Folding kinetic pathway of phosphofructokinase-2 from Escherichia coli: A homodimeric enzyme with a complex domain organization

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Phosphofructokinase-2 is a 66 kD homodimer whose subunits are associated by means of a bimolecular domain, the ?-clasp, which is linked to the larger portion of each subunit by a reentrant chain topology. To investigate how this structural organization determines the folding pathway of Pfk-2, unfolding and folding kinetic experiments were performed. The folding pathway shows an unstructured monomeric intermediate and that most part of the dimer structure is reached as a slow concerted folding/association step with a quite folded transition state in terms of solvent exposure. Unfolding kinetics show a transient intermediate, probably a partially unfolded dimer. We propose that these characteristics arise by a mutual constrain between the large domain and the ?-clasp domain imposed by their interrupted chain connectivity. Structured summary of protein interactions: Pfk-2 binds to Pfk-2 by fluorescence technology (View interaction) Pfk-2 binds to Pfk-2 by circular dichroism (View interact