

Abstract Submitted
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Substrate protein recognition mechanism of archaeal and eukaryotic chaperonins POOJA SHRESTHA, GEORGE STAN, University of Cincinnati — Chaperonins are double ring-shaped biological nanomachines that assist protein folding under non-permissive conditions. Spectacular conformational changes take place within each chaperonin ring using energy derived from ATP hydrolysis. These changes result in transitions from opened to closed chaperonin ring via partially closed state. Substrate proteins bind to the open chaperonin ring and are encapsulated within the closed cavity. We focus on the substrate protein recognition mechanism of group II chaperonins. We predict substrate protein binding sites using structural and bioinformatic analyses of functional states. Based on large changes in solvent accessible surface area and contact maps we glean the functional role of chaperonin amino acids. During the transition between open to closed chaperonin ring, the largest change in accessible surface area is found in two helices located at the cavity opening. Based on these calculations and the bioinformatic prediction of protein interaction regions we suggest that these two helices constitute the substrate protein binding site.

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