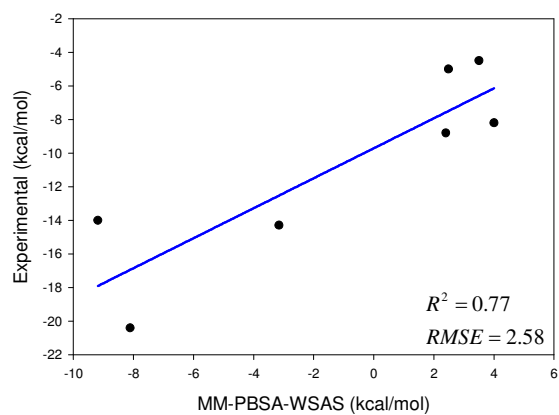
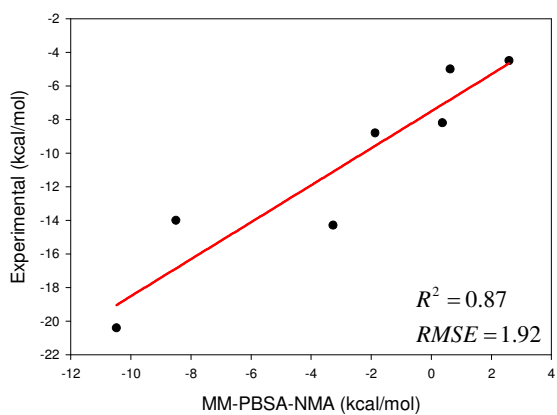
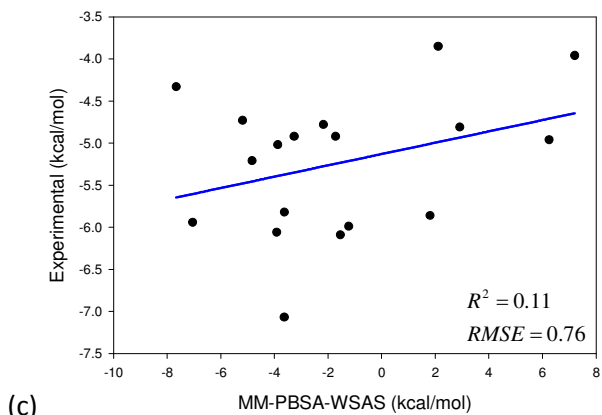
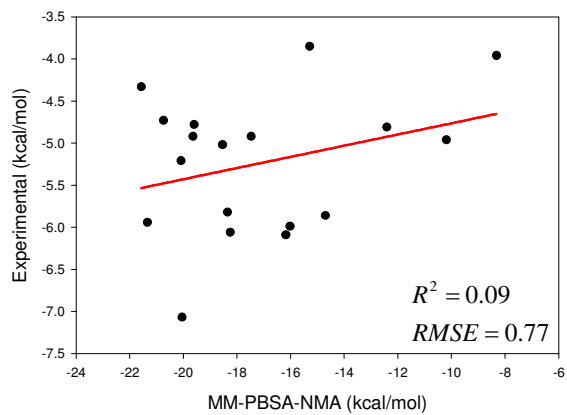


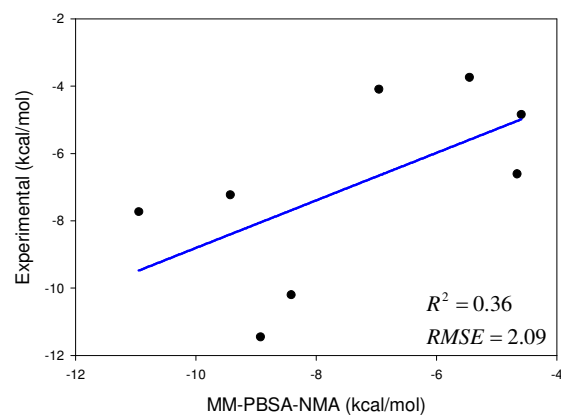
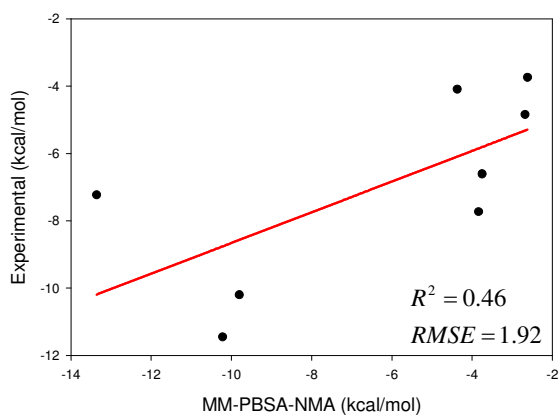
(a)



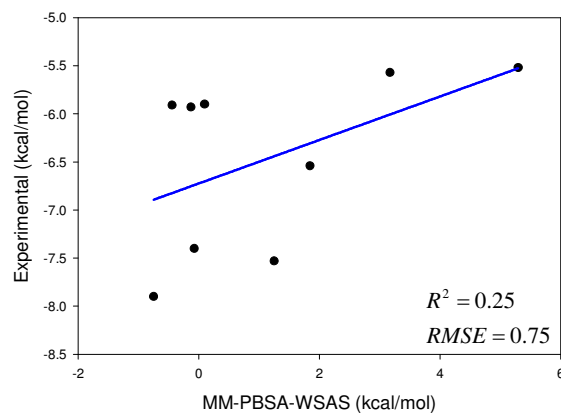
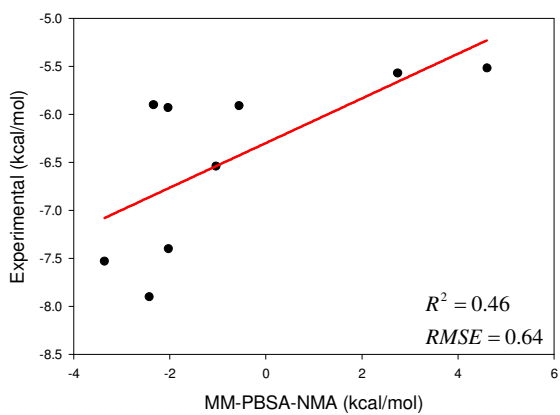
(b)



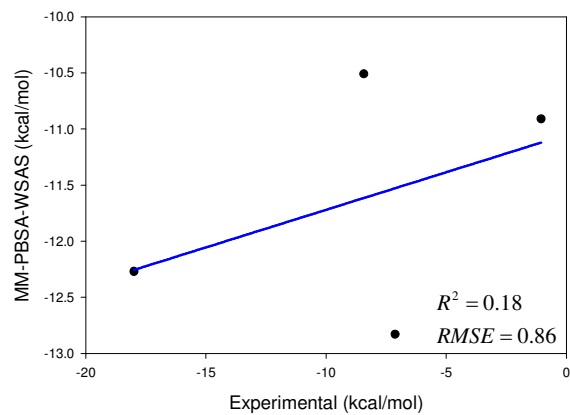
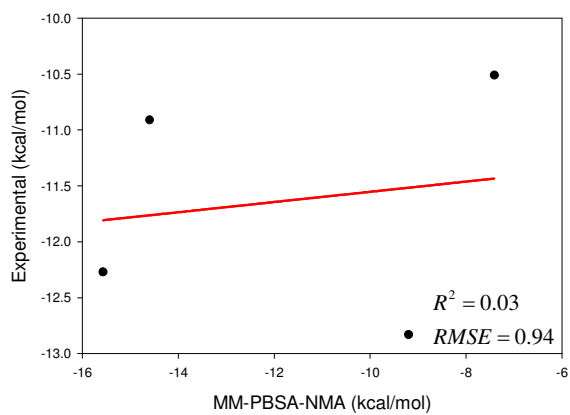
(c)



(d)



(e)



(f)

Figure S1. Comparison of two MM-PBSA protocols, MM-PBSA-NMA (right) and MM-PBSA-WSAS (left) in binding free energy calculations for six protein-ligand systems: (a) α -thrombin, (b) avidin, (c) cytochrome C peroxidase, (d) neuraminidase, (e) P450cam, (f) penicillopepsin.