

# **Dynamic Protein Quality Control by the CHIP/Hsp70 Complex**

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Protein quality control fulfills the need for a rapid and robust response to protein misfolding that is ubiquitous in human physiology. Defects in protein quality control pathways can lead to a wide range of diseases including cystic fibrosis and recessive hereditary cerebellar ataxias. Within the field of protein quality control, the ubiquitin ligase CHIP and chaperone Hsp70 play crucial roles in directing misfolded client proteins to either the refolding, or degradative pathways. Together, CHIP and Hsp70 form a complex that exhibits functions characteristic of an information processor. Our results suggest that the complex takes inputs from the both dynamic motions and posttranslational modifications in determining the fate of the misfolded protein. Guided by our 2.91 Å resolution structure of the TPR domain of CHIP in complex with the  $\alpha$ -helical “lid” subdomain and unstructured “tail” of Hsc70, we can now assemble full-length models of the CHIP/Hsp70 complex. This structural data, combined with nuclear magnetic resonance, small angle X-ray scattering, and electron paramagnetic resonance, and biochemical data are beginning to identify the mechanisms by which posttranslational modifications and dynamics regulate the activity and structure of the CHIP/Hsp70 complex.

**Meet the Speaker, 2:15 – 3:00pm, Student Lounge, 3144  
Seminar, 3:35pm, ISAT 159**