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Supporting information for article:

Hydrogen bonds are a primary driving force for *de novo* protein folding

Schuyler Lee, Chao Wang, Haolin Liu, Jian Xiong, Renee Jiji, Xia Hong, Xiaoxue Yan, Zhangguo Chen, Michal Hammel, Yang Wang, Shaodong Dai, Jing Wang, Chengyu Jiang and Gongyi Zhang

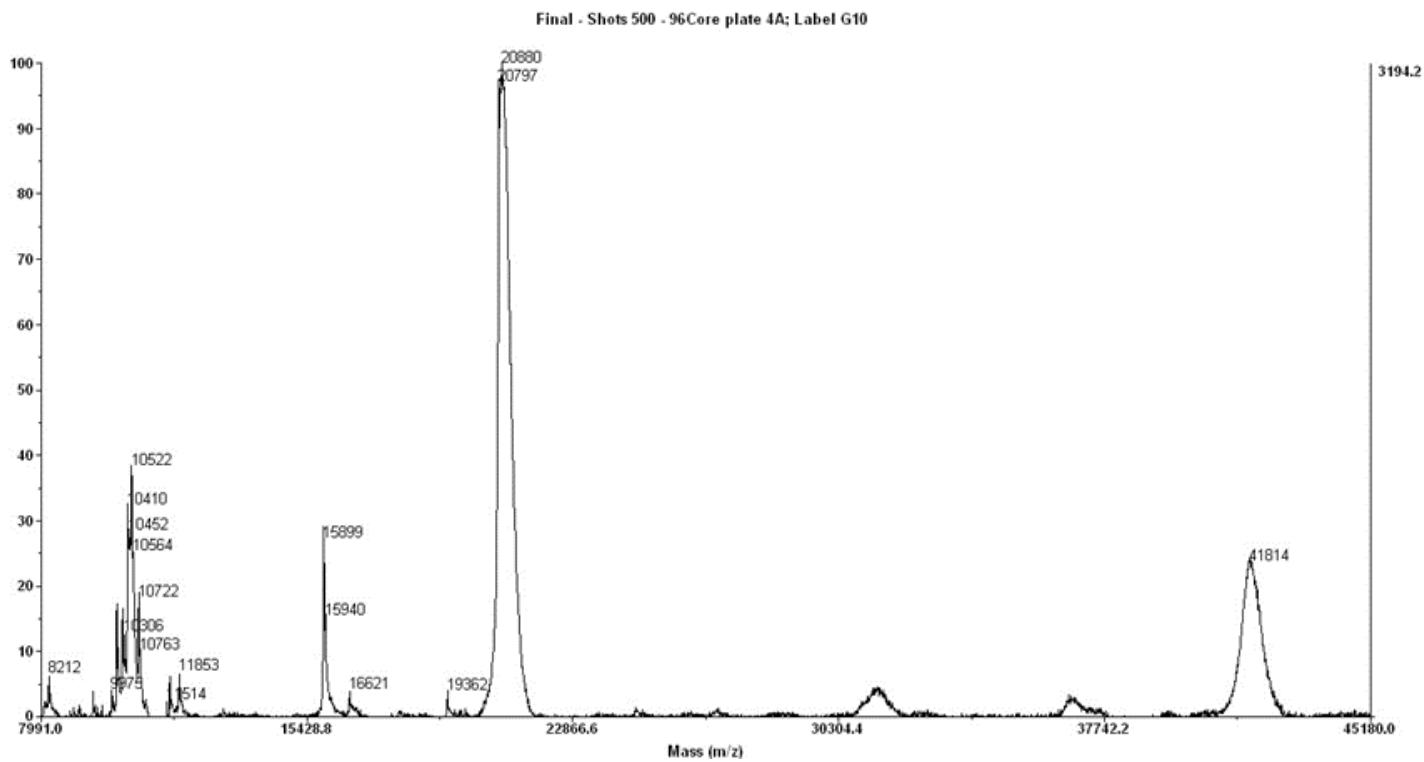


Figure S1 Mass spectra of AID¹⁵³ used for crystallization and structural determination. Major peak observed at 20880 Da. His⁶-AID containing residues 1-153 is expected to be a molecular weight of 20884 Da.

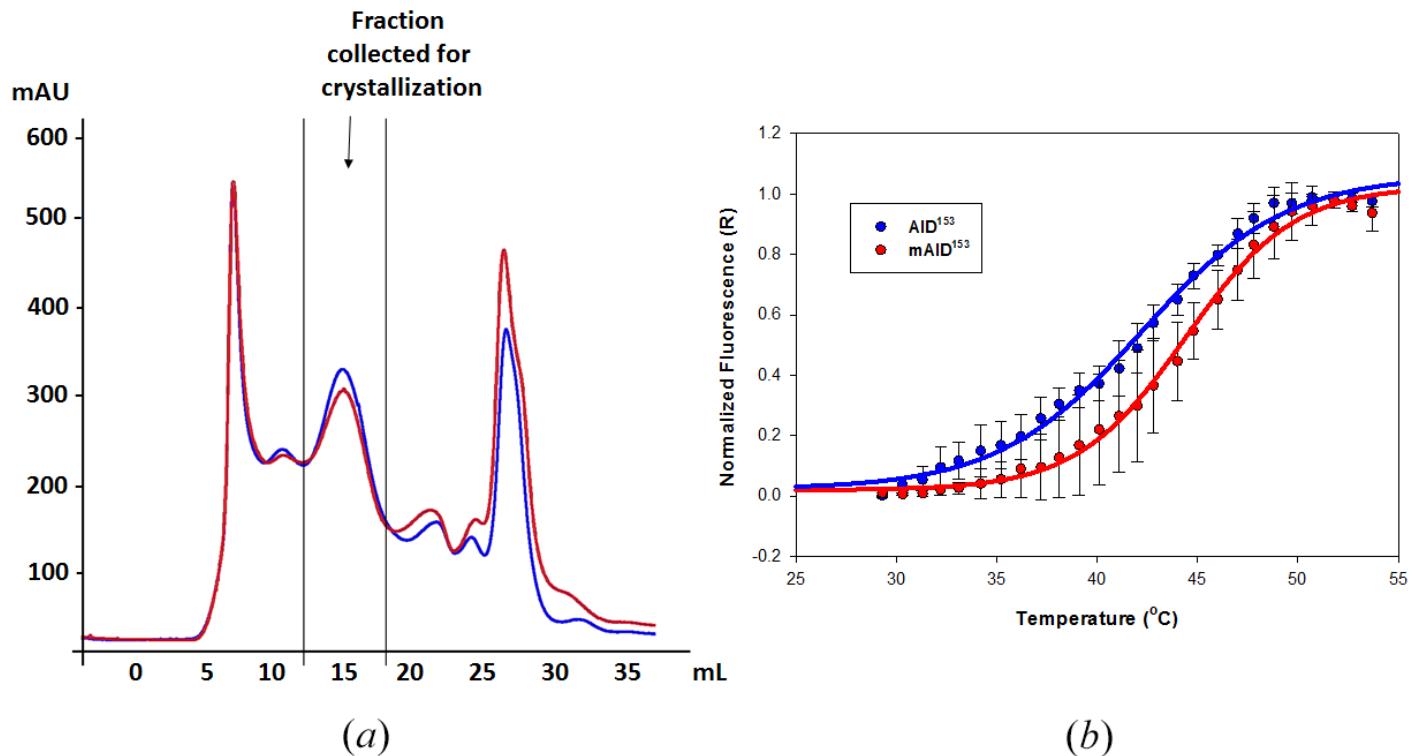


Figure S2 (a) Size exclusion chromatography assay of AID¹⁵³ (blue) and mAID¹⁵³ (red). (b) Thermal denaturation assay of AID¹⁵³ and mAID¹⁵³. AID¹⁵³ exhibited a T_m of 315.34 ± 0.28 K and mAID¹⁵³ exhibited a T_m of 317.53 ± 0.38 K.

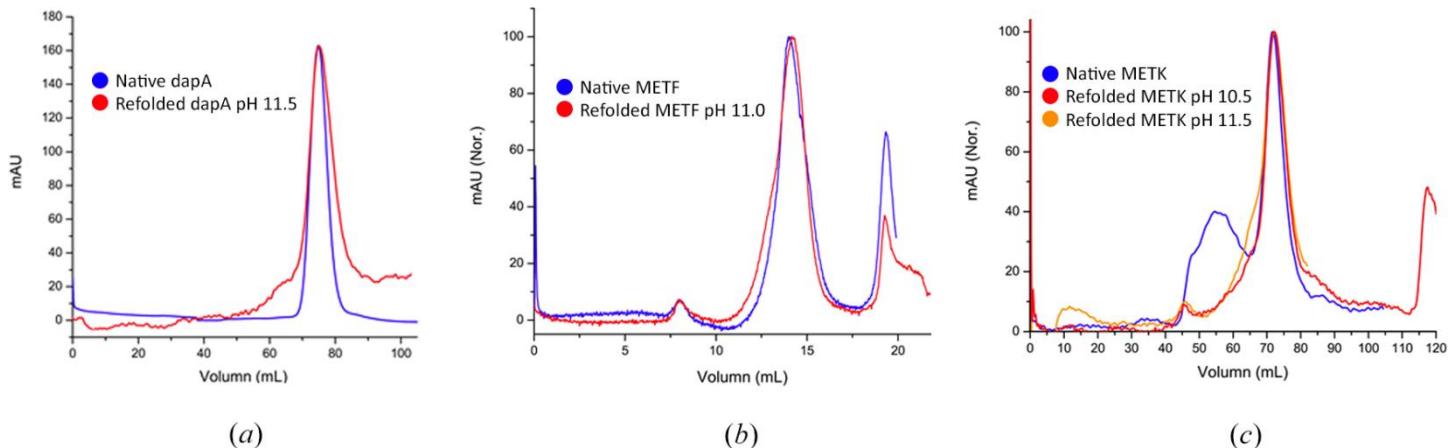


Figure S3 (a) Size exclusion chromatography assay of native dapA (blue) and dapA refolded at pH 11.5 (red). (b) Size exclusion chromatography assay of native METF (blue) and METF refolded at pH 11.0 (red). (c) Size exclusion chromatography assay of native METK (blue) and METK refolded at pH 10.5 (red) and METK refolded at pH 11.5 (orange).

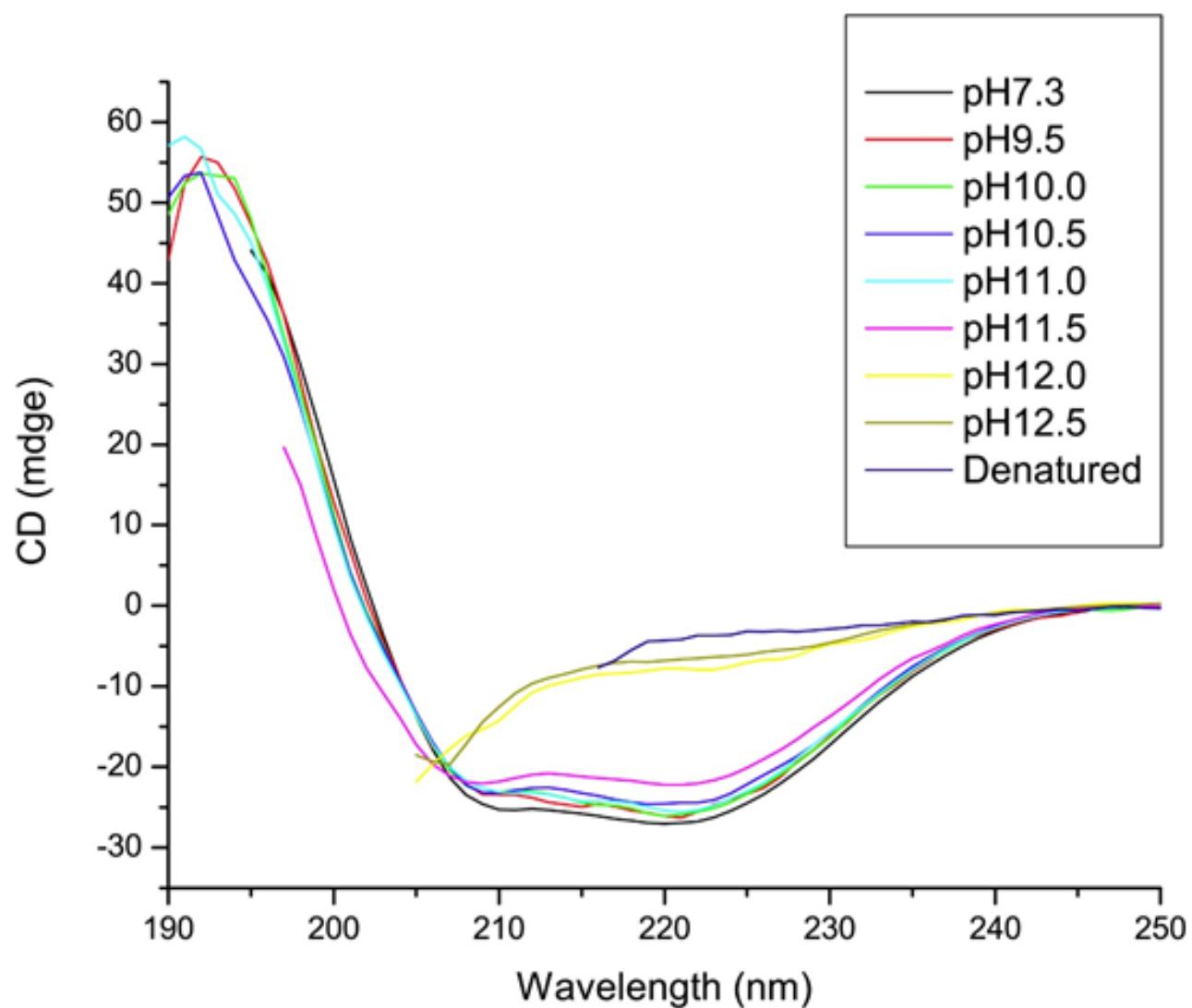


Figure S4 Native dapA unfolded at pH 12 or greater.

Table S1 Buffer recipes for the various pH conditions used for the protein refolding experiments.

| pH | Buffer conditions for protein folding |
|------|--|
| 8.5 | 20mM Tris-HCl, 50mM NaCl |
| 9.5 | 25mM Na ₂ B ₄ O ₇ , 50mM NaCl |
| 10.5 | 25mM NaHCO ₃ , 50mM NaCl |
| 11.5 | 20mM KCl, 0.00316M NaOH |
| 12.0 | 20mM KCl, 0.01M NaOH |
| 12.5 | 20mM KCl, 0.0316M NaOH |
| 13.0 | 20mM KCl, 0.1M NaOH |