

(PL-3)

**Crystal Structure of Zinc-binding Domain
of ClpX in Complex with SspB-tail**

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The degradation of *ssrA*(AANDENYALAA)-tagged proteins in the bacterial cytosol is carried out by the proteolytic machine ClpXP (a complex between AAA-ATPase, ClpX and serine protease, ClpP) and is markedly stimulated by an adaptor protein SspB (Stringent starvation protein B). It has been reported previously that the amino-terminal zinc-binding domain of ClpX (ZBD) is involved in the complex formation with SspB-tail. In order to understand recognition of the SspB by ClpX and the mechanism of delivery *ssrA*-tagged substrates to ClpXP, we have determined the crystal structures of ZBD alone at 1.5, 2.0, and 2.5 Å resolution in each different crystalline lattice and also in complex with SspB-tail peptide at 1.6 Å resolution. The structure shows similar fold with treble clef zinc-finger proteins as reported by previous solution structure. SspB-tail forms anti-parallel β-sheet with two β-strands of ZBD and the structure reveals that there are two independent SspB-tail binding sites in ZBD. The high-resolution ZBD-tail peptide complex structure explains key determinants for recognition of the SspB-tail by ClpX and sheds light on delivery of target substrates to the prokaryotic degradation machine.