

Crystal structure of CodW in *Bacillus Subtilis* - the first N-terminal serine protease

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CodWX, encoded by the *cod* operon in *Bacillus subtilis*, is a member of the ATP-dependent protease complex family, and is homologous to the eukaryotic 26S proteasome. It consists of two multimeric complexes: two hexameric ATPase caps of CodX and a protease chamber consisting of CodW dodecamer. Prior structural studies have shown that the N-terminal threonine residue is solely functional as a proteolytic nucleophile in ATP-dependent proteases such as HslV and certain β -type subunits of 20S proteasome, which have a primary sequence similarity of -50% and -20% with CodW respectively. Here we present a 3.0 Å resolution crystal structure of CodW, which is the first N-terminal serine protease among the known proteolytic enzymes. In spite of the same fold and the conserved contacts between subunits with HslV in *E. coli* and *H. influenza*, this structure shows the five additional residues extending from conserved Thr1 among the other ATP-dependent protease and extraordinary basic proteolytic chamber.