Supporting Information: Thermodynamic compensation in peptides following liquid-liquid phase separation

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Supplementary Information

The tails of the MIE 3$^{\text{rd}}$ order entropy (S^{MIE_3}) curves generated from $p\ln(p)$ calculation methods are known to exhibit $1/t$ behavior, and we took advantage of this property to estimate the asymptotes of the entropy curves we calculated. Data sets were individually fit to a hyperbolic function, $f(t) = a - b/t$, for all four sequences, similar to the approaches of previous work both in and outside of the Pettitt group.[S1–S3] The asymptotes (a) were used as a more accurate approximation of (S^{MIE_3}) at infinite time lengths. Figure S1 shows, for the conformational entropy of peptides in the aqueous state of the GGGGG system, the fitting function used and the location of its asymptote.

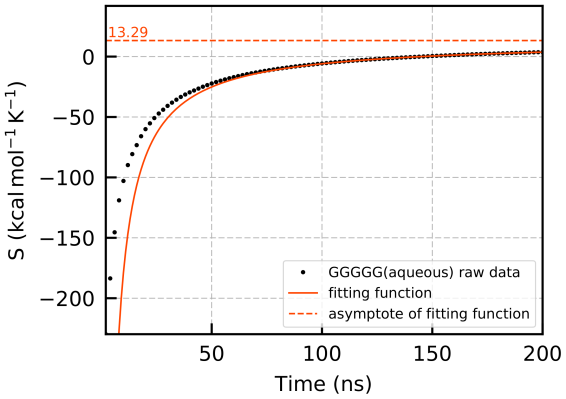

Figure S1: Black dots represent conformational entropy vs. time for aqueous state GGGGG peptides, while the orange solid line signifies the fitting function used to describe the tail behavior. Finally, the orange dotted line and number shows the location of the fit's asymptote, a in the function $f(t) = a - b/t$.

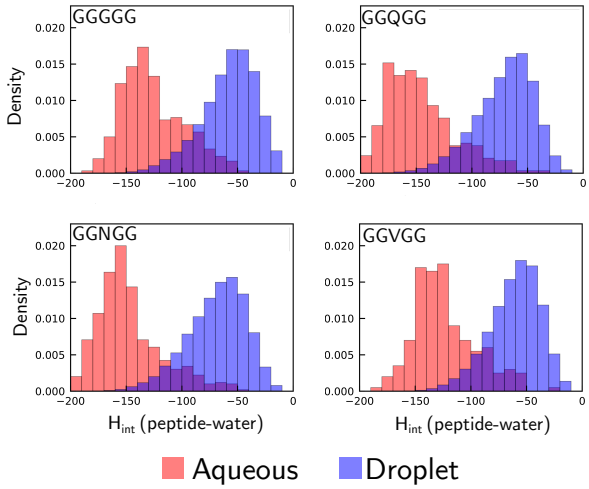

Figure S2: Histograms of the enthalpy of peptide-water interactions for each peptide in the aqueous (red) and droplet (blue) states. Overlapping bins are colored purple.

References

(S1) Killian, B. J.; Yundenfreund Kravitz, J.; Gilson, M. K. Extraction of configurational entropy from molecular simulations via an expansion approximation. *The Journal of Chemical Physics* **2007**, *127*, 024107.

(S2) Hnizdo, V.; Darian, E.; Fedorowicz, A.; Demchuk, E.; Li, S.; Singh, H. Nearest-neighbor nonparametric method for estimating the configurational entropy of complex molecules. *Journal of Computational Chemistry* **2007**, *28*, 655–668.

(S3) Drake, J.; Pettitt, B. Thermodynamics of Conformational Transitions in a Disordered Protein Backbone Model. *Biophysical Journal* **2018**, *114*, 2799–2810.