

An MBoC Favorite: Proteasomal proteomics: identification of nucleotide-sensitive proteasome-interacting proteins by mass spectrometric analysis of affinity-purified proteasomes

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In celebration of MBoC's first 20 years, members of the Editorial Board, members of the ASCB Council, and others comment on their favorite MBoC papers from the past two decades.

The proteasome is a complex multifunctional machine that destroys proteins marked for ubiquitin-mediated proteolysis. In this paper, the authors employ an elegant approach to isolate and define yeast proteasomes and their suite of interacting proteins (Verma *et al.*, 2000). This paper has something for everyone. The method the authors developed has now become the standard in the field for rapid proteasome purification. They identified and validated a new subunit of the proteasome. And their work gave a powerful glimpse into the role of the proteasome as a node of intracellular protein interactions, with dozens of proteasome-interacting proteins (PIPs) associating with core proteasome subunits in a nucleotide-dependent manner. The technological achievement and unique biological insight provided by this study justify its place as one of MBoC's most-cited articles.

REFERENCE

Verma R, Chen S, Feldman R, Schieltz D, Yates J, Dohmen J, Deshaies RJ (2000). Proteasomal proteomics: identification of nucleotide-sensitive proteasome-interacting proteins by mass spectrometric analysis of affinity-purified proteasomes. *Mol Biol Cell* 11, 3425–3439.

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