Novel Interactions of the TRTK12 Peptide with S100 Protein Family Members: Specificity and Thermodynamic Characterization.

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Supplementary Information

Figure S1: Representative EDTA-induced peptide dissociation kinetic traces. S100B-WT peptide dissociation at 35 ^{o}C in no salt (circles) 86±8 s^{-1} and with 150 mM NaCl added to buffer (triangles) 73±5 s^{-1}. Solid and dashed lines are single exponential fits to the data as described by Eq. 9. The K_d value measure in no salt, 1.7 ± 0.1 µM, was within error of that measured in 150 mM NaCl, 2.0 ± 1.0 µM.

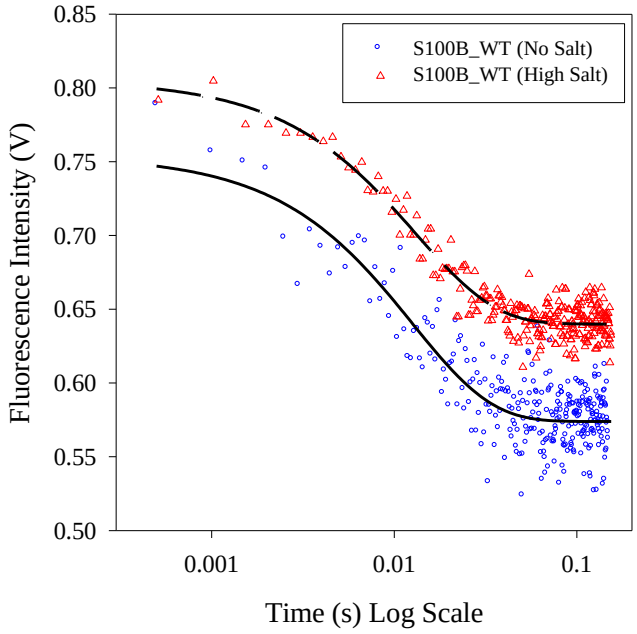

Figure S2: Example data of a fluorescence anisotropy experiment. Raw anisotropy values (●) as a function of the molar ratio of protein to peptide and the fit to the experimental data using Eq. 3 (—) for binding of TRTK12 to S100B at 25 °C.

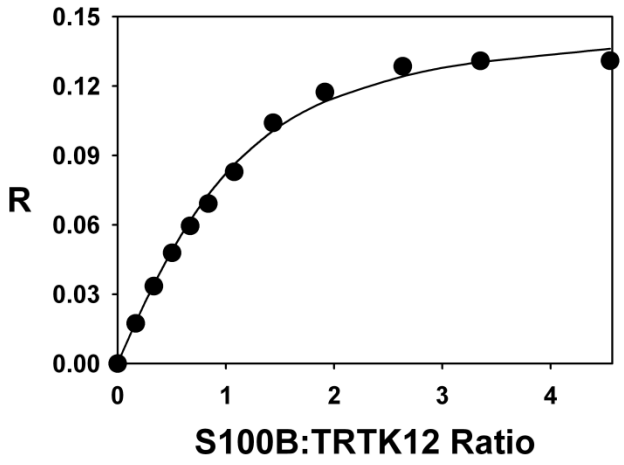

Figure S3: Dynamic quenching of tryptophan (W7) fluorescence using acrylamide for free TRTK12 (black circles), the S100B-TRTK12 complex (gray, upside-down triangles), the S100A2-TRTK12 complex (gray squares), and the S100P-TRTK12 complex (gray diamonds) in the presence of 5 mM calcium chloride.