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Thermal stability and folding kinetics analysis of intrinsically disordered protein, securin[1] CHIA-CHING CHANG[2], HSUEH-LIANG CHU, LI-PING HO, Department of Biological Science and Technology, National Chiao Tung University — Lacking a stable tertiary structure, intrinsically disordered proteins (IDPs) possess particular functions in cell regulation, signaling, and controlling pathways. The study of their unique structure features, thermal stabilities, and folding kinetics is intriguing. In this study, an identified IDP, securin, was used as a model protein. By using a quasi-static five-step (on-path) folding process, the function of securin was restored and analyzed by isothermal titration calorimetry. Fluorescence spectroscopy and particle size analysis indicated that securin possessed a compact hydrophobic core and particle size. The glass transition of securin was characterized using differential scanning microcalorimetry. Furthermore, the folding/unfolding rates (k_{obs}) of securin were undetectable, implying that the folding/unfolding rate is very fast and that the conformation of securin is sensitive to solvent environment change. Therefore, securin may fold properly under specific physiological conditions. In summary, the thermal glass transition behavior and undetectable k_{obs} of folding/unfolding reactions may be two of the indices of IDP.

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