

## **Structure of the ATP-Dependent Protease Lon from Escherichia coli**

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Lon (or La) protease, the production of lon gene, is a soluble ATP-dependent protease that degraded specific, unstable regulatory proteins and abnormally unfolding proteins in E. coli. LonR9, an unusual lon mutation, were capable of inhibiting ATP-dependent hydrolysis by protease Lon. In order to examine the structural organization of Lon and LonR9, we have used electron microscopy and image analysis. The structure of Lon and LonR9 reveal two stacked hexameric rings enclose a central channel; thus, protease Lon and LonR9 behave as dodecamer. Base on the structure of complex Lon/LonR9, we discuss the molecular mechanism of inhibition for ATP-dependent proteolytic activity of protease Lon. To confirm complexes oligomeric organization, we examined the samples of incubated with and without various nucleotides and Mg<sup>++</sup> using electron microscopy. In this study, we also compared the structures derived from two different methods: first one is obtained by individual particles of protease complex i.e. electron tomography. Second one is averaged from two dimension crystals obtained by Negative Staining-Carbon Film (NS-CF) technique i.e. electron crystallography.

ATP-Dependent Protease Lon, Structure, Electron microscopy and Image Processing