Supporting Information for:
Zinc Induced Conformational Transitions in Human Islet Amyloid Polypeptide and Their Role in the Inhibition of Amyloidosis

Author Affiliation;
*Alexandre I. Ilitchev†, Maxwell J. Giammona†, Jurgen N. Schwarze†, Steven K. Buratto†, Michael T. Bowers†**

† Department of Chemistry and Biochemistry, University of California, Santa Barbara, California 93106, USA

* E-mail: bowers@chem.ucsb.edu. Phone: 805-893-2893. Fax: 805-893-8703.

Ion Mobility Experimental Details

A constant velocity (v_d), or length (L) over drift time (t_d), can be maintained for an ion in the cell dependent upon the sample's mobility (K) and a fixed field strength (E).

$$v_d = L/t_d = K \cdot E \tag{1}$$

Where the field strength can be written as the applied voltage (V) over drift length (L);

$$E = V/L \tag{2}$$

and the mobility can be expressed in terms of the reduced mobility (K_0) which is independent of pressure (P) and temperature (T).

$$K = K_0 \left(\frac{760\ Torr}{P}\right)\left(\frac{T}{273\ K}\right) \tag{3}$$

Equations 1-3 can be combined into a linear expression relating the measured drift time to the experimentally set pressure and voltage. By tuning to different drift voltages, a set of drift times is measured and the slope of the resulting trend line is directly proportional to K_0.

$$t_d = \frac{L}{K \cdot E} = \frac{L^2(273\ K)}{K_0(760\ Torr)} \cdot \frac{P}{V} \tag{4}$$

Finally, reduced mobility is often converted to the spatially intuitive collision cross-section, which describes the 2 dimensional projection of the analyte averaged across all possible collision trajectories with the buffer gas.

$$K_0 = \left(\frac{3e}{16N_0}\right)\left(\frac{2\pi}{\mu k_B T}\right)^{\frac{1}{2}}\left(\frac{1}{\sigma}\right) \tag{5}$$

Here e is the ionic charge, N_0 is the buffer gas number density, μ is the reduced mass of the ion and buffer gas, and σ describes the collision cross section.[1]

Arrival time distribution (ATD) peaks are fit as a function of ion flux at the exit of the drift cell.[2] Assuming no additional ions are lost or generated within the cell, all ions comprising a peak can be treated as periodic delta function packets moving relative to a constant drift velocity. This resulting flux is modeled as;

$$\Phi(0, L, t) = \frac{sa}{4(\pi D_L t)^{1/2}} \left(v_d + \frac{L}{t}\right) \times \left[1 - \exp\left(-\frac{r_0^2}{4D_T t}\right)\right] \exp\left[-\frac{(L - v_d)^2}{4D_L t}\right] \quad (6)$$

Where L is the drift distance, t is drift time, s is the source packet density, a is the exit aperture area, r_0 is the radius of the initial ion packet, D_L and D_T are the longitudinal and transverse diffusion coefficients, and v_d is the measured drift velocity.

REFERENCES

(1) Gidden, J.; Ferzoco, A.; Baker, E. S.; Bowers, M. T. Duplex Formation and the Onset of Helicity in Poly D(Cg)(N) Oligonucleotides in a Solvent-Free Environment. *J. Am. Chem. Soc.* **2004,** *126* (46), 15132-15140.

(2) Mason, E. A.; McDaniel, E. W., *Transport Properties of Ions in Gases*. Wiley: New York, 1988; p xvi, 560 p.

Supporting Figure 1

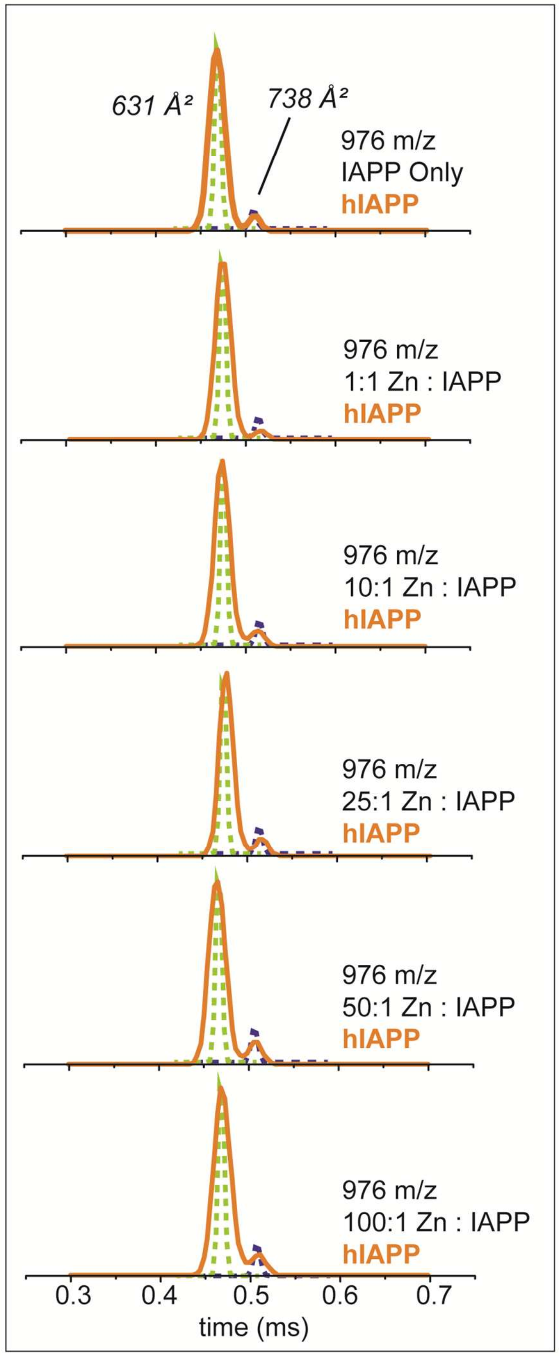

Figure S1: Arrival time distribution of +4 charged hIAPP monomer. Peaks are annotated with collision cross sections and fit using the procedure described previously. The relative ration of compact alpha-helix to extended beta-hairpin remains static regardless of zinc concentration, indicating that zinc does not modulate the structure of unbound hIAPP species.

Supporting Figure 2

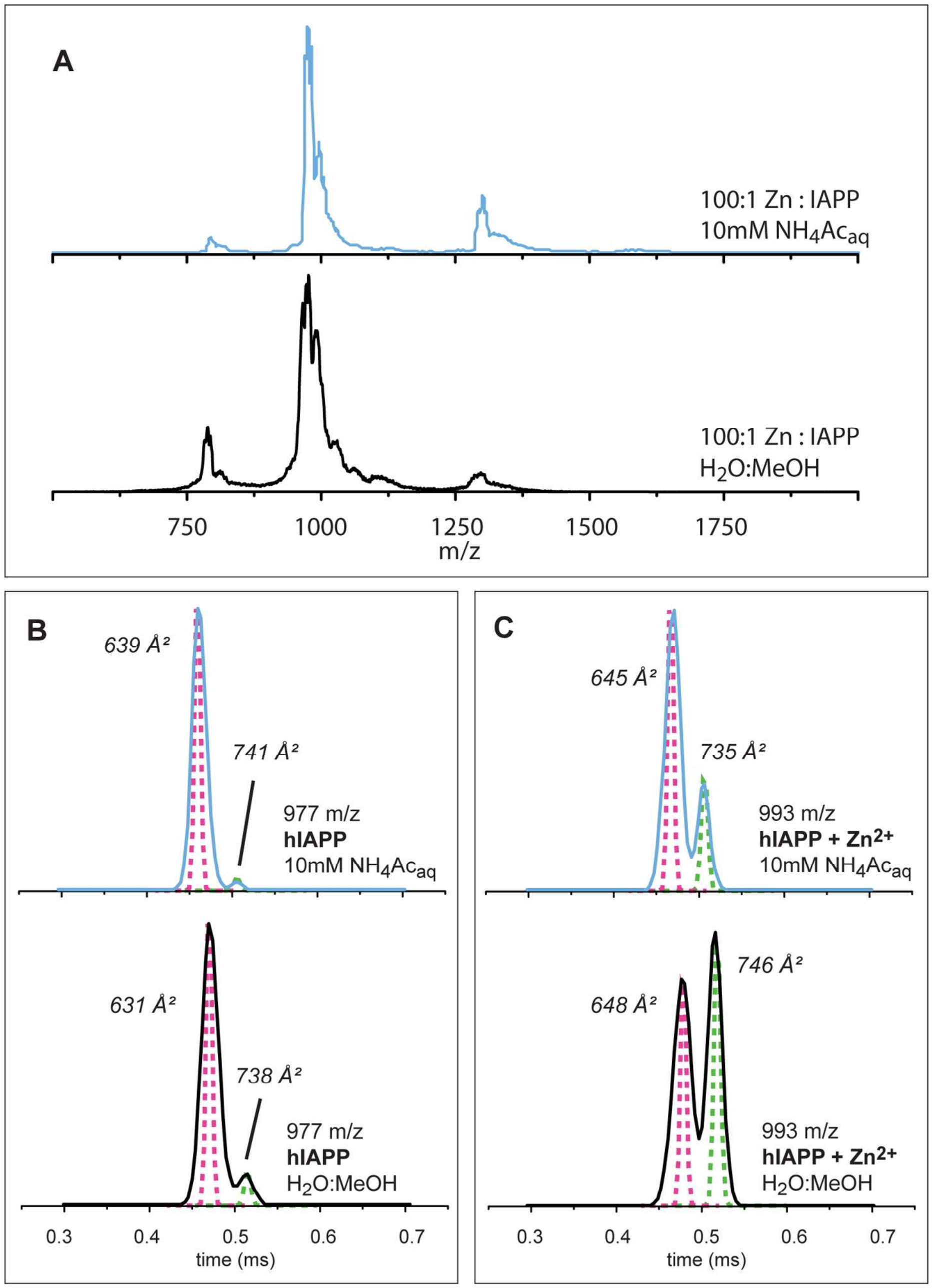

Figure S2: Comparison of mass spectra (A) and arrival time distributions (B-C) for 100:1 $ZnCl_2$:human IAPP in aqueous 10mM ammonium acetate (blue) and 1:1 water:methanol (black). Similar shifts to extended conformations are seen for zinc adducts in both solvent systems (C) but the effect is more pronounced for unbuffered water:methanol, likely due to the fact that ammonium ions compete for the zinc binding sites on IAPP. Arrival time peaks are annotated with collision cross sections and fit using the procedure described previously.