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Supplemental Information

Conformational Dynamics and Cooperativity Drive the Specificity of a

Protein-Ligand Interaction

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SUPPORTING MATERIAL

Conformational Dynamics and Cooperativity Drive the Specificity of a Protein-ligand Interaction

Xu Liu^{1, a}, Lisa C. Golden^{1, b}, Josue A. Lopez^{1, c}, Tyson R. Shepherd^{1, d}, Liping Yu^{1, 2} and Ernesto J. Fuentes^{1, 3 *}

¹Department of Biochemistry, University of Iowa, Iowa City, IA 52242, USA.

²Carver College of Medicine Medical Nuclear Magnetic Resonance Facility, University of Iowa, Iowa City, IA 52242, USA.

³Holden Comprehensive Cancer Center, University of Iowa, Iowa City, IA 52242, USA.

^aPresent Address: Department of Biochemistry, Emory University, Atlanta, GA 30322, USA

^bPresent Address: Department of Neurology, University of California Los Angeles, Los Angeles, CA 90024, USA

^cPresent Address: Department of Molecular Physiology and Biophysics, University of Iowa, Iowa City, IA 52242, USA.

^dPresent address: Department of Biological Engineering, Massachusetts Institute of Technology, Cambridge, MA 02139, USA

*Correspondence:

E.J.F., University of Iowa, Department of Biochemistry, Roy J. and Lucille A. Carver College of Medicine, 4-632 Bowen Science Building, Iowa City, IA 52242. Email: ernesto-fuentes@uiowa.edu Fax: 319-335-9570

INVENTORY OF SUPPLEMENTAL INFORMATION:

Figure S1. Methyl-bearing ¹³C-HSQC spectra of Tiam2 WT and QM PDZ domains.

Figure S2. SDC1 and Caspr4 binding to Tiam2 WT and QM PDZ domains monitored by solution NMR.

Figure S3. Relaxation dispersion curves for the Tiam2 WT PDZ domain.

Figure S4. Relaxation dispersion curves for the Tiam2 QM PDZ domain.

Figure S5. Guanidine hydrochloride denaturation unfolding curves for Tiam2 WT and QM PDZ domains.

Supporting Figures



Figure S1. Methyl-bearing ¹³**C-HSQC spectra of Tiam2 WT and QM PDZ domains.** Overlay of ¹H-¹³C HSQC spectrum of Tiam2 PDZ WT (red) Tiam2 PDZ QM (black).



Figure S2. SDC1 and Caspr4 binding to Tiam2 WT and QM PDZ domains monitored by solution NMR. (A) Overlay of ¹H-¹⁵N HSQC spectrum of Tiam2 PDZ WT in apo (red) and SDC1-bound (blue) state. (B) Overlay of ¹H-¹⁵N HSQC spectrum of Tiam2 PDZ QM in apo (black) and Caspr4-bound (green) state.



Figure S3. Relaxation dispersion curves for the Tiam2 WT PDZ domain. Data for the 8 residues having R_{ex} were collected at 500 and 800 MHz and plotted in red and blue, respectively. The curves are plotted using parameters from global fitting.



Figure S4. Relaxation dispersion curves for the Tiam2 QM PDZ domain. Data for the 34 residues having R_{ex} were collected at 500 and 800 MHz and plotted in red and blue, respectively. The curves are plotted using parameters from local fitting.



Figure S5. Guanidine hydrochloride denaturation unfolding curves for Tiam2 WT and QM PDZ domains. The CD signal at 220 nm of Tiam2 PDZ WT (\blacktriangle) and QM (\bullet) was monitored as a function of guanidine hydrochloride concentration and fit to a two-state unfolding model, respectively. The experiments were carried out in triplicate.