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A large scale membrane-binding protein conformational change that initiates at small length scales TREVOR GRANDPRE, MATTHEW ANDORF, DePaul University, SRINIVAS CHAKRAVARTHY, Illinois Institute of Technology, ROBERT LAMB, TAYLOR POOR, Northwestern University, ERIC LANDAHL[1], DePaul University — The fusion (F) protein of parainfluenza virus 5 (PIV5) is a membrane-bound, homotrimeric glycoprotein located on the surface of PIV5 viral envelopes. Upon being triggered by the receptor-binding protein (HN), F undergoes a greater than 100Å ATP-independent refolding event. This refolding event results in the insertion of a hydrophobic fusion peptide into the membrane of the target cell, followed by the desolvation and subsequent fusion event as the two membranes are brought together. Isothermal calorimetry and hydrophobic dye incorporation experiments indicate that the soluble construct of the F protein undergoes a conformational rearrangement event at around 55 deg C. We present the results of an initial Time-Resolved Small-Angle X-Ray Scattering (TR-SAXS) study of this large scale, entropically driven conformational change using a temperature jump. Although we the measured radius of gyration of this protein changes on a 110 second timescale, we find that the x-ray scattering intensity at higher angles (corresponding to smaller length scales in the protein) changes nearly an order of magnitude faster. We believe this may be a signature of entropically-driven conformational change.

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