Thermodynamic Origin of α-Helix Stabilization by Side-Chain Cross-Links in a Small Protein

Conor M. Haney, Halina M. Werner, James J. McKay and W. Seth Horne*
Department of Chemistry, University of Pittsburgh, Pittsburgh, PA 15260

Supporting Information

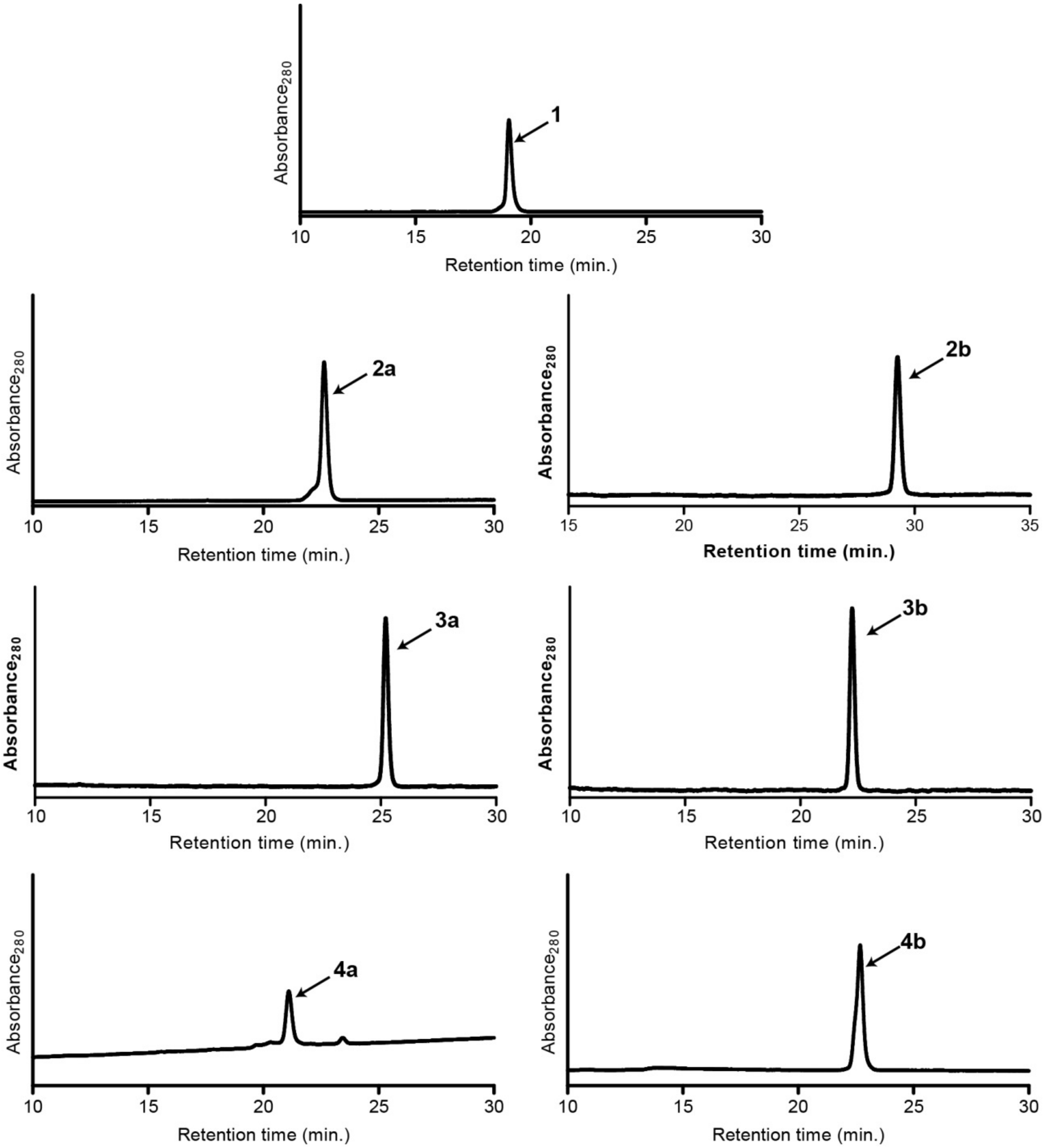

Fig. S1. Analytical HPLC chromatograms of purified peptides **1**, **2a-4a** and **2b-4b.**

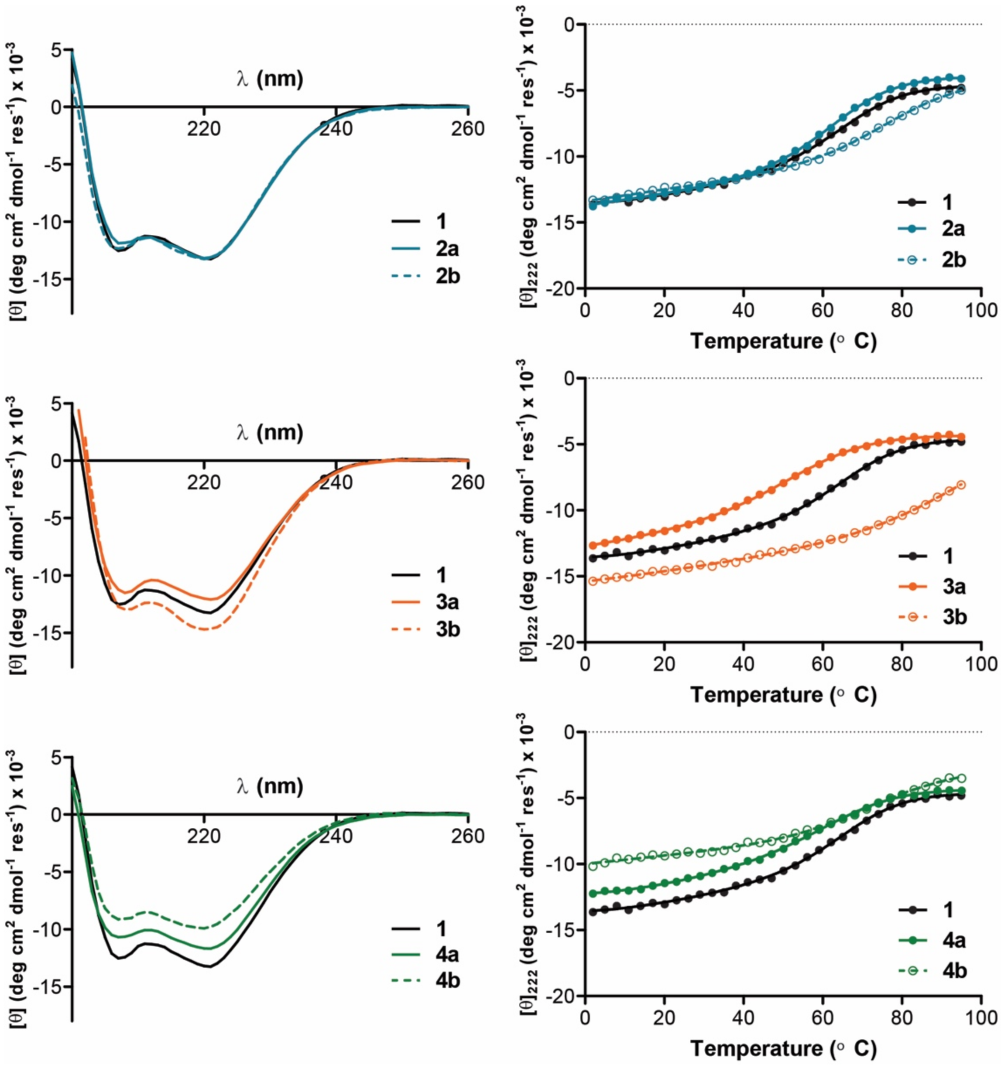

Fig. S2. Circular dichorism (CD) data for peptides **1**, **2a-4a** and **2b-4b** at 50 μM concentration. Left: CD scans acquired at 20 °C. Right: CD thermal melts obtained by monitoring molar elipticity at 222 nm as a function of temperature; circles represent measured elipticity values, while dashed or solid lines represent the nonlinear fit to a two-state thermal denaturation model.

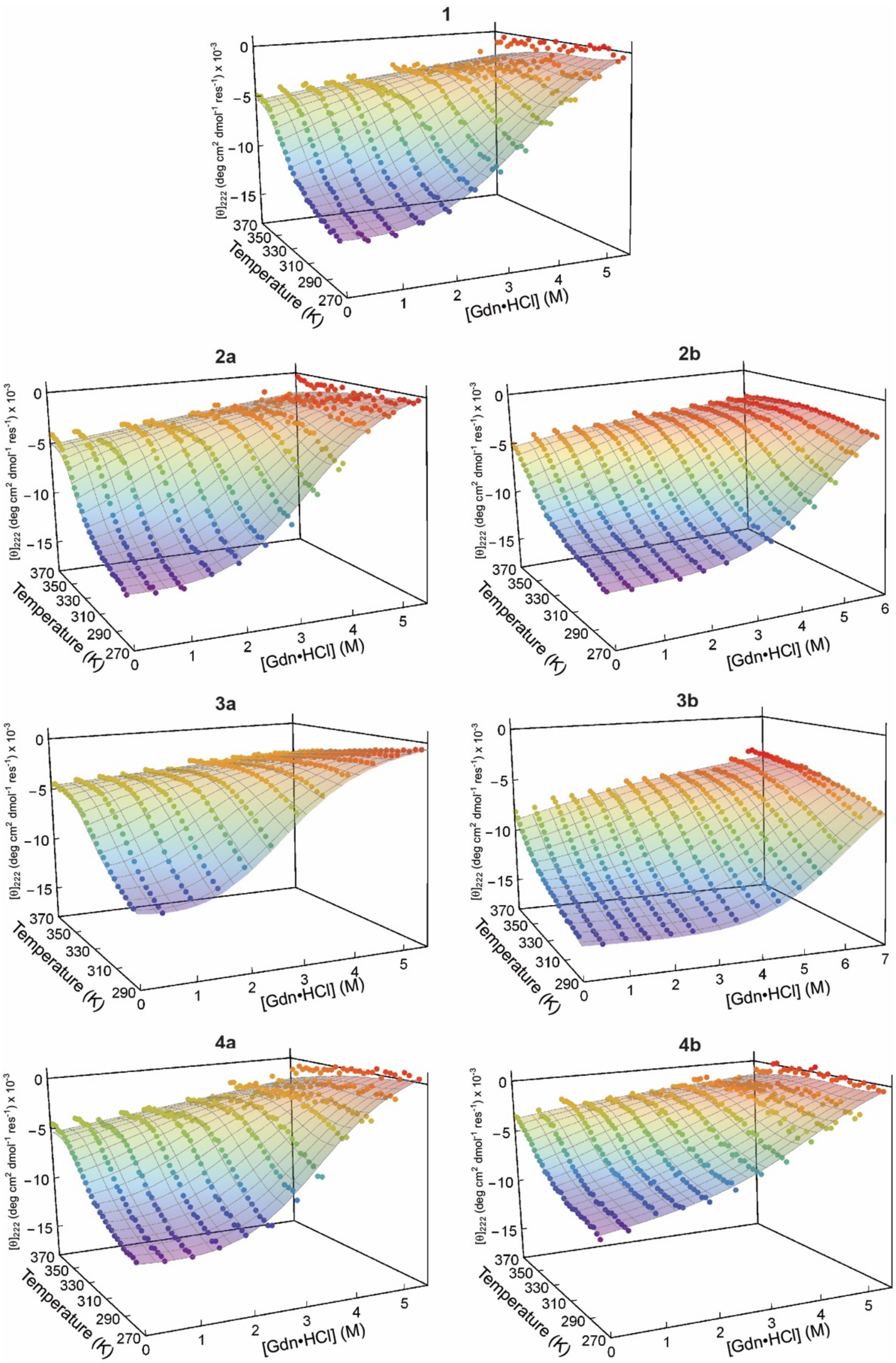

Fig. S3. Thermal-chemical denaturation plots for peptides **1**, **2a-4a** and **2b-4b**. Raw data (points) are fit (surface) to extract thermodynamic parameters for the folding equilibrium.

Table S1. MALDI-TOF data for peptides **1**, **2a-4a** and **2b-4b**.

	$[M+H]^+$ (*m/z*)	
Peptide	**Calculated**	**Observed**
1	4151.3	4151.1
2a	4138.2	4138.0
2b	4120.2	4120.3
3a	4146.8	4146.0
3b	4146.8	4146.5
4a	4212.3	4212.3
4b	4163.2	4163.0