



Structure of the mitochondrial inner membrane AAA+ protease YME1 gives insight into substrate processing

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Feeding a protease step by step

Proteins that degrade damaged or misfolded mitochondrial proteins are essential for mitochondrial function. A key player is the hexameric protease YME1, in which each subunit is anchored in the inner mitochondrial membrane by a helix and has an adenosine triphosphatase (ATPase) domain and a protease domain in the intermembrane space. Puchades *et al.* report a high-resolution structure that shows that the ATPase domains form an asymmetric spiral staircase that stacks above a planar protease ring. Conserved tyrosine residues in the central pore of the spiral staircase interact with a substrate peptide. The ATP hydrolysis cycle is sequential and coordinated with changes in the position of the tyrosine residues that result in stepwise translocation of the substrate into the protease chamber.

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