

Abstract Submitted
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Substrate protein recognition mechanism of archaeal and eukaryotic chaperonins.¹ POOJA SHRESTHA, MANORI JAYASINGHE, GEORGE STAN — Chaperonins are double ring-shaped biological nanomachines that assist protein folding. Spectacular conformational changes take place within each chaperonin ring using energy derived from ATP hydrolysis. These changes result in transitions from the open to the closed ring. Substrate proteins bind to the open ring and are encapsulated within the closed ring cavity. We focus on the substrate protein recognition mechanism of archaeal and eukaryotic chaperonins. We predict substrate protein binding sites using structural and bioinformatic analyses of functional states during the chaperonin cycle. 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 of amino acids is found in helical protrusion and two helices located at the cavity opening. Our calculations suggest that the helical protrusion and two helices constitute the substrate protein binding site.

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