

Supporting Figures and Tables

Figure S1. Brønsted plots from four model proteins 2CI2, 1R69, 1SHF and 1RIS using G \ddot{o} model with scale 0.25, 0.50, 0.90 for residue mutation. The correlation coefficient r is 0.84, 0.83 and 0.81, and corresponding fitting slope s is 0.55, 0.54 and 0.52 respectively.

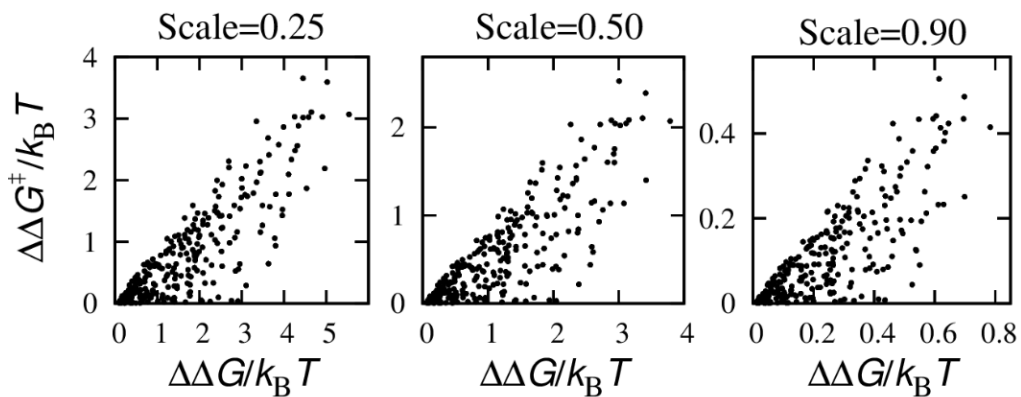


Figure S2. Folding free energy profiles as function of native contact fraction by different models for nine studied proteins. The number within the parentheses after “mb” denotes the value of many-body parameter ε_{mb} in corresponding mb-MJ model.

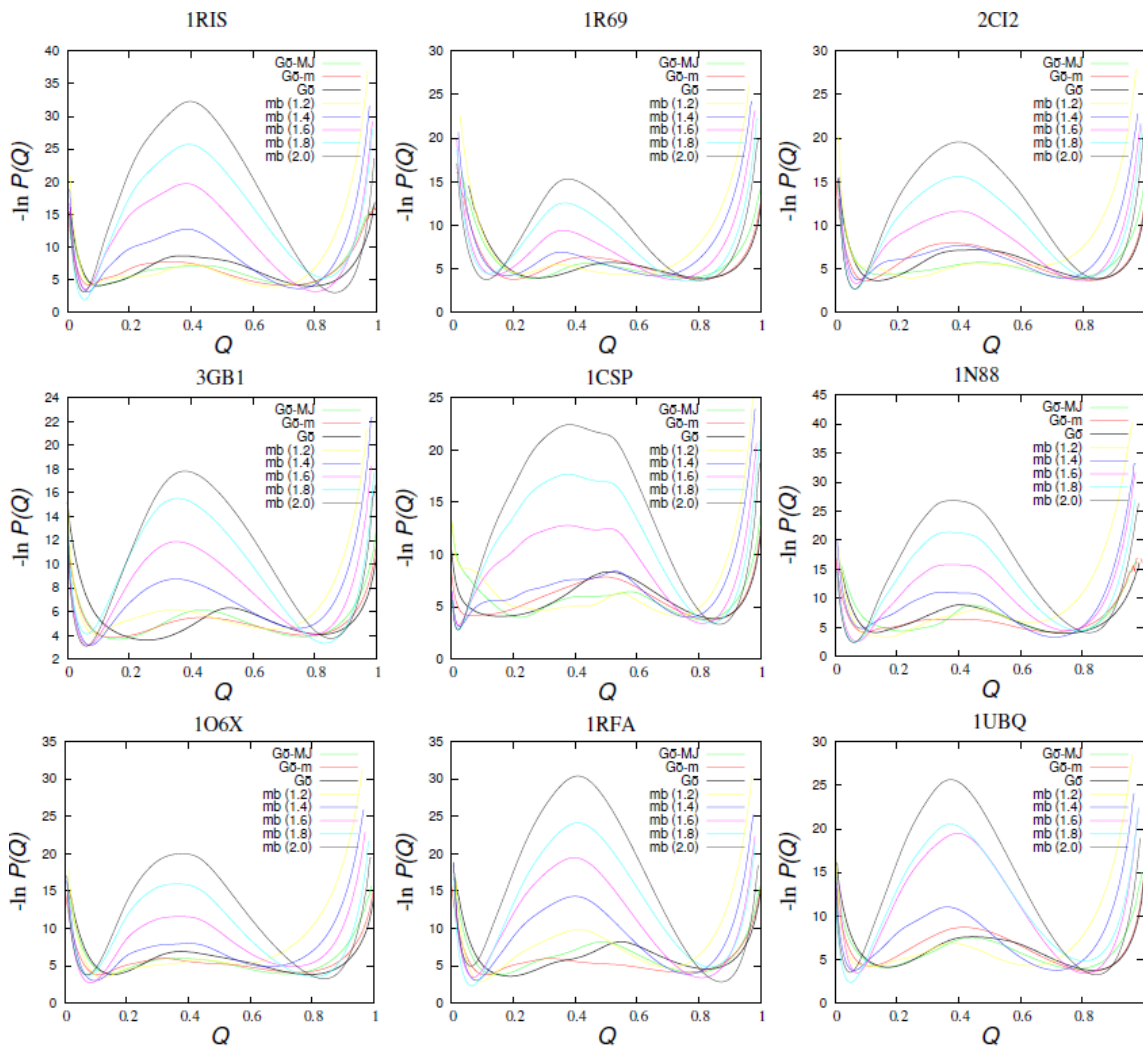


Figure S3. The residue ϕ -values for proteins 2CI2, 1CSP, 1UBQ and 1RIS predicted by G \ddot{o} , G \ddot{o} -MJ, mb-MJ (ϵ_{mb} 1.6) models and those from experiments¹⁻⁴.

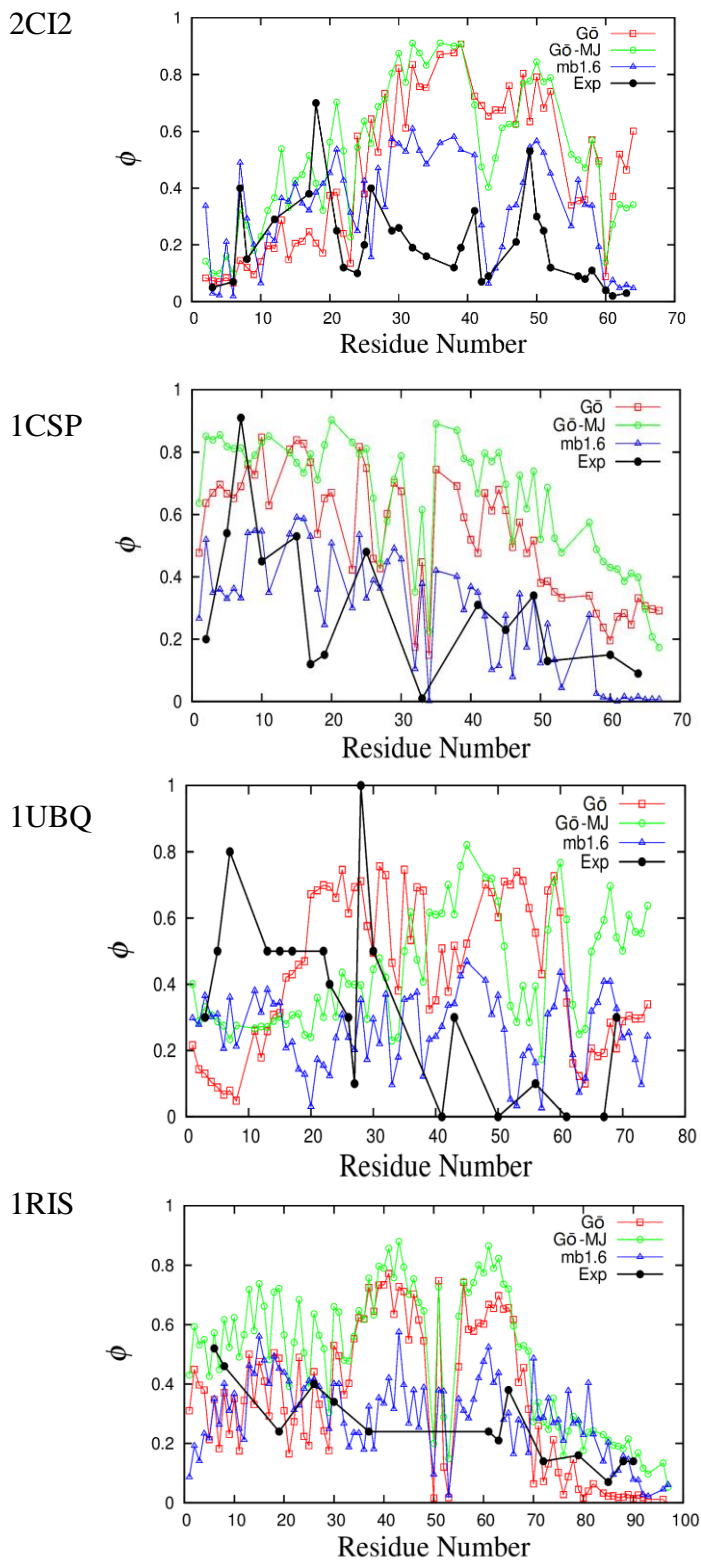


Table S1. Proteins studied in this work.

Protein PDB ID	Residue Number	Structure class
2CI2	20-83	α/β
1SHF	84-142	β
1R69	1-63	α
1RIS	1-97	α/β
1UBQ	1-76	α/β
1N88	1-96	α/β
1CSP	1-67	β
3GB1	1-56	α/β
1O6X	1-81	α/β
1RFA	55-132	α/β
1APS	1-98	α/β
1FKB	1-107	α/β
1DIVC	58-149	α/β
1DIVN	1-57	α/β
1SHG	6-62	β
1COA	20-83	α/β
1FMK	82-140	β
1HZ6	2-64	α/β
2ABD	1-86	α
1PGB	1-56	α/β
1SSO	1-62	β
1IMQ	1-86	α
1YYJ	1-106	α
1ST7	1-86	α
1E0L	1-37	β
1W4E	126-170	α
1SS1	1-60	α
1W4J	125-175	α

Table S2. Topology dependence of average ϕ -value (fitting slope of Brønsted plot) by all the models used in this study.

Model Topology	Gō	Gō-m	Gō-MJ	mb-MJ (ϵ_{mb})				
				1.2	1.4	1.6	1.8	2.0
α	0.42	0.44	0.40	0.41	0.37	0.35	0.30	0.25
β	0.54	0.58	0.58	0.41	0.53	0.35	0.31	0.26
α/β	0.50	0.57	0.57	0.59	0.46	0.38	0.30	0.27

References

1. L.S. Itzhaki, D.E. Otzen and A.R. Fersht. *J. Mol. Biol.*, 1995, **254**, 260-288.
2. M.M. Garcia-Mira, D. Boehringer and F.X. Schmid. *J. Mol. Biol.*, 2004, **339**, 555-569.
3. H.M. Went and S.E. Jackson. *Protein. Eng. Des. Sel.*, 2005, **18**, 229-237.
4. M.O. Lindberg, E. Haglund, I.A. Hubner, E.I. Shakhnovich and M. Oliveberg. *Proc. Natl. Acad. Sci. USA.*, 2006, **103**, 4083-4088.