

Abstract

The selective and timely degradation of proteins in the cell is important for overall protein homeostasis as well as an integral part of many cellular processes. One of the major proteases involved in the degradation of these polypeptide chains is the proteasome. The proteasome is formed by 66 subunits that have to assemble into a 2.5 MDa complex. It can be divided into two subcomplexes, the core particle and the regulatory particle. The core particle harbors the proteolytic active sites on the inner surface of its cylindrically shaped structure. The regulatory particle (RP) facilitates protein degradation by unfolding substrates and regulating entry into the CP.

The formation of proteasomes is assisted by nine proteasome-specific assembly chaperones. Several of these chaperones are able to regulate the interaction between CP and RP, indicating an important role in regulating this association.

The proteasome-associated protein Ecm29 can stabilize the RP-CP interaction, however, this protein is not a chaperone. I will discuss our recent structural and functional insights into several of these chaperones and our proposed role of Ecm29 as a quality control factor that specifically recognizes “faulty” proteasomes and inhibits them.