

ABSTRACT

To explore if the hydrophobic collapse model (HCM) usually tested in single domain compact proteins is extendable to multi-domain system with sequentially similar domains, we obtained small angle X-ray scattering (SAXS) data on six-domain, one-domain and three domain constructs of gelsolin as function of increasing and decreasing urea in buffer. Kratky plots, estimated Porod exponent and radius of gyration (R_G) values supported that with increase in urea, protein molecules transformed from globular to Gaussian-chain like to unfolded profiles. Upon removal of urea by dialysis, profiles reversed back except upon addition of Ca^{2+} ions or lowering of buffer pH and in some cases, increasing the temperature of unfolding/refolding experiments. Interestingly, Porod exponent mapping in presence of glycerol, arginine and sucrose indicated that latter two promote unfolding and folding to occur via similar intermediates. Together, our communication provides biophysical evidence on extension of HCM to proteins with similar multiple domains.
