

Crystal structure of the protease domain of an ATP-independent heat shock protease HtrA

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HtrA (high temperature requirement A), a periplasmic heat shock protein, is known to have molecular chaperone function at low temperatures and proteolytic activity at elevated temperatures. To investigate the mechanism of functional switch to protease, we have determined the crystal structure of the N-terminal protease domain (PD) of HtrA from *Thermotoga maritima*. HtrA PD shares the same fold with chymotrypsin-like serine proteases. However, crystal structure suggests that HtrA PD is not an active protease at current state since its active site is not formed properly and blocked by an additional helical lid. On the surface of the lid, HtrA PD has hydrophobic patches that could be potential substrate binding sites for molecular chaperone activity. Present structure suggests that the activation of the proteolytic function of HtrA PD at elevated temperatures might occur by the conformational change .