ARTICLE TYPE

Supplementary Information Thermodynamic and Kinetic Characterization of Transmembrane Helix Association[†]

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1 Supplementary Tables

System	Simulations No.	Lipids No.	Water No.	Box Size (nm)	Simulation Length (µs)
Long Unbiased	1	256	4000	12X6	320
Biased	36 windows	256	4000	12X6	6
Multiple Short Unbiased	100	94	863	5X5	1

Supplementary Table 1 Overview of the coarse-grain simulations simulations performed

[†] Electronic Supplementary Information (ESI) available. For review purposes, see attached file. For the final version see DOI: 10.1039/b000000x/

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Supplementary Figures 2

Supplementary Fig. 1 A contact map of the helix-helix interface for (a) 1-5 μ s (b) 300-320 μ s of the long unbiased simulation. A value of 1.0 correspond to a well preserved contact where as 0.0 correspond to no contacts. A cut-off of 0.8nm was used to calculate the contacts.



(a) 1-5 μs



Supplementary Fig. 2 The population distribution of the inter-helical angles sampled during (a)1-5 μ s (b) 300-320 μ s of the long unbiased simulations.



Supplementary Fig. 3 The potential of mean force (PMF) of polyalanine transmembrane helices along the inter-helical distance calculated from long ms-timescale unbiased simulations. The profiles where calculated for 0-10 μ s (red), 0-50 μ s green, 0-100 μ s (blue) and 0-320 μ s (magenta) time intervals.



Supplementary Fig. 4 The PMF of polyalanine transmembrane helices along the inter-helical distance calculated from umbrella sampling biased simulations. The PMF were calculated at different time intervals: 0-1 μ s (red), 0-2 μ s (green), 0-3 μ s (blue), 0-4 μ s (magenta), 0-5 μ s (cyan) and 0-6 μ s (brown).



Supplementary Fig. 5 The PMF of polyalanine transmembrane helices along the inter-helical distance calculated from the ensemble of biased simulations. The profiles were calculated for the time intervals: 600-700 ns (red), 700-800 ns green, 800-900 ns (blue), 900 ns-1 μ s (magenta).



Supplementary Fig. 6 The time evolution of the percentage of the dimers formed in the meso-scale simulation at protein-lipid ratios (a)1:20, (b)1:50, and (c)1:200.