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ATP dependent conformational change and protein folding mechanism of group II chaperonin

グループII型シャペロニン(Hsp60)のATP依存的構造変化とタンパク質フォールディング機構

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午後3時から

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Protein folding is assisted by molecular chaperones *in vivo*. Molecular chaperone system of hyperthermophilic archaea is composed of only four groups of chaperones, **group II chaperonin (CPN)**, prefoldin (PFD), sHsp and PPIase. ATP drives the conformational change of the group II chaperonin from the open-lid substrate binding conformation to the closed-lid conformation to encapsulate an unfolded protein in the central cavity for its correct folding. To elucidate detailed conformational change and protein folding mechanism, we have performed kinetic studies of conformational change using CPN from *Thermococcus* strain KS-1 by stopped-flow fluorometry, stopped-flow small angle X-ray scattering (SAXS) and Diffracted X-ray Tracking (DXT). Our study has given clear insights for the conformational change and also protein folding mechanism of CPN.