Supplemental Data
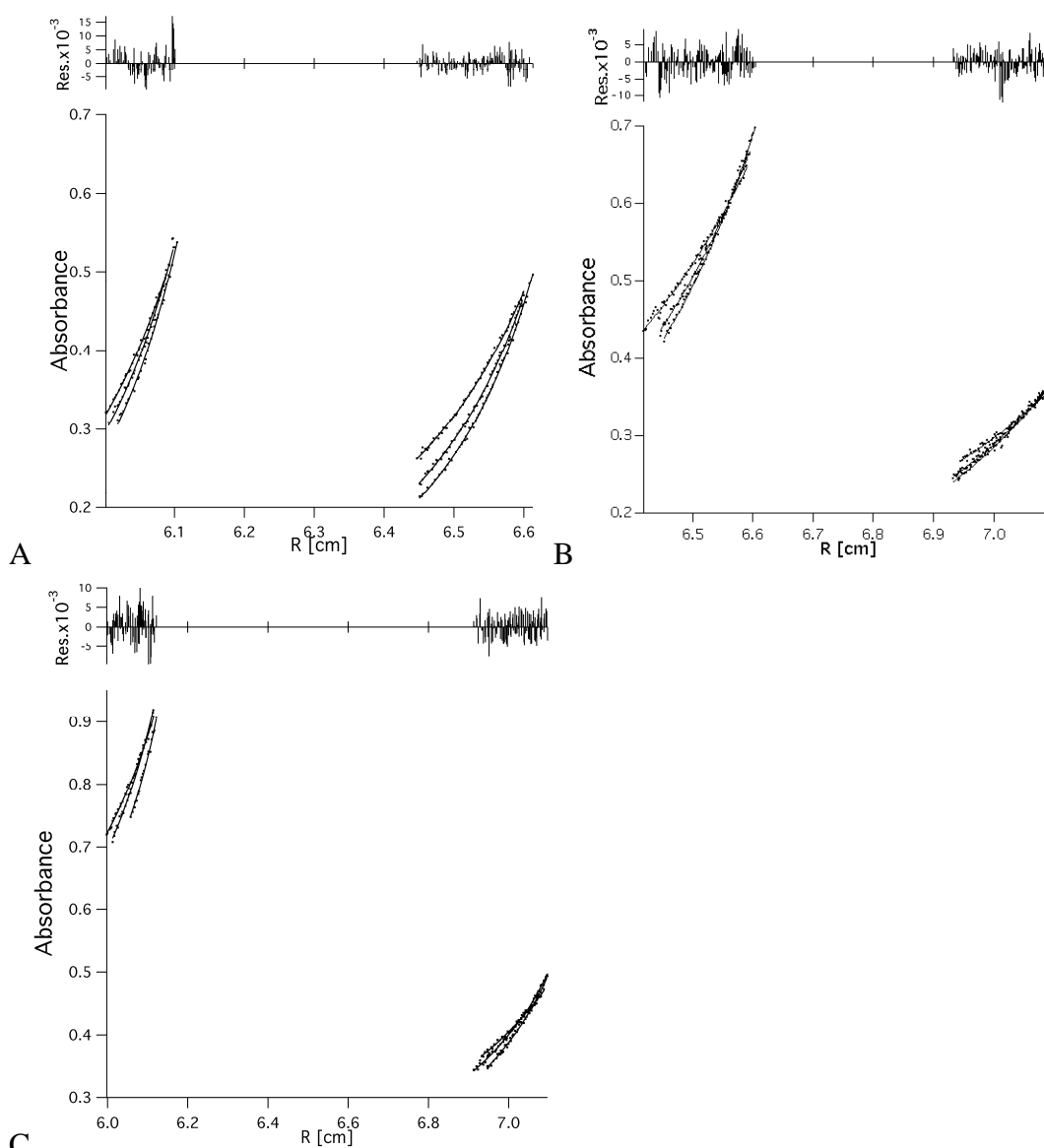
The Interplay of Functional Tuning, Drug Resistance,

and Thermodynamic Stability in the Evolution

of the M2 Proton Channel from the Influenza A Virus

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Figure S1. Sedimentation Equilibrium Analytical Ultracentrifugation of (A) $M2TM_{22-46}$ S31N, (B) $M2TM_{22-46}$ H37A, and $M2TM_{22-46}$ WT in DPC Detergent Micelles Radial absorbance profiles (data points) for two samples of different concentration (40-60 uM) were collected at equilibrium at 40, 45, and 48 Krpm. The data for each peptide is globally fit to a theoretical curve set describing a monomer/tetramer equilibria. The residual values for the curve set are located above each plot. The degree of curvature for samples of similar absorbance is proportional to tetramer population (i.e. $M2TM_{22-46}$ S31N > $M2TM_{22-46}$ WT > $M2TM_{22-46}$ H37A).