231	0.143	1.000	1.000
<b>641</b>	2.275	2.275	1.031	0.243	1.000	1.000
<b>651</b>	2.275	2.275	1.031	0.243	1.000	1.000
<b>662</b>	2.479	3.929	0.921	0.213	1.601	1.228
<b>672</b>	2.475	2.475	0.931	0.243	1.000	1.000
<b>682</b>	3.763	2.462	1.202	0.481	1.479	1.437
<b>742</b>	3.763	2.462	1.202	0.481	1.479	1.437
<b>862</b>	3.763	2.462	1.202	0.481	1.479	1.437
<b>871</b>	2.475	2.475	1.000	0.363	1.000	1.000

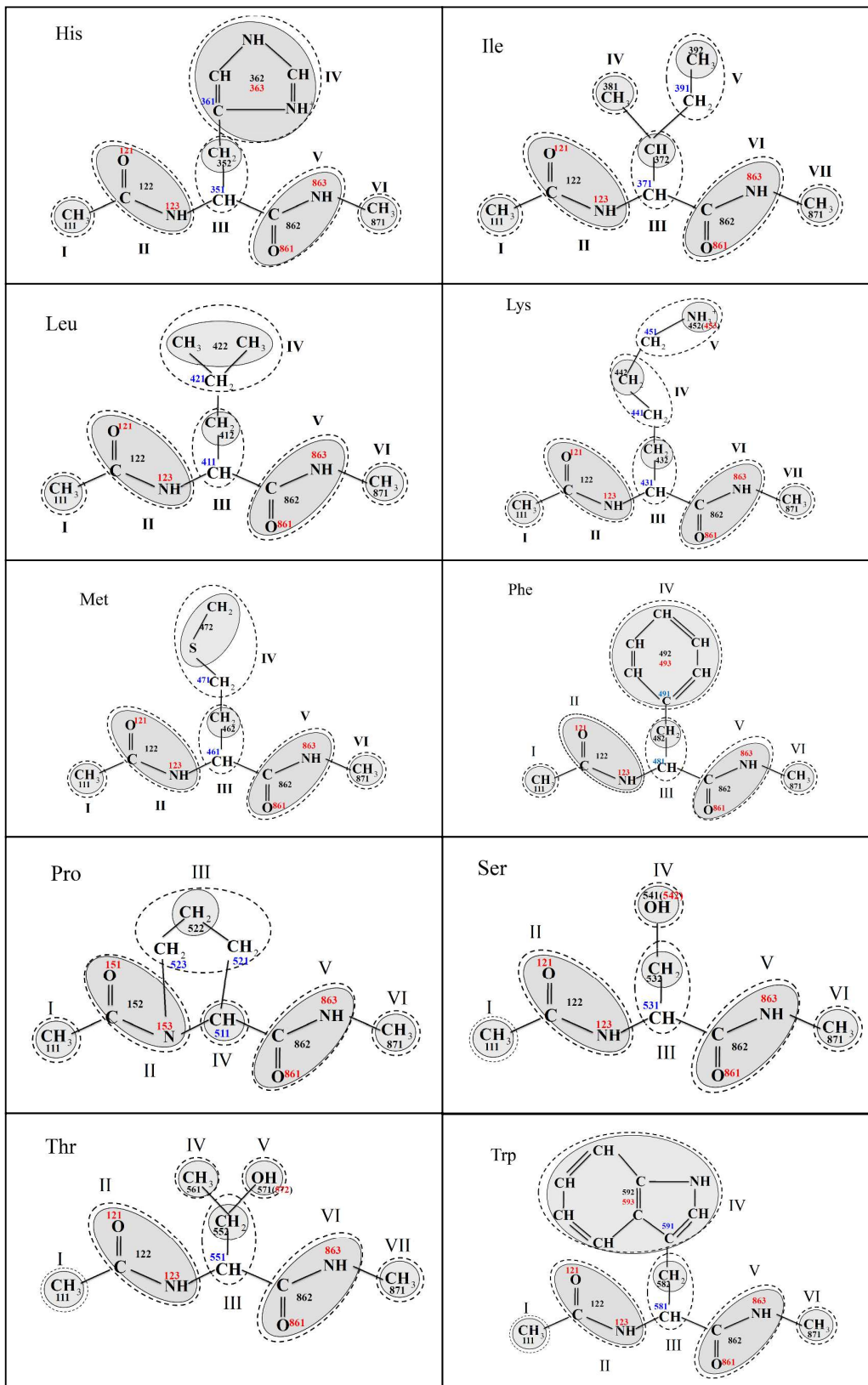
**Table S2.** EMP parameters for the coarse-grained particles defined in dipeptide models.

<b>Index of EMP site</b>	<b>Charge</b>	<b>dipole</b>	<b>Qudrupole</b>		
<b>121</b>	0.000	-1.463 0.281 -0.003	2.001 -1.148 -0.014	-1.148 -0.927 0.009	-0.014 0.009 -1.074
<b>123</b>	0.000	0.879 -0.437 -0.024	1.067 -1.148 0.138	-1.148 1.258 -0.128	0.138 -0.128 -2.325
<b>151</b>	0.000	-1.463 0.281 -0.003	2.001 -1.148 -0.014	-1.148 -0.927 0.009	-0.014 0.009 -1.074
<b>153</b>	0.000	0.879 -0.437 -0.024	1.067 -1.148 0.138	-1.148 1.258 -0.128	0.138 -0.128 -2.325
<b>223</b>	1.000	-2.743 -0.762 1.818	6.435 -3.860 -0.061	-3.860 2.459 -1.957	-0.061 -1.957 -8.894
<b>243</b>	0.000	-3.653 0.835 -0.086	-0.632 1.318 -0.330	1.318 2.936 0.391	-0.330 0.391 -2.305
<b>263</b>	-1.000	-3.378 0.670 -0.043	-0.632 0.318 -0.230	0.318 1.936 0.491	-0.230 0.491 -1.305
<b>313</b>	0.000	-3.653 0.835 -0.086	-0.632 1.318 -0.330	1.318 2.936 0.391	-0.330 0.391 -2.305
<b>363</b>	1.000	1.241 -1.801 -0.021	-0.605 0.604 -0.501	0.604 -0.700 -0.073	-0.501 -0.073 -1.305
<b>403</b>	0.000	-1.316 5.155 -0.260	3.729 3.893 -0.911	3.893 -13.165 0.044	-0.911 0.044 9.436
<b>453</b>	0.000	-1.316 5.155 -0.260	3.729 3.893 -0.911	3.893 -13.165 0.044	-0.911 0.044 9.436
<b>493</b>	0.000	-1.316 5.155 -0.260	3.729 3.893 -0.911	3.893 -13.165 0.044	-0.911 0.044 9.436
<b>542</b>	0.000	-3.653 0.835 -0.086	-0.632 1.318 -0.330	1.318 2.936 0.391	-0.330 0.391 -2.305

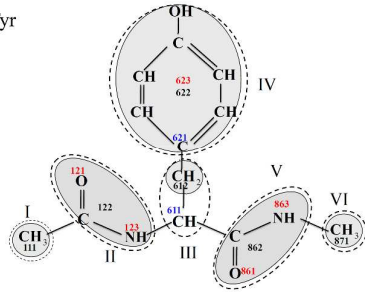
<b>572</b>	0.000	-3.653 0.835 -0.086	-0.632 1.318 -0.330	1.318 2.936 0.391	-0.330 0.391 -2.305
<b>593</b>	0.000	-3.653 0.835 -0.086	-0.632 1.318 -0.330	1.318 2.936 0.391	-0.330 0.391 -2.305
<b>623</b>	0.000	-3.653 0.835 -0.086	-0.632 1.318 -0.330	1.318 2.936 0.391	-0.330 0.391 -2.305
<b>681</b>	0.000	-1.463 0.281 -0.003	2.001 -1.148 -0.014	-1.148 -0.927 0.009	-0.014 0.009 -1.074
<b>683</b>	0.000	-0.879 -0.437 -0.024	1.067 -1.148 0.138	-1.148 1.258 -0.128	0.138 -0.128 -2.325
<b>863</b>	0.000	0.879 -0.437 -0.024	1.067 -1.148 0.138	-1.148 1.258 -0.128	0.138 -0.128 -2.325

**Figure S1.** GBEMP mapping schemes for amino acid dipeptides. Each rigid body, being enclosed by a dash line, consists of a Gay-Berne particle (represented by shadowed ellipsoid, sphere or disk) with a few electric multipoles or without any electric multipole. The indices of rigid bodies, Gay-Berne sites, interacting EMP sites and non-interaction EMP sites (just serve as connecting different rigid bodies), are indicated by Roman numbers and Arabic numbers in black, red and blue, respectively.

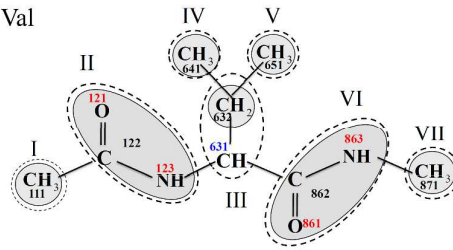




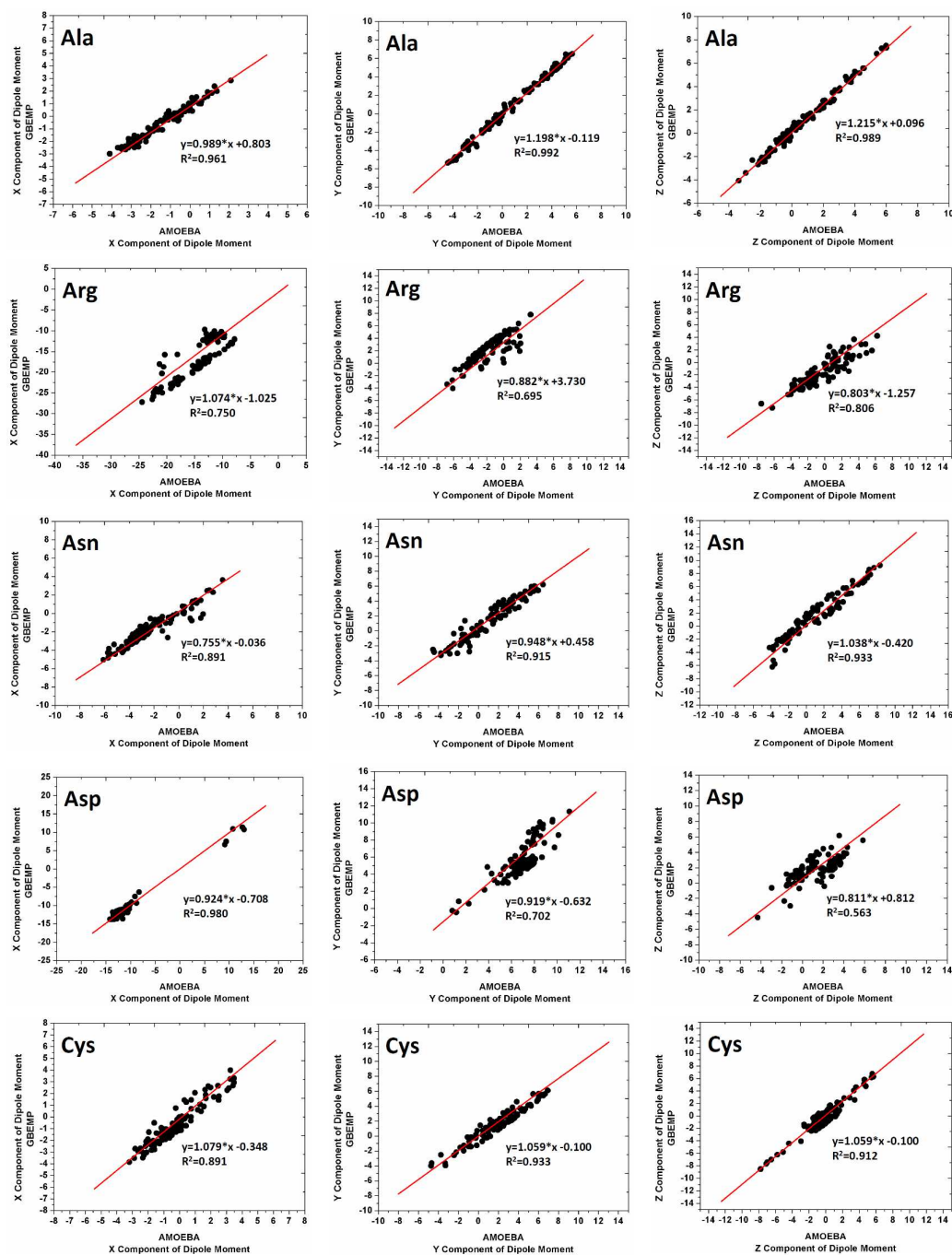
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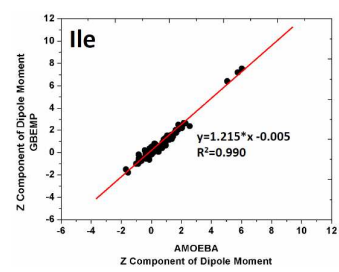
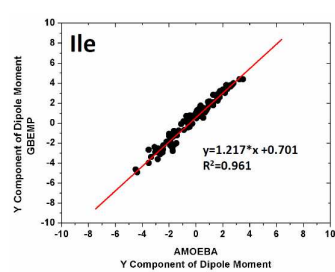
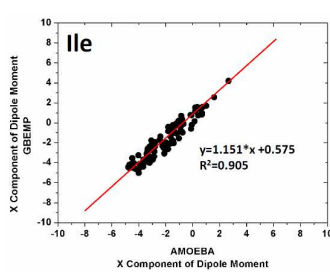
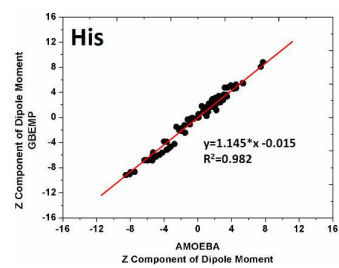
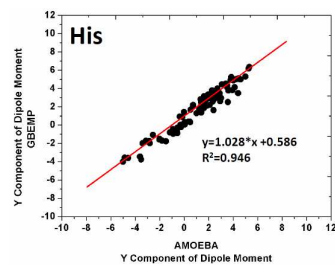
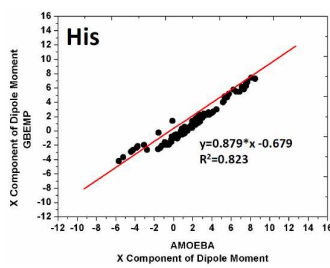
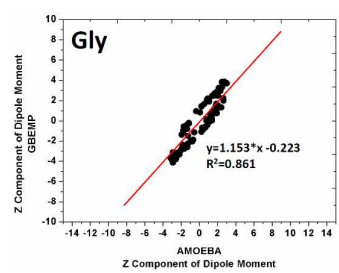
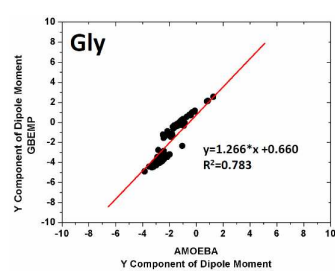
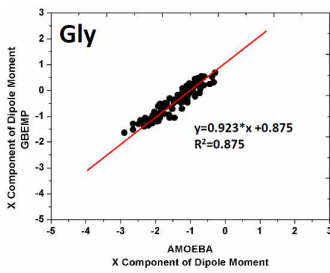
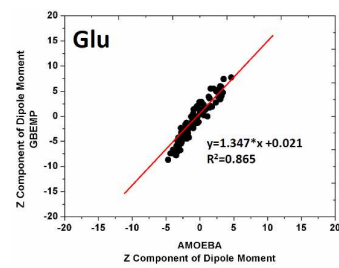
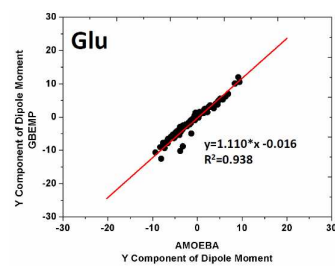
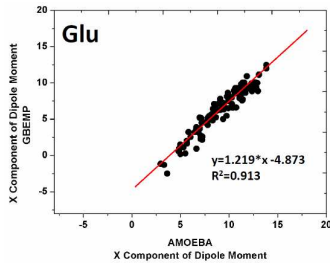
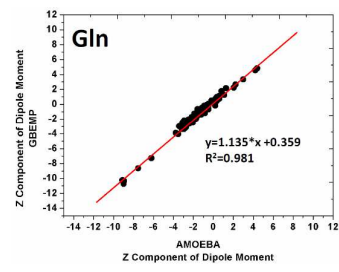
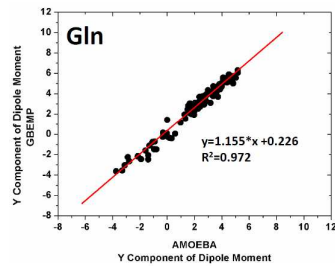
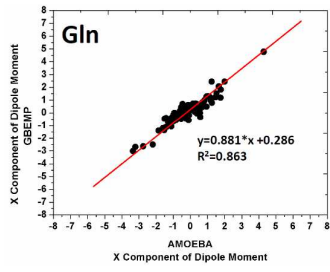
Val

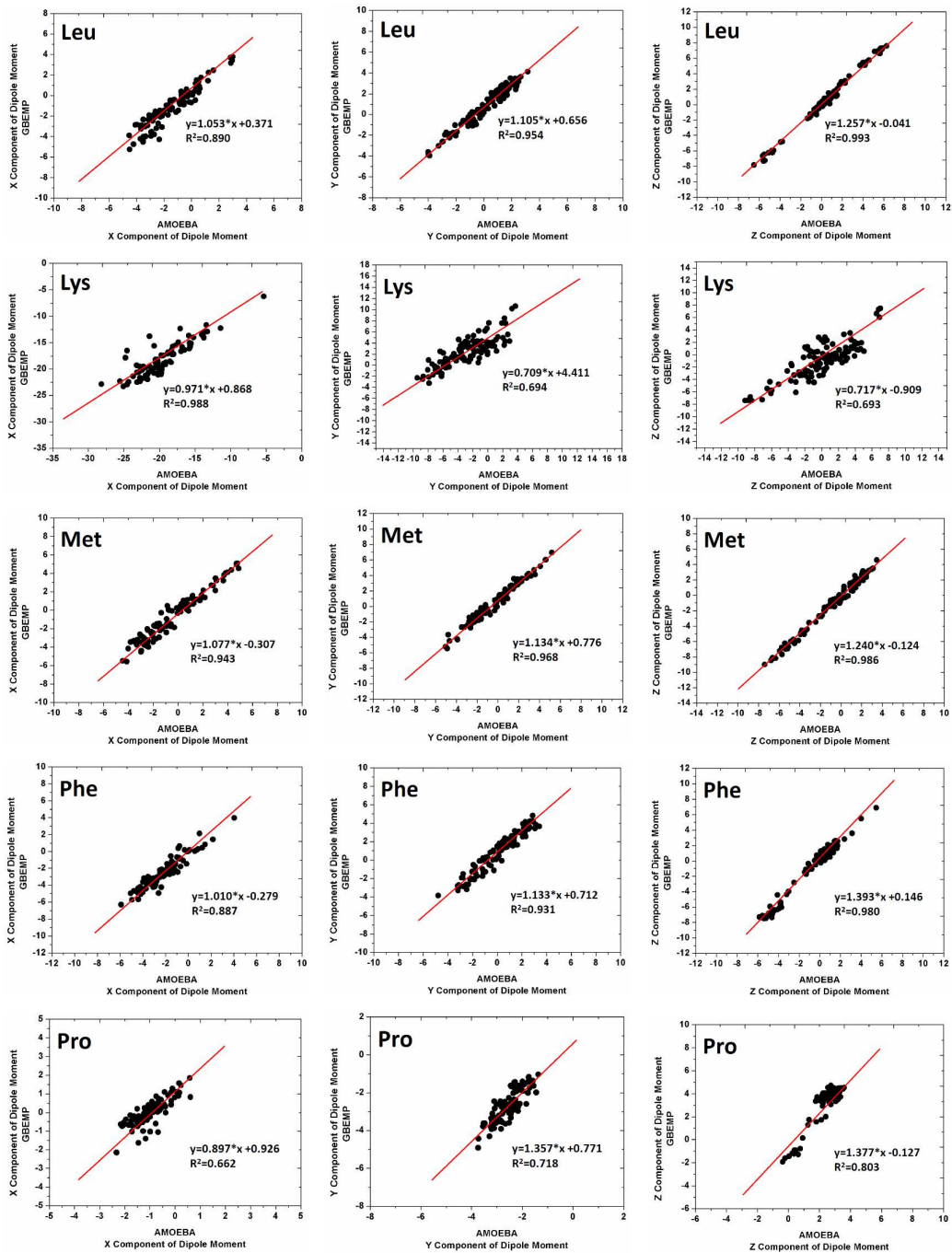


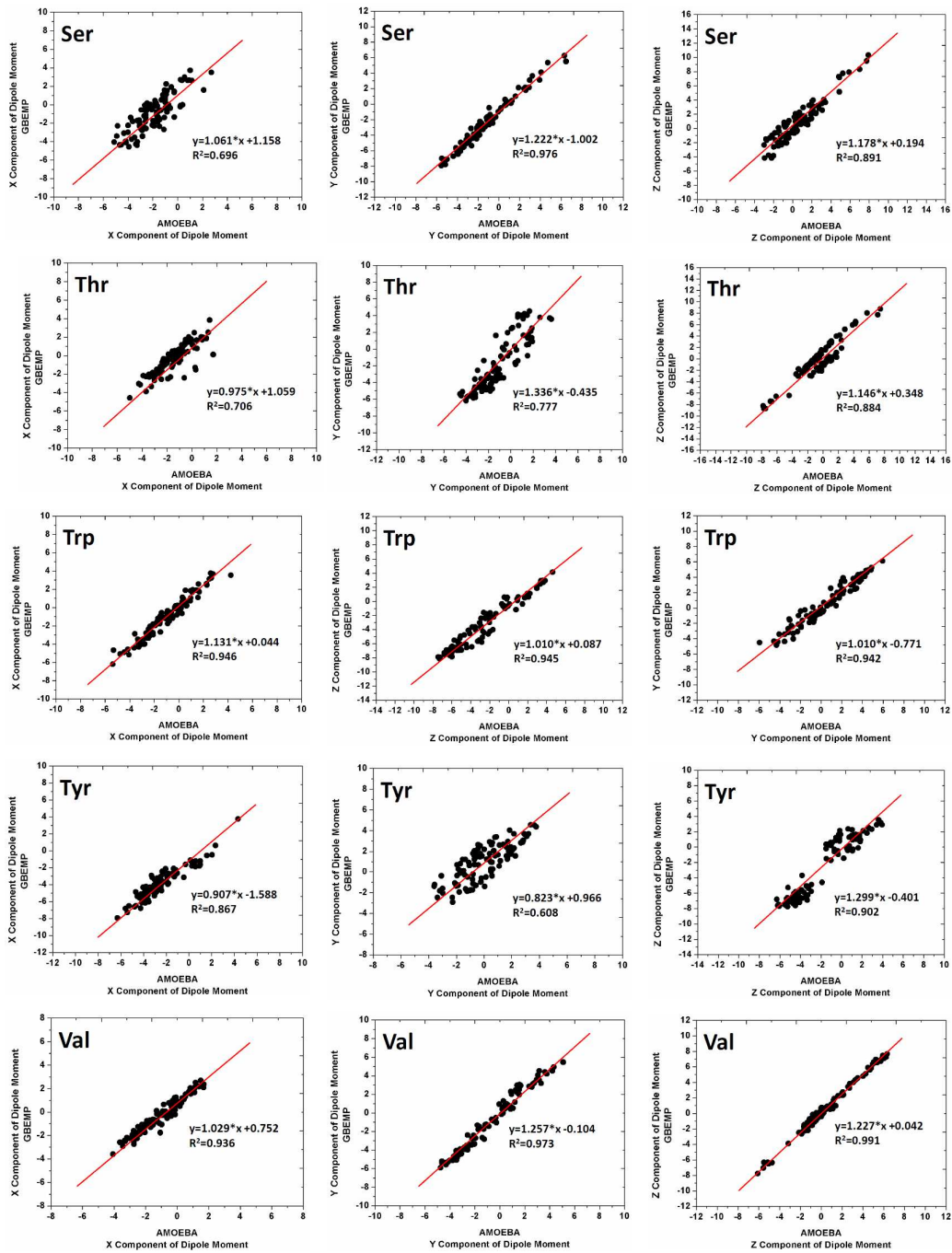
**Figure S2.** Correlations between GBEMP and AMOEBA results for calculating the x (left panel), y (middle panel) and z (right panel) components of the dipole moment of different dipeptide models (20 kinds of dipeptides in total). For each dipeptide, the conformations were chosen randomly from atomistic structures generated from atomistic MD simulation (AMOEBA force field).



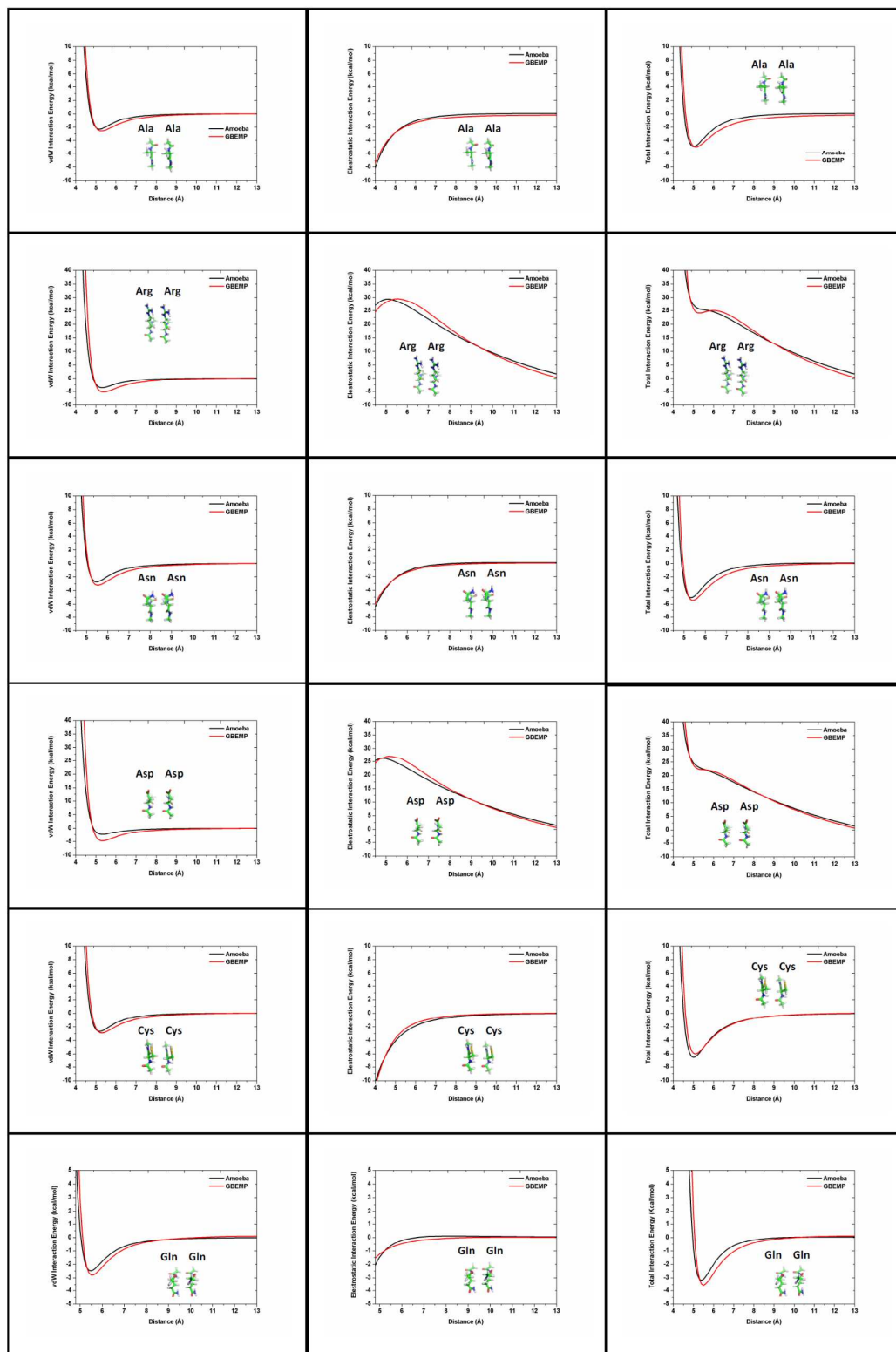


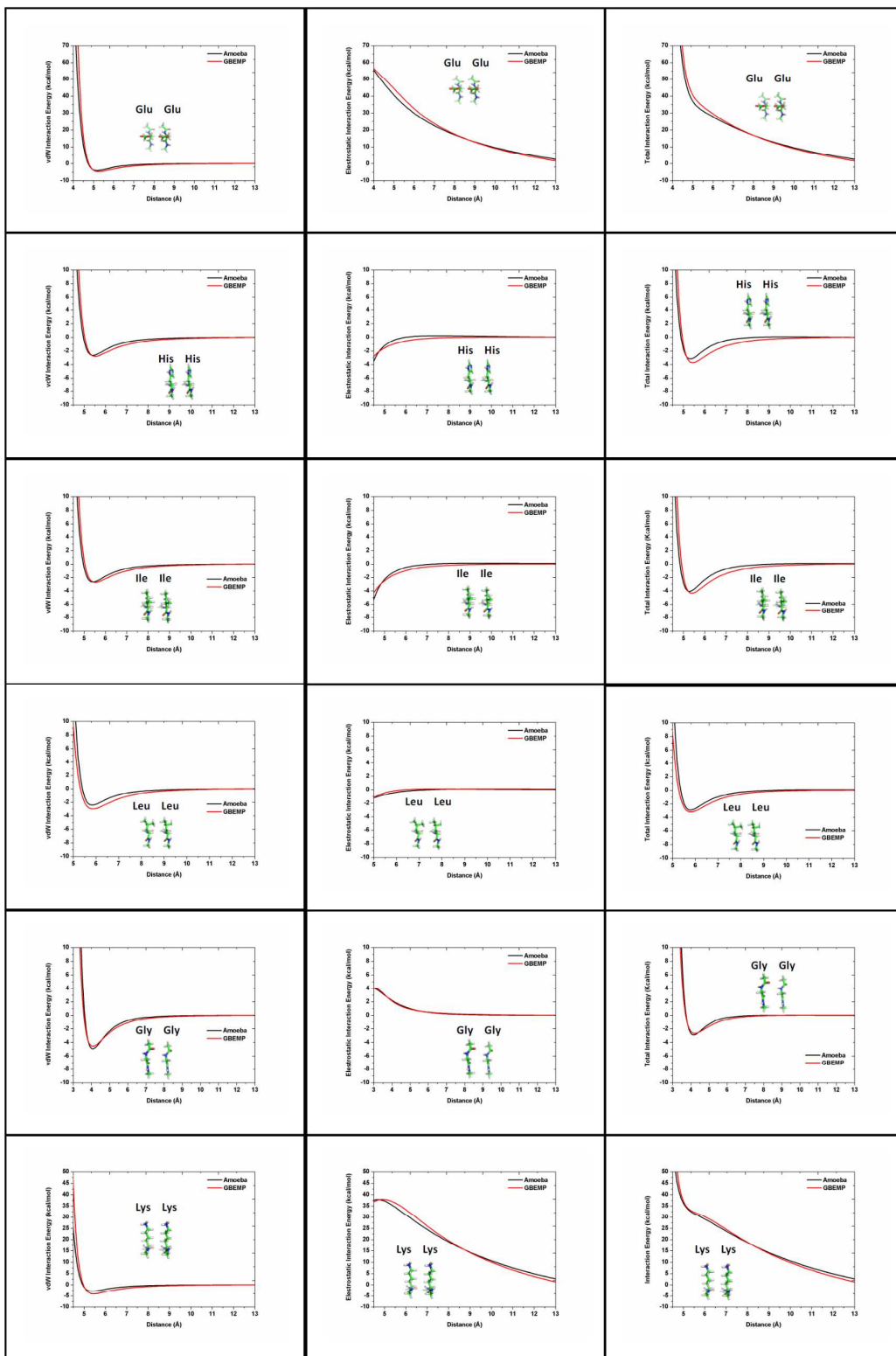


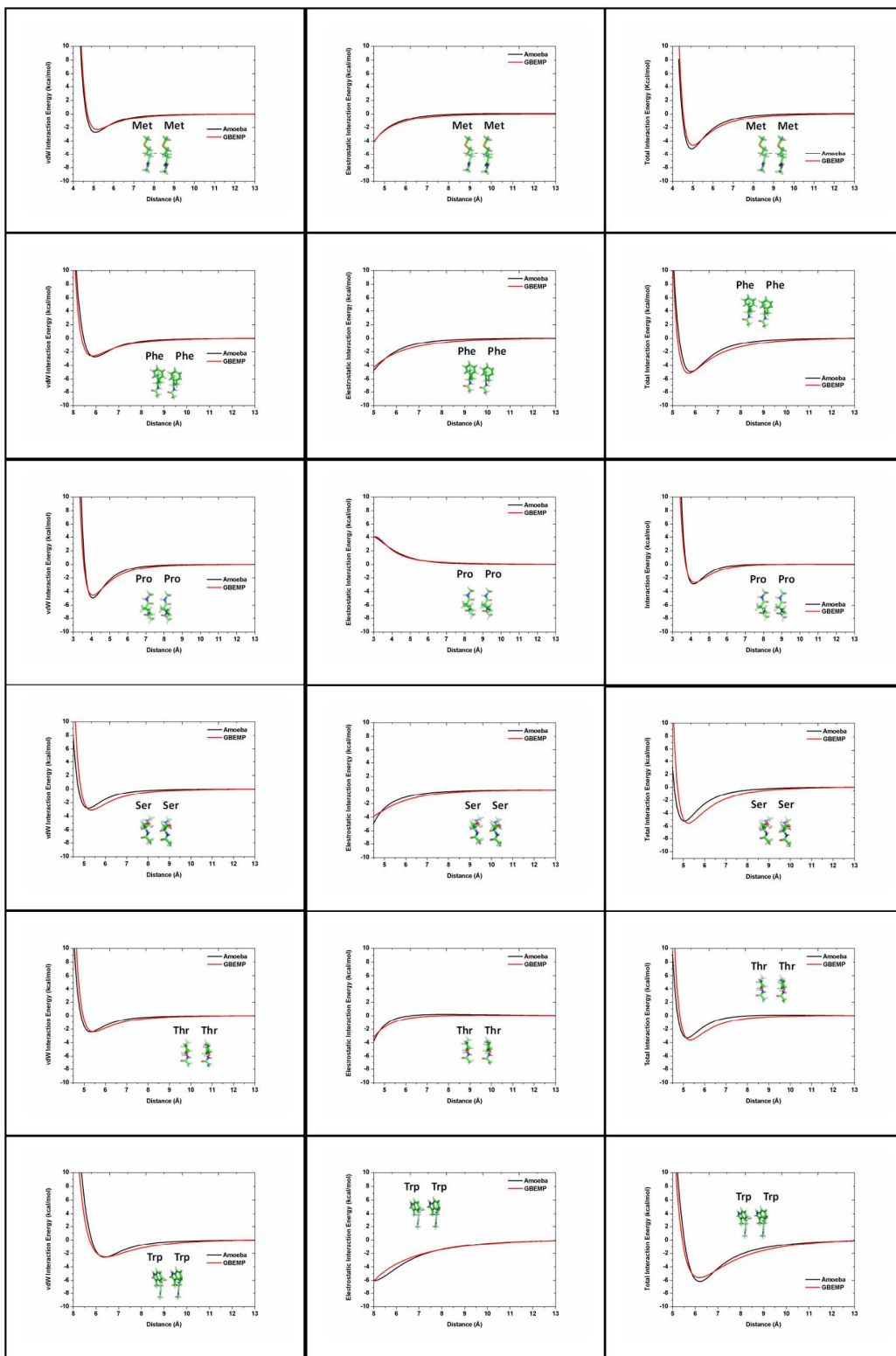


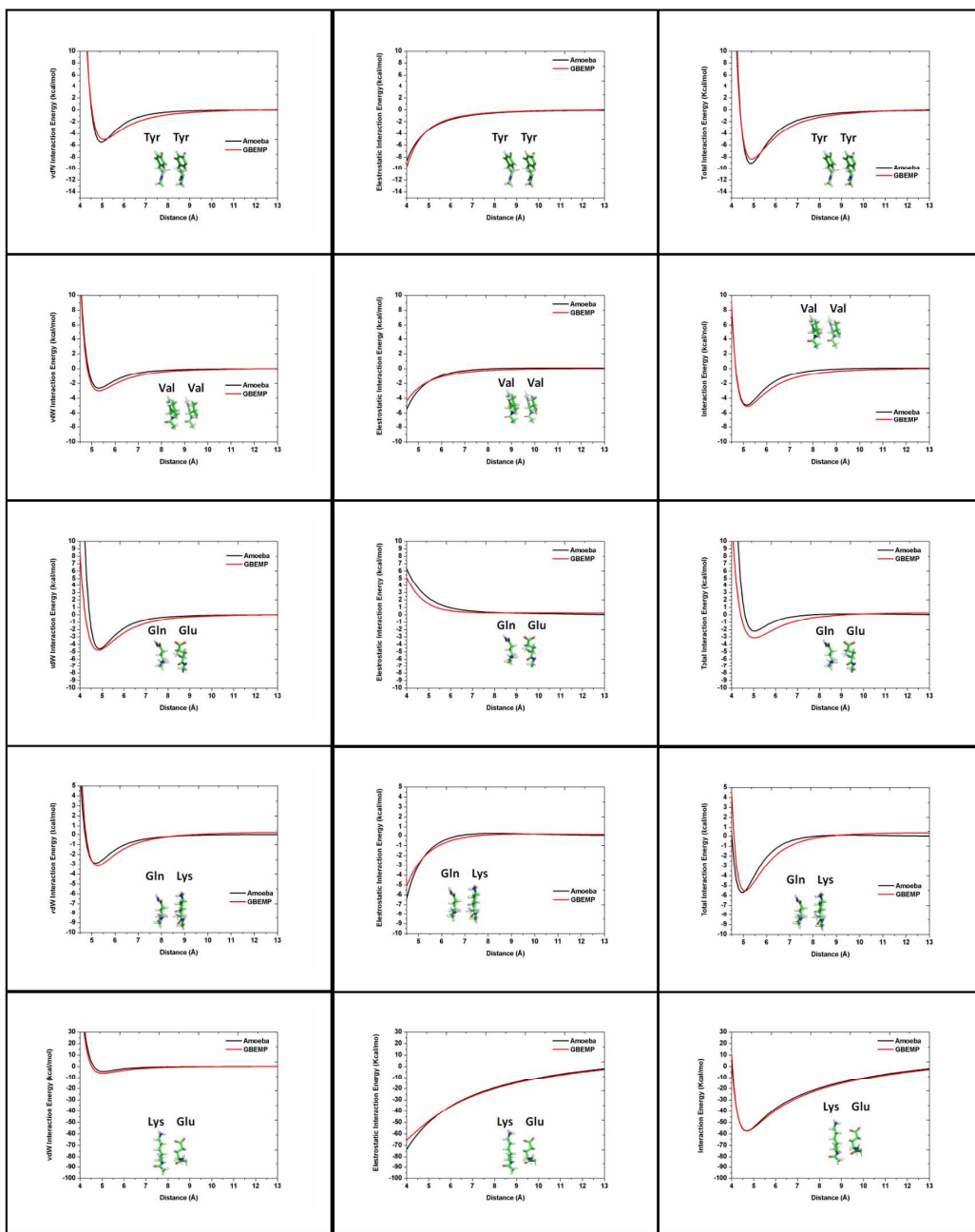


**Figure S3.** Intermolecular interaction energies for 20 dipeptide homodimers and 3 dipeptide heterodimers, obtained from AMOEBA atomistic force field (in black) and GBEMP coarse-grained force field (in red). Left, middle and right columns show van der Waals, electrostatic and total interaction energies respectively.

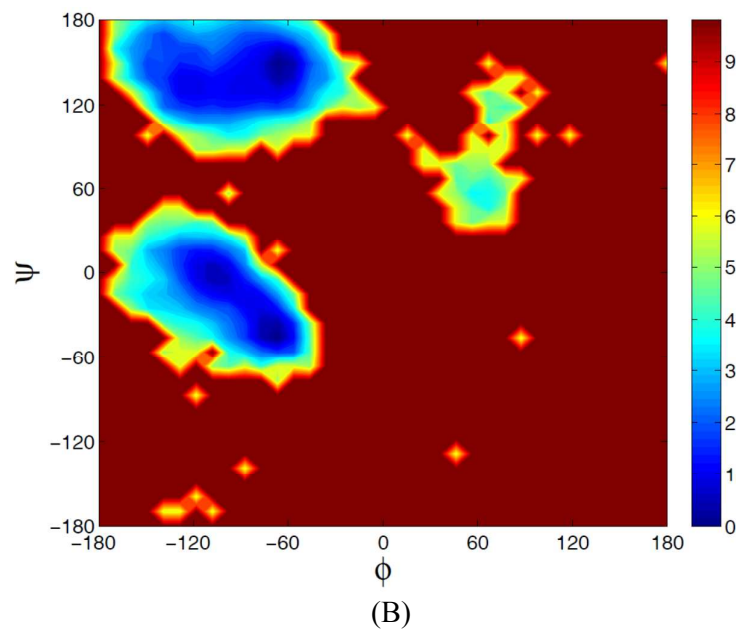
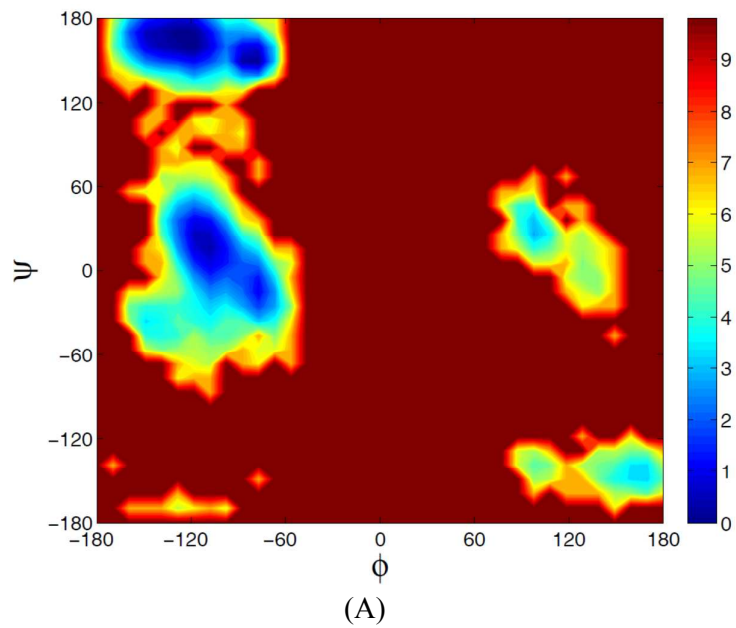






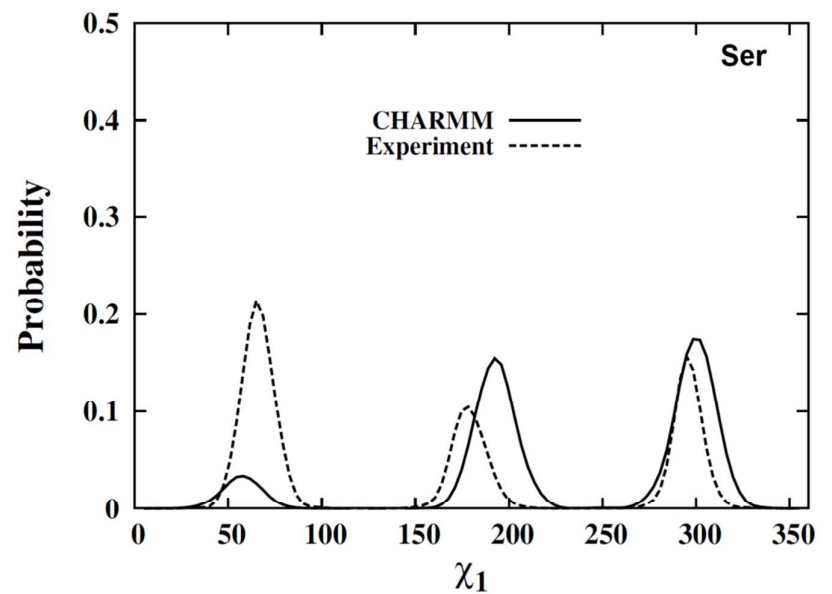


**Figure S4.** Potentials of mean force (PMFs) for the  $(\phi/\psi)$  distribution for valine (Val), calculated from (A) GBEMP and (B) CHARMM simulations. The color bars represent free energy in the unit of kcal/mol.

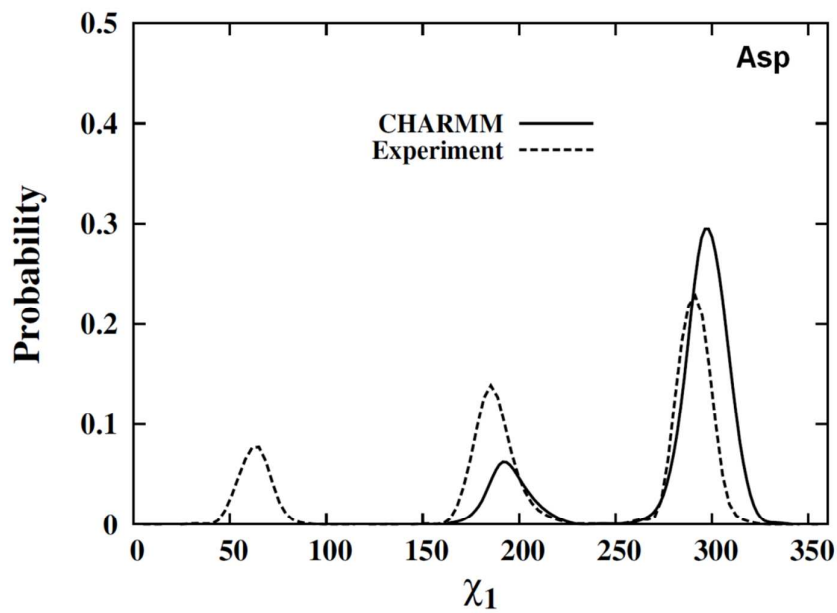




**Figure S5** Distribution of the side chain torsion  $\chi_1$  for (A) serine (Ser) and (B) aspartic acid (Asp) from the protein structures (Dunbrack Library) and CHARMM atomistic simulations of dipeptides. Experimental and CHARMM results are represented by the dash and solid lines respectively.



(A)



(B)